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RESULT 11
AAY98153
ID AAY98
CC The peptide can be used in the method of the invention. The invention of the production of transgenic plants that express a protein cC able to produce hydrogen peroxide. The production method comprises cC transforming a plant cell with Agrobacterium rhizogenes containing a cC vector that carries a gene encoding the protein to be expressed in the cC transgenic plant, selection is made for the expression of the gene in a cC colorimetric test using peroxidase. Plants are transformed to produce a cC protein of interest, specifically oxalate oxidase (OO):

CC (i) to impart resistance to pathogens (OO degrades oxalic acid, a cC phytotoxin produced by many phytopathogens); or cC (ii) as a selection system for plants transformed with a second gene, cencoding another protein of interest, introduced in the same vector as cC the gene encoding the first protein of interest. Particularly the second cC protein confers resistance to pathogens (fungi, bacteria, insects, insects, and is specifically endo-chitinase. The method uses a cC simple and rapid method, based on a colorimetric test, to select for transformation, particularly using as test sample roots induced by CC Agrobacterium rhizogenes. It is not necessary that the cells being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        producing transgenic plants expressing a hydrogen peroxide-producing protein, useful for imparting pathogen resistance or as marker for
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6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grison R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     represents a protein localisation signal sequence sed in the method of the invention. The invention
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9.3e+05;
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Query Match Best Local Matches

Similarity 6; Conserv

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Score 29; DB Pred. No. 9.3 % Mismatches

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RESULT 12
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                                      The present sequence is that of an endoplasmic reticulum (ER)

CC retention peptide obtained from pCMV/myc/ER. An aspect of the

CC invention is a phage display library which expresses a heavy chain

CC capable of inhibiting the activity of a secreted protein. Sequences

CC encoding heavy chains capable of binding the desired secreted

CC protein and inhibiting its activity are inserted into a eukaryotic

CC expression vector such that thay are operably linked to sequences

CC coding for signal peptides which direct the resulting fusion

CC proteins to the ER. Preferably, the heavy chains are also linked to

CC a sequence which encodes a polypeptide directing the retention of

CC is synthesised on the ribosomes on the surface of the ER and passed

CC through a pore to the ER awaiting further modification for

CC secretion. The heavy chain binds its target in the ER, causing the

CC identify the target protein as misfolded and escort the target

CC protein/heavy chain complex out of the ER and into the cytoplasm by

CC described the retrograde pathway, and the misfolded complex is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                    Modulating inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endoplasmic reticulum retention peptide; signal heavy chain; phage display; proteosome target 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endoplasmic reticulum retention peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                             Mulligan-Kehoe
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                                                                                                                                                                                                                                                                                                                          Example
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                            degraded
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                                                                                                                                                                                                                                                                                                                         14; Page 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEKDEL
                           by proteosomes.
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                                                                                                                                                                                                                                                                                                                                                    proteolytic degradation of intracellular targets useful for the activity of intracellular components \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEPT HEALTH & HUMAN SERVICES
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Pred. No.
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target library.
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Matches 6
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   Mason HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-terminus via a protesse cleavage site. On administration of the drug, the antibody binds the drug, localising it at the target cells but maintaining it in an inactive state. As the antibody is degraded (the timescale for which is dependent upon the N-terminal or stabilon amino acids), the drug is released at its site of action where it can exert its effects. The antibody encoded by the expression construct (and therefore the therapeutic agent) can be targetted to particular subcellular locations (e.g., the nucleus) by including the appropriate cellular localisation signals. The novel method may be used to deliver therapeutic agents to patients with a variety of conditions such as the properties and contents with a variety of conditions such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding an antibody (particularly a single chain antibody) to the drug to be delivered. The antibody contains a modulator of intracellular half-life; this can either be a stabilising or destabilising residue located in the N-terminus after the initial methionine, or a peptide ("stabilon") containing a stabilising residue linked to the antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endoplasmic reticulum retention signal.
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                                                                                                                                                                                                                                     23-DEC-1999;
                                                                                                                                                                                                                                                                                                        29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant expression vector; antigen; hepatitis B surface antigen; HBsAg;
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                                                              (HEAL-) HEALTH
                                                                                                 (BOYC-) BOYCE THOMPSON INST PLANT RES
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in a patient are transformed with an expression consti
                                                              RES INST
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Arntzen CJ,
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Pred. No.
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Richter E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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RESULT 10
AAY96657
ID AAY96
CCCCCCXxxxqqqqxxxxxxqxqxxqxxqxxqxxqxxqxx
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes a plant expression vector which comprises two expression cassettes, the first comprising a polynucleotide encodir an antigen and the second comprising a non-identical polynucleotide encoding the same antigen. The antigen is especially a hepatitis B surface antigen (HBsAg). The expression vector is used to transform bacterial and plant cells to elicit the production of anti-hepatitis B antibodies and are useful as vaccines. The present sequence represents
                                                                                     Claim 9;
                                                                                                              elicit immune
                                                                                                                          New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic composition
                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                           Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral; adjuvant; anti-bacterial; microsomal retention signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                  C-terminal microsomal retention signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96657 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                               WPI; 2000-442653/38
                                                                                                                                                                                                                              (BOYC-)
                                                                                                                                                                                                                                                                   22-DEC-1998;
                                                                                                                                                                                                                                                                                                                    29-JUN-2000
                                                                                                                                                                                                                                                                                                                                             WO200037609-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY96657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an endoplasmic reticulum retention signal, course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 12; Page 79; 144pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New expression vector for transforming plants comprising two expression cassettes useful for producing plant material comprising anti-hepatitis
                                                                                                                                                                                                                                                                                          22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-452181/39.
                                                                                                                                                                                                                   (ARNT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibodies -
                                                                                                                                                                                         L HS,
                                                                                                                                                                                                                             BOYCE THOMPSON MASON H S.
                                                                                                                                                                                                                MASON H S.
ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 6; Conser
                                                                                    Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEKDEL 6
                                                                                                                                                                                         Arntzen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                    71; 103pp; English.
                                                                                                             responses
                                                                                                                                                                                                                                                                   98US-0113507
                                                                                                                                                                                                                                                                                           99WO-US30747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide; 6 AA
                                                                                                                                                                                                                                            INST PLANT
                                                                                                              in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29; DB 21;
Pred. No. 9.3e+05;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                          compositions to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding
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Novel polynucleotides encode a mutant Escherichia coli heat-labile (LT-A) polypeptide or a mutant Vibrio cholerae cholera toxin (CT) subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at 10 of the codons is altered to a plant preferred codon. The polynucle further comprises a nucleic acid sequence encoding LT B subunit ()

Escherichia coli heat-labile

(CT) A

toxin

least

one

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RESULT 7
AAB15683
ID AAB1
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 Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a signal peptide used in the fusion gene constructs of the invention. The specification describes DNA constructs that encode a fusion protein that comprises a subunit of an enterotoxin and a signal peptide. When transgenic plants containing the constructs are fed to mammals or birds, they induce immunity against the enterotoxin, specifically that of cholera. Alternatively, the plants are consumed to provide an adjuvant effect, in conjunction with administration of a live, dead or attenuated dose of pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-1998;
07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion protein; enterotoxin; transgenic plant; immunity;
                                                                                                                                                               Endoplasmic reticulum retention signal; single-chain antibody; kappa light chain constant region; stabilon; stabilising fusion peptide; kappa light chain constant region stabilon; protein stability;
                                                                                                                                                                                                                                       08-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plants useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-264031/22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYLO-) UNIV LOMA LINDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-APR-1999
                                                                                                                             Unidentified
                                                                                                                                                     vaccine; gene therapy; protein degradation modulation; protein
Alzheimer's disease.
                                                                                                                                                                                                                 Carboxy terminal
                                                                                                                                                                                                                                                               AAB15683
                                                                                                                                                                                                                                                                                     AAB15683 standard;
(MIND-)
                                  11-JAN-1999;
                                                          11-JAN-2000; 2000WO-US00558.
                                                                                  20-JUL-2000
                                                                                                       WO200042185-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of expressing cholera toxin B subunit useful for producing oral vaccines
                                                                                                                                                                                                                                                                                                                                                \vdash
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MINDSET BIOPHARMACEUTICALS USA INC MCINNIS \mathcal P A.
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page
                                                                                                                                                                                                                                                                                                                                                 SEKDEL 6
                                                                                                                                                                                                                                                                                                                                                                        SEKDEL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chong D,
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0061265
97US-0061265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US21237
                                  99US-0115505.
                                                                                                                                                                                                                endoplasmic reticulum retention signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragments).
                                                                                                                                                                                                                                                                                     Peptide; 6
                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Langridge WHR,
                                                                                                                                                                                                                                                                                                                                                                                               <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                          Score 29; DB 20;
Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Merritt JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein in transgenic
                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6;
                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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B S

Delivering a drug, to a patient suffering from cancer or diabetes,

at

WPI; 2000-572044/53

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RESULT 8
AAB22836
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a carboxy terminal endoplasmic reticulum retention signal. The nucleotide sequence encoding this signal may be incorporated into a primer used to amplify DNA encoding the kappa light chain constant region of human antibodies. The protein encoded by the PCR product will contain a signal for the endoplasmic reticulum. A heavy chain and a light chain may be joined through a linke to form a single-chain antibody. A stabilising fusion peptide, referred to as a stabilon, may be linked to the N-terminus of the single-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody to increase stability of the antibody against proteolysis in vivo. Degradation of the antibody may be modulated by linking the stabilon to the antibody through a protease-sensitive linker region. The stabilon is removed upon induction of expression of a specific restriction protease by means of an inducible promoter, and this renders the antibody susceptible to proteolysis by the N-end rule pathway. This method for regulating protein stability allows removal of the antibody after it has bound to its target antigen. Stabilised recombinant proteins may be used in gene therapy for the treatment of disorders such as
                                                                                                                                                                                                                                                                                                                                              Controlled release delivery system, drug targetting, drug-specific antibody; intracellular half-life; gene therapy; diabetes; autoimmune disease; inflammatory disease; infectious cancer; side effect; subcellular localisation sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modulating degradability of protein or peptide useful for gene therapy involving antibodies, comprises altering a gene at the N terminus to render protein or peptide metabolically stable -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-terminal ER retention signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB22836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB22836 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   render protein or peptide metabolically
                                                                                                                                                                        31-AUG-2000.
                                                                                                                                                                                                                                                                                       Unidentified
                                                    26-FEB-1999;
                                                                                                           25-FEB-2000; 2000WO-US04749
                                                                                                                                                                                                                                  WO200050089-A2
(MIND-) MINDSET BIOPHARMACEUTICALS USA INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SEKDEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                       99US-0122103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29; DB 21;
Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                      disease;
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RESULT 5
AAW96344
ID AAW9
XX
AC AAW9
XX
AC AAW9
XX
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                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                    to treat, prevent or diagnose tumors (e.g. as tumor vaccines), autoimmune diseases and inflammation (e.g. transplant rejection and arthritis), blood disorders (e.g. of the coagulation and/or circulatory systems, such as anemia, leucopenia, thrombocytopenia and hypertension), nervous system disorders and/or infections (by viruses or bacteria, or malaria), including, when (I) include a fusogenic peptide, use for gene transfer.

(I) are produced simply and in predominantly homogeneous form, in a wide variety of hosts, either in secreted or membrane-bound forms. This sequence represents a VH-VL domain linker peptide which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               multiple antigens and comprises two variable domains of heavy immunoglobulin chains (VH), having specificities A and B and two variable domains of light chains (VL), also with specificities A and B. The domains are provided as two VH-VL constructs which are attached via a peptide (P). Any VH and VL may be replaced by their functional fragments. The products of the invention have anticancer, antiviral, antibacterial, antimalarial and antiinflammatory activity. (1) are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polyspecific binding agents containing variable heavy and light constructs connected via peptide linker, used for treatment, prevention or diagnosis of e.g. cancer -
 19-JUL-1999
                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 16; 20pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-581511/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen binding; single chain; variable domain; VH domain; light chain heavy immunoglobulin chain; VL domain; anticancer; antiviral; tumor; antibacterial; antimalarial; antiinflammatory; treatment; prevention; diagnosis; vaccine; autoimmune disease; inflammation; blood disorder;
                                    AAW96344;
                                                                      AAW96344 standard; Peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a novel single-chain molecule (I) that binds multiple antigens and comprises two variable domains of heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kontermann R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VH-VL domain linker peptide #6.
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                                                                                                                                                                                               SEKDEL 6
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                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                      ξ,
 (first entry)
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                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                 Score 29;
Pred. No.
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                   9.3e+05;
                                                                                                                                                                                                                                                                  DB 20;
                                                                                                                                                                                                                                                                Length 6;
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RESULT 6
AAY01625
ID AAY0
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                                                                                                                                                                                                                                                                                                                                                                                              Intracellular binding to a desired target by an intracellularly cappressed antibody (i.e. an intrabody) can be used to knock out multiple locuses of immunomodulatory receptor molecules (IRMs), so that the expression of multiple major histocompatibility (MHC) molecules is blocked. This selective targeting of IRMs, their pathways or components, can be used to selectively regulate the immune system by controlling expression of these molecules and preventing an undesired immune response in a cell. Any component of the MHC pathway or the MHC assembly line or antigen presentation can be targeted. Intrabodies can be used to knock out the immune response in a particular tissue or portion of the body to prepare it for cell or tissue transplantation. Alternatively, an organ for transplantation can be perfused with the intrabody ex vivo. The intrabodies can comprise whole antibodies, heavy chains, Fab' fragments, single-chain antibodies and diabodies. The intrabodies also comprise an intracellular localisation signal to facilitate interception of expressed proteins. For example, if the target was a cell surface receptor, the antibody would comprise a leader retention signal. This peptide is an endoplasmic reticulum (ER) or Goldi apparatus
                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 6
             Signal peptide used in the
                                              21-JUN-1999 (first entry)
                                                                                                                AAY01625 standard; Peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                      AAW96345-W96377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody, immune response; modulation; MHC; IRM; receptor; intrabody; major histocompatibility complex; graft rejection; immunomodulatory response molecule; regulation; transplantation; retention signal; localisation signal; golgi apparatus; ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 25; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Altering the regulation of the immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marasco W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9914353-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                retention signal. This peptide is an endoplasmic retricult retention signal This percentage and the retricult retricult sequences. For other localisation sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endoplasmic reticulum localisation signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DAND ) DANA FARBER CANCER INST INC
                                                                                                                                                                                                                                 1 SEKDEL 6
                                                                                                                                                                                                                                                                 6; Conserv
                                                                                                                                                                                                  TECNES
                                                                                                                                                                                                                                                                                                                                   6 AA;
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                                                                                                                                                                                                                                                                    Conservative
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             fusion
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Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                    Mismatches
            gene
               constructs
                                                                                                                                                                                                                                                                                                  Length 6;
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               invention
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Query Match
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intracellular binding of antigens -
with vector system, for e.g. tumour
                                             A transgenic plant comprising or expressing a DNA sequence encoding an immunogenic agent can be be used as an orral vaccine for animals. The vaccine is administered by the oral consumption of the plant and provides the first known functional method for immunising animals using transgenic plants, where the plants express bacterial antigens that act as both immunogens and adjuvants. The method provides an inexpensive production and delivery system for such antigens to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
 animals. This sequence acts as a microsomal retention signal and was used to modify the LT-B Escherichia coli toxin subunit C-terminal sequence. The sequence coding for the whole LT-B gene was used in the
                                                                                                                                                                                                                   Transgenic plants contg. E. coli heat labile enterotoxin subunits used as oral vaccines for animals which consume the plant
                                                                                                                                                                                                                                                                   WPI; 1996-230602/23.
                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adjuvant; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxin; subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified heat labile enterotoxin B subunit (LT-B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-1996
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UNIV TEXAS A & M SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 AA;
                                                                                                                                                                                 Page 45; 130pp;
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                                                                                                                                                                                                                                                                                                      Clements
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RESULT 3
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 construction of such a transgenic plant. The immunogenic agent preferably comprises the LT-B or CT-B (cholera toxin B subunit) optionally LT-A or CT-A.
                                                                                                                     The endoplasmic reticulum retention signal sequence was used in the method of the invention to generate lymphocytes that are resistant to HIV infection due to the lack of an expressed co-receptor. The products and methods can be used for inhibiting phenotypic expression of a chemokine receptor in a cell. In particular they can provide lymphocytes that are resistant to HIV infection due to the lack of an expressed co-receptor. They can be used in the therapy or prevention of HIV infection and in the prevention or treatment of opportunistic infections in AIDS or ARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV resistant lymphocyte; chemokine receptor; HIV; intracellular retention signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endoplasmic reticulum retention signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW61472;
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                                                                                        Sequence
                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                   chemokine encoding gene, useful for, e.g. treating
                                                                                                                                                                                                                                                                                                                        Bai X,
                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                           Inhibition of expression of chemokine receptors in cells -
                                                                                                                                                                                                                                                                                                  WPI; 1998-333340/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-1998
                                                                                                               patients.
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RESULT 4 AAY33594

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Transmit tector		ŧ				,
Endonlasmic reticu	AAY93737	2	ע	100.0	29	φ
C-terminal ER rete	AAB22836	21	o	100.0	29	80
Carboxy terminal e	AAB15683	21	σ	100.0	29	7
Signal peptide use	AAY01625	20	6	100.0	29	6
Endoplasmic reticu	AAW96344	20	6	100.0	29	₅
VH-VL domain linke	AAY33594	20	6	100.0	29	4
Endoplasmic reticu	AAW61472	19	6	100.0	29	ω
Modified heat labi	AAR94943	17	6	100.0	29	N
C-terminal endopla	AAR48284	15	6	100.0	29	,
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į	96	AAY44959	AAY44958	AAY44966	AAY44965	AAY44963	AAY44962	AAY44961	AAY44960	ABP10603	AAY44964	AAE19253	AAE19255	AAE19257	AAE19259	AAB69627	AAY95252	AAE19261	AAE28217	AAE19266	AAE28223	AAB85342	AAR94942	AAY44968	85		AAM47850		041	AAU97200	822	534	94	5864	9	AAY96657
		KDEL receptor inhi		receptor		receptor	receptor	receptor	KDEL receptor inhi	ORFX pro	KDEL receptor inhi	Human recombinant	Human recombinant		Human recombinant	ER retention signa	Fluorescein-labell	Human recombinant	Tobacco mosaic vir	Human alpha-galact	Tobacco mosaic vir	C-terminal sequenc	Heat labile entero	Peptide-1 binding	Plant endoplasmic	Endoplasmic reticu	Plant endoplasmic	ER-retention signa		lasmic retic	Ę	lasmic retic	н	c re	\sim	C-terminal microso

ALIGNMENTS

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RESULT 1
AAR48284
WPI; 1994-048868/06.
N-PSDB; AAQ56576.
                                                                                                                                                                       Single chain antibody; sFv; heavy chain; light chain; kappa; variable domain; hydrophilic linker; antibodies; PCR; polymerase chain reaction; endoplasmic reticulum retention.
                                                                                                                                                                                                              C-terminal endoplasmic reticulum retention signal.
                                                                                                                                                                                                                                25-MAR-2003
29-JUL-1994
                           Haseltine WA,
                                                                 17-JUL-1992;
17-MAR-1993;
                                                                                             16-JUL-1993;
                                                                                                                03-FEB-1994.
                                                                                                                                   WO9402610-A1.
                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                             AAR48284;
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                                              (DAND ) DANA
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(first entry)
                                              FARBER CANCER INST INC
                           Marasco WA;
                                                                 92US-0916939.
93US-0045274.
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RESULT 39
QUAJKS
AC QUAJK
AC STRU
AC STR
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                                              RESULT 40
Q9DPC9
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InterPro; IPR001623; DnaJ N.
InterPro; IPR00133; T.Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00217; T.Ag_DNA_bind; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS50076; DNAJ 2; 1.
PROSITE; PS50076; DNAJ 2; 1.
SEQUENCE 688 AA; 79210 MW; AACE7669D588B3EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8JJK3;
Q8JJK3;
01-OCT-2002
01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=MT-2, MT-14, TD-4, TD-6, TD-15, TD-19, MN-6, and MN-7;

STRAIN=MT-2, MT-14, TD-4, TD-6, TD-15, TD-19, MN-6, and MN-7;

Saruwatari L., Zheng H.Y., Takasaka T., Sugimoto C., Sakai E.,

Aung N., Kitamura T., Yogo Y., Ohno N.;

"Peopling of Myanmar as revealed by genotyping of urinary JC v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "JC Virus Genotypes in the Western Pacific Suggest Asian Mainland Relationships and Virus Association with Early Population Movements."; Hum. Biol. 74:473-488 (2002).
Q9DPC9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EMBL; AB077860; BAC02982.1; -. EMBL; AB077861; BAC02984.1; -. EMBL; AB077862; BAC02994.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Large T antigen4.
Polyomavirus JC.
Viruses; dsDNA viruses,
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InterPro; IPR003133; T_Ag_DN
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AB077867;
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PF02217; T_Ag_DNA_bind; 1.
; SM00271; DnaJ; 1.
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AB077865;
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8; Conserv
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                                                                                                                                                                                                                                                                                                                           PS50076; DNAJ_2; 1.
688 AA; 79350 MW;
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llarity 88.9%;
Conservative
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BAC03006.1;
BAC03012.1;
BAC03018.1;
BAC03024.1;
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Last sequence update)
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Pred. No.
                                                                                                                                                                                                                                 Score 45; DB 12; Length 688; Pred. No. 3.7; Indels
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Search completed: December 11, Job time: 39.8 secs

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Best Local Similarity
Matches 8; Conserv
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01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                   MEDLINE=97314152; PubMed=9170494; Agostini H.T., Ryschkewitsch C.F., Brubaker G.R.,
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=309A;
                                                                                                                                                                                                                                                                                                                                                     Polyomavirus JC.
Viruses; dsDNA viruses,
                                                                                      PROSITE; PS50076; DNAJ_2; 1.
SEQUENCE 688 AA; 79156 MW;
                                                                                                         EMBL; AF295731; AAG34668.1; ...
InterPro; IPR001623; DnaJ N.
InterPro; IPR003133; T Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF002217; T Ag_DNA_bind; 1.
SMART; SM00271; DnaJ; 1.
                                                                                                                                                                         Agostini H.T., Ryschkewitsch C.F., Brubaker G.R., Shao J., Stoner G.I.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=309A;
                                                                                                                                                                                                                                                       Americans.
                                                                                                                                                                                                                                                                            Stoner G.L.;
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10632;
                                                                                                                                                                                                                                                                                                                                                                          Large T antigen.
                                                                                                                                                                                                                                          Arch. Virol.
                                                                                                                                                                                                                                                               Five complete genomes of JC virus type 3 from Africans and African
 125
TPPKKKKKV
              TPPKKKRKV
                                            Conservative
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   133
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                                                      Pred. No. 3.
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RESULT
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EMBL; AF281605; AAK70259.1; -.
EMBL; AF396425; AAM69549.1; -.
EMBL; AF396425; AAM69620.1; -.
InterPro; IPR001623; DnaJ N.
InterPro; IPR003133; T Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF02216; T Ag_DNA_bind; 1.
PROSITE; PS50076; DNAJ 2; 1.
SEQUENCE 688 AA; 79320 MW; F8767D
  Sugimoto C.,
           SEQUENCE FROM N.A. STRAIN=G5;
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STRAIN=234E, and 233E;
Stoner G.L., Jobes D.V., R.
Stoner G.L. analysis of
                                                   Polyomavirus JC.
Viruses; dsDNA viruses,
                                                                                            01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                  Yanagihara R., Neyurkar V.R., Scheirich I., Agostini H.T., Mgone C.S., Cui X., Jobes D.V., Cubitt C.L., Ryschkewitsch C.F., Hardy D.B., Friedlaender J.S., Stoner G.L.;
"JC Virus Genotypes in the Western Pacific Suggest Asian Mainland Relationships and Virus Association with Early Population Movements.";
Hum. Biol. 74:473-488(2002).
                                       NCBI_TaxID=10632;
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Viruses; dsDNA viruses,
NCBI_TaxID=10632;
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01-OCT-2002
                                                                      LARGE T ANTIGEN.
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MEDLINE=22168078; PubMed=12180767;
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 Zheng
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Pred. No.
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 Demenev V.,
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                                                   Polyomaviridae;
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3.7;
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RESULT 38
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Q8V6F7
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Matches 8
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A Mitsunobu Y., Ikegaya H., Kobayashi N., Kitamura T., Yogo Y.;

"JC virus strains indigenous to northeastern Siberians and Canadian

I nuits are unique but evolutionally related to those distributed

I throughout Europe and Mediterranean areas.";

Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

REMBL; AB074581; BAB93045.1; -.

REMBL; AB074581; BAB93045.1; -.

RINterPro; IPR001313; T.Ag_DNA_bind.

RPfam; PF00226; DnaJ; 1.

RPfam; PF00227; Tag_DNA_bind; 1.

RPfam; PF00217; Tag_DNA_bind; 1.

RP Pfam; PF0075; DNaJ; 1.

RP Pfam; PF0075; DNaJ; 1.

RP PROSITE; PS00077; DnaJ; 1.

RR PGOSTER; PS00076; DNAJ_2; 1.

RR PGOSTER; PS00076; DNAJ_2; 1.
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Best Local Similarity
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InterPro; IPR001623; DnaJ N.
InterPro; IPR003133; T.Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00217; T.Ag_DNA_bind; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS50076; DNAJ 2; 1.
SEQUENCE 688 AA; 79258 MW; 0C807;
                                                                                                                                                                                                                                                                   Q8JUB9;
Q8JUB9;
01-OCT-2002
01-OCT-2002
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Q8V6F7;
01-MAR-2002
                                                                                                                                Polyomavirus JC.
Viruses; dsDNA viruses,
SEQUENCE FROM N.A. STRAIN=#808B;
                                                                                                NCBI_TaxID=10632;
                                                                                                                                                                                                        Large T antigen.
                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stoner G.L., Jobes D.V., Ryschkewitsch C.F., I "Evolutionary analysis of the human polyomaviz Submitted (JUN-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Large T antigen.
Polyomavirus JC.
Viruses; dsDNA viruses,
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01-JUN-2002
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the human polyomavirus
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Last seq
Last ann
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Pred. No. 3.7;
1; Mismatches 0
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Pred. No. 3
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Matches 8
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01-MAR-2002
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Polyomavirus JC.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00226; DnaJ; 1
Pfam; PF02217; Tag DA bind; 1.
SMART; SM00271; Tag DnaJ; 1.
PROSITE; PS50076; DNAJ_2; 1.
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Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                MEDLINE=98227930; PubMed=9568975;
Agostini H.T., Ryschkewitsch C.F., Stoner
"JC virus Type 1 has multiple subtypes: th
J. Gen. Virol. 79:801-805(1998).
EMBL, AF015527; AAC59332.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9WM10;
01-NOV-1999
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InterPro; IPR003133; T_Ag_
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=type 1B;
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                                                                                                                  InterPro; IPR001623; DnaJ N.
InterPro; IPR003133; T Ag_DNA_bind
Pfam; PP00226; DnaJ; 1.
Pfam; PF02217; T Ag_DNA_bind; 1.
SMART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10632;
                                                                                           PROSITE; PS50076; DNAJ
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                                                            AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNAJ_2; 1.
; 79287 MW;
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INTEGRATO; IPR001623; DNAJ N.
INTEGRATO; IPR003133; T_Ag_DNA_bind.
Pfam; PF00226; DNAJ; 1.
Pfam; PF002217; T_Ag_DNA_bind; 1.
SMART; SM00271; DNAJ; 1.
PROSITE; DS50076; DNAJ; 2; 1.
SEQUENCE 688 AA; 79454 MW; AFEB4
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Q8JUC9;
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Viruses; dsDNA viruses,
NCBI_TaxID=10632;
                                                                                                      Sugimoto C., Kato A., Zheng H., Kitamura T., Yogo Y.;
"Evolution of the Human Polyomavirus JC Virus: Support f
Aspects of the Differentiation and Migration of Modern H
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB048553; BAB68822.1;
                                                                                                                                                                                                                          POLYOMAVITUS JC.
Viruses; dsDNA viruses,
NCBI_TaxID=10632;
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Cui X., Jobes D.V., Cubitt C.L., Ryschkewitsch C.F.,
Friedlaender J.S., Stoner G.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003
                         Pfam; PF00226; DnaJ; 1.
Pfam; PF02217; T_Ag_DNA_bind; 1.
SMART; SM00271; DnaJ; 1.
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                 SMART; SM00271;
PROSITE; PS50076
                                                               InterPro; IPR001623; DnaJ_N.
InterPro; IPR003133; T_Ag_DNA_bind
Pfam; PF00226; DnaJ; 1.
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                                                                                                                                                                                                                                                                              Large T antigen.
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Relationships and Virus Association with Early Population Movemen
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688 AA; 79286 MW;
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Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                            Polyomavirus JC.
Viruses; dsDNA viruses,
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Stoner G.L., Jobes D.V.,
                                                                                                                                                                                                                                                                                                                               STRAIN=804;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10632;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          тррккккки 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            889
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88.9%;
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  93.8%; Score 45;
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Pred. No. 3
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     DB 12;
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RESULT 30
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ID Q993Y
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DT 01-JU
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DR Pfam;
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Best Local
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Q993Y4;
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C STRAIN-AM-18;

XA Sugimoto C., Hasegawa M., Zheng H., Demenev V., Sekino Y., Kojima K., RA Honjo T., Kida H., Hovi T., Vesikari T., Schalken J.A., Tomita K., RA Honjo T., Kida H., Hovi T., Vesikari T., Schalken J.A., Tomita K., RA Mitsunobu Y., Ikegaya H., Kobayashi N., Kitamura T., Yogo Y.;

RT "JC virus strains indigenous to northeastern Siberians and Canadian RT Innits are unique but evolutionally related to those distributed RT throughout Europe and Mediterranean areas.";

Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

BMBL; AB074575; BAB93009.1; -.

DR EMBL; AB074575; BAB93009.1; -.

DR InterPro; IPR001163; DnaJ N.

DR Ffam; PF00226; DnaJ; 1.

DR Pfam; PF002271; T Ag DNA bind.

PR Ffam; PF002217; T Ag DNA bind; 1.

DR PRASTI; SM00271; DnaJ; 1.

DR PRASTI; SM00271; DnaJ; 1.

DR PROSTIF; PS0076; DNAJ 2; 1.

SQ SEQUENCE 688 AA; 79296 MW; 4C95B143DAC7C7D6 CRC64;
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Matches 8; Conserv
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01-JUN-2001
01-OCT-2001
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Q8JZK0;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                             Stoner G.L., Fernandez Cobo M., Jobes D.V., Ryschkewitsch C.F.;
"JC virus distribution in the Americas.";
"Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF295734; AAK28467.1; -.
InterPro; IPR001623; DnaJ.N.
InterPro; IPR003133; T Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00227; T Ag_DNA_bind; 1.
SMART, SM00271; DnaJ; 1.
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Viruses; dsDNA viruses,
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LARGE T ANTIGEN.
                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                      Polyomavirus JC
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                                                                                                                                                                                                                                                                                                        Large T antigen.
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PS50076; DNAJ 2; 1.
688 AA; 79257 MW;
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45;
Pred. No.
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 157B97C8F6DDA0E8 CRC64;
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RESULT
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Matches 8
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Matches
                                                                                       Stoner G.L., Jobes D.V., Ryschkewitsch C.F., Fernandez Cobo
"Evolutionary analysis of the human polyomavirus JC.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL, AF281.624; AAK70313.1; -.

R InterPro; IPR001623; DnaJ N.
R InterPro; IPR003133; T_Ag_DNA_bind.

R Pfam; PF00226; DnaJ; 1.

R Pfam; PF002217; T_Ag_DNA_bind; 1.

R Pfam; PF002217; T_Ag_DNA_bind; 1.

R SMART; SM00271; DnaJ; 1.

R PROSITE; PS50076; DNAJ; 2; 1.

SEQUENCE 688 AA; 79282 MW; 1F7D65407A1D5824 CRC64;
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Pfam; PF00226; DnaJ; 1.
Pfam; PF002217; T Ag DNA bind; 1.
SMART; SM00271; DnaJ; 1
PROSITE; PS50076; DNAJ 2; 1.
PROSITE; PS50076; DNAJ 2; 1.
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01-OCT-2002
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InterPro; IPR001623; DnaJ N.
InterPro; IPR003133; T Ag DNA bind.
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Polyomavirus JC.
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EMBL; AF015532; AAC59497.1; -.
EMBL; AB048554; BAB68828.1; -.
InterPro; IPR001623; DnaJ N.
InterPro; IPR003133; T_Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00217; T_Ag_DNA_bind; 1.
SMART; SM00271; DnaJ; 1.
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"Evolution of the Human Polyomavirus JC Virus: Support for Various
Aspects of the Differentiation and Migration of Modern Humans.";
Submitted (SEP-200) to the EMBL/GenBank/DDBJ databases.
EMBL, AB048573; BAB68942.1;
InterPro; IPR001623; DnaJ N.
InterPro; IPR003133; T Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00226; DnaJ; 1.
SMART; SM00271; T Ag_DNA_bind; 1.
SMART; SM00271; T Ag_DNA_bind; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS50076; DNAJ_2; 1.
SEQUENCE 688 AA; 79296 MW; 3A27A50A2B45F731 CRC64;
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Viruses; dsDNA viruses,
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Agostini H.T., Shishido-Hara Y., Baumhef
Ryschkewitsch C.F., Stoner G.L.;
"JC virusType 2: definition of subtypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polyomavirus JC.
Viruses; dsDNA viruses,
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"Evolution of the Human Polyomavirus JC Virus: Support for Various
Aspects of the Differentiation and Migration of Modern Humans.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB04856; BAB68900.1;
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Pfam; PF02217; T Ag DNA bind; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS50076; DNAJ; 2; 1.
SEQUENCE 688 AA; 79268 MW; 6
                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50076; DNAJ_2; 1. SEQUENCE 688 AA; 79324 MW;
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InterPro; IPR003133; T Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF02211; T Ag_DNA_bind; 1.
SMART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=SP-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses,
NCBI_TaxID=10632;
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InterPro; IPR003133; T_Ag_DNA_bind.
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8; Conserv
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8; Conservative
dsDNA viruses,
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RNA stage; Polyomaviridae; Polyomavirus.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                           Score 45; DB Pred. No. 3.7; 1; Mismatches
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Pred. No. 3.
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3.7;
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RESULT 22
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Best Local S
Matches 8
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Best Local
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                                                                                                                                                                                           STRAIN=type 3;
Agostini H.T., Ryschkewitsch C.F., Bagostini H. S., Rysch C.F., Rysch C.F., Rysch C.F., Rysch C.F., Dadj 1.

Pfam; PF002217; T.Ag_DNA_bind; 1.

Pfam; PF02217; T.Ag_DNA_bind; 1.

SMART; SM00271; Dnadj; 1.

PROSITE; PS50076; DNAJ_2; 1.

PROSITE; PS50076; DNAJ_2; 1.

VARIANT 653 653 F -> S.

VARIANT 323 323 N -> S.

VARIANT 323 323 N -> S.
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InterPro; IPR001623; DnaJ N.
InterPro; IPR003133; TAg_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF022217; TAg_DNA_bind; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS50076; DNAJ 2; 1.
SEQUENCE 688 AA; 79413 MW; 892071
                                                                                                                                                                             SEQUENCE
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STRAIN=type 3;
MEDLINE=97314152; PubMed=9170494;
ASOStini H.T., Ryschkewitsch C.F.,
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Viruses; dsDNA viruses,
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01-DEC-2001
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01-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22168078; PubMed=12180767;
Yanagihara R., Nerurkar V.R., Scheirich I., Agostini H.T., Mgone C.S.,
Cui X., Jobes D.V., Cubitt C.L., Ryschkewitsch C.F., Hardy D.B.,
Friedlaender J.S., Stoner G.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Five complete
Americans.";
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                                                                                                          93.8%;
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                                                                                     Score 45; DB Pred. No. 3.7; 1; Mismatches
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Pred. No. 3
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CF35E42B0457EC34 CRC64;
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                                                                                                            DB 12;
3.7;
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3.7;
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RESULT 16
Q9WM07
ID Q9WM0
AC Q9WM0
DT 01-NC
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DT 01-DE
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01-MAR-2002
01-JUN-2002
Large T anti
                                 Q8V6G6
Q8V6G6;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                    STRAIN=type 2A;
MEDLINE=9826491; PubMed=9603329;
Agostini H.T., Shishido-Hara Y., Baumhef.
Ryschkewitsch C.F., Stoner G.L.;
"JC virusType 2: definition of subtypes
                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                          of ten complete genomes.";
J. Gen. Virol. 79:1143-113(1998).
EMBL; AP015530; AACE9485.1;
InterPro; IPR001623; DnaJ_N.
InterPro; IPR003133; T_Ag_DNA_bind.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inuits are unique but evolutionally related to those distributed throughout Europe and Mediterranean areas.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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Polyomavirus JC.
Viruses; dsDNA viruses,
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01-NOV-1999
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InterPro; IPR003133; T_Ag
Pfam; PF00226; DnaJ; 1.
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                                                                                                                                                                                                                                                        Ptam;
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nes 8; Conserv
                                                                                                                                                                                                       m; PP00226; DnaJ; 1. — m; PP00226; DnaJ; 1. — RT; SM00271; DnaJ; 1. SITE; PS50076; DNaJ; 1. UBNCE 688 AA; 79349 MW; B7
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PF02217; T Ag DNA bind; 1.
; SM00271; DnaJ; 1.
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8; Conserv
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Y., Ikegaya H., Kobayashi N., Kitamura T., Yogo
strains indigenous to northeastern Siberians and
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Pred. No. 3.7;
1; Mismatches
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Pfam; PF00226; DnaJ; 1.

Pfam; PF002217; T Ag_DNA_bind; 1.

SMART; SM00271; DnaJ; 1.

PROSITE; PS50076; DNAJ 2; 1.

PROSITE; PS50076; DNAJ 2; 1.

PROSITE; PS50076; DNAJ 2; 1.
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InterPro; IPRO03133; T.Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF002217; T.Ag_DNA_bind; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS50076; DNAJ 2; 1.
PROSITE; PS50076; DNAJ 2; 1.
SEQUENCE 688 AA; 79307 MW; E9C920
Q9WM08 PRELI
Q9WM08;
01-NOV-1999 (TrEM
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01-UN-2001 (TrEM
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Large T antigen.
Polyomavirus JC.
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Q8JWJ4;
01-OCT-2002
01-OCT-2002
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Aung N., Kitamura T., Yogo Y., Ohno
"Peopling of Myanmar as revealed by
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"Evolutionary analysis of the human polyomavirus JC.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF281615; AAL37672.1;
                                                                                                                                                                                                                                                 EMBL; AB077858; BAC02970.1; -.
InterPro; IPR001623; DnaJ N.
InterPro; IPR003133; T_Ag_DNA_bind
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Viruses; dsDNA viruses,
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Viruses; dsDNA viruses,
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Best Local Similarity
Matches 8; Conserv
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Pfam; PF00226; DnaJ; 1.

Pfam; PF002217; T Ag DNA bind; 1.

SMAXT; SM00271; DnaJ; 1.

PROSITE; PS50076; DNAJ 2; 1.

PROSITE; PS50076; DNAJ 2; 1.
                                                                                                                                                                        Q8JUC5;
01-OCT-2002
01-OCT-2002
01-MAR-2003
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Pfam; PFOO
Pfam; PFOO
SEQUENCE FROM N.A.
STRAIN#811A;
MEDLINE=22168078; PubMed=12180767;
MEDLINE=22168078; PubMed=12180767;
Yanagihara R., Nerurkar V.R., Scheirich I., Agostini H.T., Mgone C.Cui X., Jobes D.V., Cubitt C.L., Ryschkewitsch C.F., Hardy D.B., Friedlænder J.S., Stoner G.L.;
"JC Virus Genotypes in the Western Pacific Suggest Asian Mainland Relationships and Virus Association with Early Population Movement Hum. Biol. 74:473-488 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q91DF4;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2003) (TrEMBLrel.
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Pfam; PF02217; T Ag DNA bind; SMART; SM00271; DnaJ; 1.
PROSITE; PS50076; DNAJ 2; 1.
                                                                                                                                    Polyomavirus JC.
Viruses; dsDNA viruses,
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Pred. No.
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RN C1]
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InterPro; IPR001623; DnaJ N.
InterPro; IPR001623; DnaJ N.
InterPro; IPR003133; T.Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
SMART; SM00271; DnaJ; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS50076; DNAM_2; 1.
SEQUENCE 688 AA; 79281 MW; A0D08:
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Pfam; PF00226; DnaJ; 1.

Pfam; PF002217; T Ag DNA bind; 1.

SMART; SM00271; DnaJ; 1.

PROSITE; PS50076; DNAJ 2; 1.

PROSITE; PS50076; DNAJ 2; 1.
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Q8JJJ0;
01-OCT-2002
01-OCT-2002
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Q8JUD5;
01-OCT-2002
01-OCT-2002
01-MAR-2003
SEQUENCE FROM N.A.
STRAIN=AM-5, AM-7, SI-1,
Sugimoto C., Hasegawa M.,
                                        Viruses; dsDNA viruses,
NCBI_TaxID=10632;
                                                                Large T antigen.
LARGE T ANTIGEN.
Polyomavirus JC.
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Friedlaender J.S., Stoner G.
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MEDLINE=22168078; PubMed=12180767;
Yanagihara R., Nerurkar V.R., Sche
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Viruses; dsDNA viruses,
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Polyomavirus JC.
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InterPro; IPR003133; T_Ag_DNA_bind
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Relationships and Virus Association with Early Population Movemen
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Cubitt C.L., Ryschkewitsch C.F.,
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and SI-7;
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Lednicky J.A., Garcea R.L., Bergsagel D.J.,
"Natural simian virus 40 strains are present
and ependymoma tumors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CPC/MEN;
Lednicky J.A., Stewart !
Submitted (JUN-1999) to
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SEQUENCE FROM N.A.
STRAIN=CPC/MEN;
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Lednicky J.A., Butel J.S., Lewis A.M.;
"Complete DNA Sequence of SV40-GM00637H Variant 1.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
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InterPro;
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Lednicky J.A.,
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Submitted (MAR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete DNA sequence
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PF02217; T Ag DNA bind; 1.
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711 AA; 81908 MW;
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SV40 strain 777,
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Pred. No. 1.1;
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RESULT 10
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ID Q8JMI
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DT 01-MA
DE Large
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OC Virus
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RT "Whol
RT SEQUE
RC STRAI
RA Ledmin
DR EMBLI
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DR Pfam,
DR Pfam,
DR PROSSI
SQ SEQUE
RESULT 11

Q9W8V1

ID Q9W8V

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AC Q9W8V

DT 01-NC

DT 01-NC

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STRAIN=B-1, and B-2;
Lednicky J.A., Stewart A.R., E
Submitted (MAY-1999) to the EN
EMBL; AF155359; AAD43805.1; --
EMBL; AF155358; AAD43799.1; --
InterPro; IPR001623; DnaJ_N.
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Q8JMI9;
01-OCT-2002
01-OCT-2002
01-MAR-2003
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"Whole genomic sequence of SV-40 isolate N128-1.";
submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX120890; AAM7/807.1; -.
InterPro; IPR001623; DnaJ.N.
InterPro; IPR003133; T.Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF002217; T.Ag_DNA_bind; 1.
SMART; SM00271; DnaJ; 1.
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Viruses; dsDNA viruses,
                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-B-1, and B-2;

MEDLINE-9824346; pubMed-9584955;

Stewart A.R., Lednicky J.A., Butel J.S.;

"Sequence analyses of human tumor-associated isolates from monkeys and humans.";

J. Neurovirol. 4:182-193(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=B-1, and B-2;
MEDLINE=97368433; PubMed=9225047;
                                                                                                                                                                                                                                                                                                                                                "Tissue culture adaptation of natural isolates of simian virus changes occur in viral regulatory region but not in carboxy-tendomain of large T-antigen.";

J. Gen. Virol. 78:0-0(0).
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01-OCT-2001
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01-NOV-1999
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711 AA; 81895 MW;
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D; Mismatches
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Best Local S
Matches
Lednicky J.A., Butel J.S., Lewis A.M.;
"DNA sequence of SV40 reference strain 776.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ da
EMBL; AR316141; AAG39204.1; -.
InterPro; IPR001623; DnaJ N.
InterPro; IPR003133; T.Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00226; DnaJ; 1.
SMART; SM00271; DnaJ; 1.
SMART; SM00271; DnaJ; 1.
SMART; SM00271; DnaJ; 1.
SROSITE; PS50076; DNA_B1623 MW; 3E37D4BAFC5D59BD
SEQUENCE 708 AA; 81623 MW; 3E37D4BAFC5D59BD
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InterPro; IPR001623; DnaJ_N.
InterPro; IPR001133; T.Ag_DNA_bind.
Pfam; PP00226; DnaJ; 1.
Pfam; PP00226; DnaJ; 1.
SMART; SM00771; DnaJ; 1.
SMART; SM00771; DnaJ; 1.
PROSITE; BS50076; DNAJ; 1.
SEQUENCE 707 AA; 81567 MW; 58C9CA33AA64B5CD
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01-JUN-1998
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01-MAR-2001
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Simian virus 40 (SV40).
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polyomavirus disease.";
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=776;
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Lednicky J.A., Arrington A.S., Stewart A.F.
Jafar S., Murphey-Corb M., Butel J.S.;
"Natural isolates of simian virus 40 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=K661;
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NCBI_TaxID=10633;
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Simian virus 40 (SV40).
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"Complete DNA sequence of SV
variant of SV40 strain H328
Submitted (OCT-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                       Lewis A.M.;
SV40 strain H328-1, a regulatory region
SV40 with an archetypal regulatory region.";
ne EMBL/GenBank/DDBJ databases.
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      3E37D4BAFC5D59BD CRC64;
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Best Local S
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Best Local S
Matches 9
                                                                           Q9WND0;
Q9WND0;
01-NOV-1999
01-NOV-1999
01-JUN-2001
               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
Large tumor antigen (Large T antigen)
Simian virus 40 (SV40).
Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00226; DnaJ; 1. — Pfam; PF02217; T Ag DNA bind; 1. SMART; SM00271; DnaJ; 1. PROSITE; PS0076; DNAJ 2; 1. SEQUENCE 709 AA; 81671 MW; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Tissue culture adaptation of natural changes occur in viral regulatory regionain of large "-antigen.";
J. Gen. Virol. 78:0-0(0).
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EMBL; AF156107; AAD38993.1; -.
EMBL; AF156105; AAD38846.1; -.
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Stewart A.R., Lednicky J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=VA45-54-1, and VA45-54-2;
Lednicky J.A., Stewart A.R., But
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STRAIN-VA45-54-1, and VA45-54-2;
MEDLINE=9736843; PubMed=9225047;
Lednicky J.A., Butel J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simian virus 40 (SV40).
Viruses; dsDNA viruses,
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01-NOV-1999
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InterPro; IPR003133; T_Ag_DNA_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                solates from monkeys and humans.";
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Conservative (
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Pred. No. 1.1;
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ion but not in carboxy-terminal
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Best Local (
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PEAM; PF00217; T Ag DNA bind; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS50076; DNAJ 2; 1.
PROSITE; PS50076; DNAJ 2; 1.
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01-DEC-2001
T1 antigen ()
T1 ANTIGEN.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
PubMed=9484845;
Kao M.C., Liu G.Y., Chuang T.C., Lin
"The N-teninal 178-anino-acid domain
"The N-teninal Total suppressor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003133; T Ag_DNA_bind.
Pfam; PF02217; T Ag_DNA_bind; 1.
NON_TER 134 134
                   Q98ZP7
Q98ZP7; PRELIMINARY;
Q1-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Large tumor antigen.
Simian virus 40 (SV40).
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Mammalia; Eutheria;
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InterPro; IPR001623; DnaJ_N.
InterPro; IPR003133; T_Ag_DNA_bind.
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"Experimental evidence for RNA trans-splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95347348; PubMed=7542587;
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S79054; AAB34944.1; -
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Pred. No.
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Pred. No.
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InterPro; IPRO03133; T_Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF002217; T_Ag_DNA_bind; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS50076; DNAJ 2; 1.
SEQUENCE 705 AA; 81203 MW; F5366.
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Viruses; dsDNA viruses, 1
NCBI_TaxID=10633;
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InterPro; IPR003133; T Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF022217; T Ag_DNA_bind; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS50076; DNAJ 2; 1.
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MEDLINE=20090224; PbbMed=10626798;

Rizzo P., Di Resta I., Powers A., Ratner H., Carbone "Unique strains of Sv40 in commercial poliovaccines readily identifiable with current testing for Sv40 i Cancer Res. 59:6103-6108(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Large t antigen.
Simian virus 40 (SV40).
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                                                                                                                                                                                                                                                                                                                STRAIN=MC-028846B;
Rizzo P., Carbone M.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ
EMBL; AF180737; AAF28270.1; -
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seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

16	. p.	13	12	11	10	9	80	7	6	ហ	4.	ω	۵	1	Result No. So
4 4 U U	4.4	4 5	4 5	48	48	48	48	48	48	48	48	48	48	48	Score
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Q9WM07	Q8JUD5	Q8JUC5	Q91DF4	Q9W8V1	Q8JMI9	Q9WND0	Q9W8G8	Q9DH70	056326	Q9J7C9	Q98ZP7	Q9W7W7	Q64142	Q64141	ID
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Q8JUB6	Q82950	QBJUB1	Q91DE6	Q9DUG1	Q9DPC9	Q8JJK3	Q8JUB9	Q8V6F7	Q8JZJ2	Q910D2	Q91DG7	Q8JUC9	Q9WM10	Q8V6G3	Q993Y4	Q8JZK0	Q91NL2	Q91NM2	Q9W8D4	Q91DF5	Q91NL8	Q8JUE2	P88898	Q8JUD8	Q91DF8	80MM60	Q8JWJ4	Q8V6G6
Q8jub6	Q82950	Q8jub1	Q91de6	Q9dug1	Q9dpc9	Q8jjk3	Q8jub9	Q8v6£7	Q8jzj2	Q910d2	Q91dg7	Q8juc9	Q9wm10	Q8v6g3	Q993y4	Q8jzk0	Q91nl2	Q91nm2	Q9w8d4	Q91df5	Q91nl8	Q8jue2	868884	Q8jud8	Q91df8	Q9wm08	Q8jwj4	Q8v6g6
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Q64141
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Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches
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Q64141;
Q64141;
Q64141;
Q64100-1996 (TEMBLrel. 01, C
Q1-NOV-1996 (TEMBLrel. 01, L
Q1-DEC-2001 (TEMBLrel. 19, L
Q64142 PRELIMINARY;
Q64142;
01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                 NON TER
SEQUENCE
                                                                                                                                                                                                    Eul J., Graessmann M., Graessmann A.;
"Experimental evidence for RNA trans-splicing
EMBO J. 14:3226-323 (1995).
EMBL; 879053; AAB34943.1; -
InterPro; IPR003133; T. Ag DNA bind.
Pfam; PF02217; T. Ag DNA bind; 1.
                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10118,
                                                                                                                                                                                                                                                                                                                                                                  T2 antigen
T2 ANTIGEN.
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MEDLINE=95347348; PubMed=7542587;
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                                                                                                      TPPKKKKRKV
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RESULT 40
ISL1_CHICK
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01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00389; HOX; 1.

SMART; SM00132; LIM; 2.

PROSITE; PS00027; HOMEDOBOX 1; 1.

PROSITE; PS00478; LIM DOMAIN 1; 2.

PROSITE; PS50023; LIM DOMAIN 2; 2.

PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D21135; BAA04670.1; -. PIR; I51739; I51739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                            Repeat; LIM
DOMAIN
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001781; LIM.
InterPro; IPR0017107; LIM homeo.
Pfam; PF00046; homeobox; 1.
Pfam; PF00412; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND DEVELOPMENTAL EXPRESSION MEDLINE=94220748; PubMed=8167375;
                                                                                                                                                                                                                                    lomeobox;
                                                                                                                                                                                                                                                                                                                  ProDom; PD000010; Homeobox; 1. ProDom; PD000094; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                   ZFIN; ZDB-GENE-980526-112; isl1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inoue A., Takahashi M., Hatta K., Hotta Y., Okamoto H.;
"Developmental regulation of islet-1 mRNA expression during neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio).
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ISL1 OR ISL-1.
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                                                                                      2 PPKKKRKV 9
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                                                                PPKKKRLI 14
                                                                                                                                                                                                                     DNA-binding; Developmental protein; Nuclear protein;
IM domain; Metal-binding; Zinc; Multigene family.
                                                                                                                                                         181
245
349
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                             Conservative
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    STANDARD;
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133 L
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39181 MW;
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GLN-RICH.
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Pred. No.
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LIM 2.
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                                                                                                             Mismatches
    349
                                                                                                                        DB 1;
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ISL1 OR ISL-1.
Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996
01-OCT-1996
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                      Homeobox; DNA-binding; Developmental protein; Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc.
DOMAIN 17 70 LIM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIM-3 AND ISL-2.

SUBCELLULAR LOCATION: Nuclear.

DEVELOPMENTAL STAGE: EXPRESSED PRIOR TO THE FORMATION OF DISTINCT MOTOR AXON PATHWAYS AND BEFORE THE SEGREGATION OF MOTOR NEURONS INTO COLUMNS. EXPRESSED THROUGHOUT THE MEDIAM MOTOR COLUMN AND THE MEDIAL SUBDIVISION OF THE LATERAL MOTOR COLUMN (LMCM).

SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00478; LIM_DOMAIN_1; 2.
PROSITE; PS50023; LIM_DOMAIN_2; 2.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00389; HOX; 1.
SMART; SM00132; LIM; 2.
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Pfam; PF000412; LIM; 2.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000094; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L35567; AAA62171.1; -. PIR; I50369; I50369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsuchida T., Ensini M., Morton S.B., Ba
Jessell T.M., Pfaff S.L.;
"Topographic organization of embryonic
expression of LIM homeobox genes.";
Cell 79:957-970(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00027; HOMEOBOX_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Spinal
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PPKKKKRLI 14
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
enhancer protein ISL-1 (Islet-1)
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                                                                                                                                                                                                                         39033 MW;
                                                                                                                                       72.9%;
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                                                                                                                                       Score 35;
Pred. No.
                                                                                                                                                                                                                         HOMEOBOX.
GLN-RICH.
; 286E2B364EE0A505 CRC64;
                                                                                                                                                                                                                                                                                                                  LIM 2.
                                                                                                            Mismatches
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49;
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                                                                                                                                                              Length 349;
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RESULT 37
PSBS_SOLSG
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                                              Matches
                                                                 Query Match
Best Local
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Q9FPP4;
16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rorat T., Havaux M., Irzykowski W., Cuine S., Becuwe N., Rey P.;
"PSII-S gene expression, photosynthetic activity and abundance of
plastid thioredoxin-related and lipid-associated proteins during
chilling stress in Solanum species differing in freezing resistance.",
physiol. Plantarum 113:72-78(2001).
-!- FUNCTION: Seems to be involved in nonphotochemical quenching, a
process maintains the balance between dissipation and utilization
of light energy to minimize generation of oxidizing molecules,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                         TRANSMEM TRANSMEM
                                                                                                                                                                                                                        REPEAT
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=Line 1;
                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00504; chloroa_b-bi\overline{n}d; 1. Photosynthesis; Photosynthesis; Photosystem II; Chloroplast; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF311720; AAG48610.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=52705;
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                                                                                                                                                                                                                                                                                                                  TRANSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN; CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thereby protecting the plant against photo-oxidative damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THYLAKOID
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                                                                   Similarity
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    PPKKKRKV
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                                                                                                                                                                                                                                                                                                                                     Transmembrane;
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(Rel. 40,
(Rel. 41,
II 22 kDa
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75.0%;
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Pred. No.
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                                                                   Score 35; DB
Pred. No. 39;
                                                                                                                                                                                                                                                                                         CHLOROPLAST
PHOTOSYSTEM
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RESULT 39
ISL1_BRARE
ID ISL1_BRARE
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28-FEB-2003 (Rel. 4
Hypothetical ABC tra
MG467.
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Y467_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                        PROSITE, PSO0211, ABC TRANSPORTER_1; 1.

PROSITE; PSO0293, ABC TRANSPORTER_2; 1.

PROSITE; PS50893, ABC TRANSPORTER_2; 1.

Hypothetical protein; ATP-binding; Transport; Complete NP BIND 122 ATP (POTENTIAL).

SEGUENCE 311 AA; 35051 MW; 67EB11B97C10F68B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC transporter; 1.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing.";
J. Bacteriol.
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01-FEB-1996
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PIR; F64251; F64251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94075230; PubMed=8253680; Peterson S.N., Hu P.-C., Bott K.F., Hut "A survey of the Mycoplasma genitalium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 14-117 FROM N.A. STRAIN=ATCC 33530 / G-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 175:7918-7930(1993).-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96026346; PubMed=7569993;
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|PPKEKQKV
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33, Last sequence update)
41, Last annotation update)
transporter ATP-binding prot
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(See http://www.isb-sib.
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by using
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STANDARD;

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Best Local S
Matches 6
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01-NOV-1990
01-NOV-1990
28-FEB-2003
       This
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SEQUENCE
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=85042103; PubMed=6495656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nonstructural protein NS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U63963; AAB51697.1; -.
InterPro; IPR000910; HMG 12_box.
Pfam; PF00505; HMG_box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The coding sequences of 40 ne analysis of cDNA clones from DNA Res. 3:17-24(1996).
                                                                                                                                                                                                                                        Nakajima K., Nobusawa E., Nakajima S.;
"Genetic relatedness between A/Swine/Iowa/15/30(H1N1)
                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA negative-strand viruses; Influenza A viruses; Influenzavirus A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andre C., Hampe A., L.
Hu W.X., Galibert F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Prediction of the coding sequences of unidentified human genes. The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced analysis of cDNA clones from human cell line KG-1.";
                                                                                                                                                                                         virology 139:194-198(1984).
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=11500;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Influenza A virus (strain A/Swine/Iowa/15/30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50118; HMG_BOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00398; HMG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D83778; BAA12107.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 HMG box domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FMS receptor tyrosine kinase genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97179223; PubMed=9027509;
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                                                                                                                                                                                                                    .nfluenza viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of two genomic regions containing
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8
                                                                                                                                                                       ALTERNATIVE PRODUCTS
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                                                                                                                         Name=NS1;
                                                                                                                                               Event=Alternative
SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 PPKKKKK 177
                                                                                             IsoId=P18295-1;
                                                 IsoId=P18295-2;
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6; Conserva
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185
1435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136
255
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85.7%;
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                                                 Sequence=Not
                                                                                           Sequence=Displayed
                                                                                                                                          splicing;
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HMG BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 1; Le
Pred. No. 1.3e+02;
1; Mismatches 0;
                                                                                                                                            Named isoforms=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404692C02E81F07A CRC64;
                                                 described;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                             Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1435;
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  collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <
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RESULT 36
PSBS_LYCES
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Best Local S
Matches 6
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InterPro; IPR000256; Flu NS1; 1.
Pfam; PF00600; Flu NS1; 1.
ProDom; PD000613; Flu NS1; 1.
Nonstructural protein; Alternative splicing.
Nonstructural protein; Alternative Splicing.
230 AA; 26090 MW; 3DB7E558C6AC30AC CRC64;
 REPEAT
TRANSMEM
                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as most modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                          REPEAT
                                                                                InterPro; IPR001344; Chloro_ABbind.
Pfam; PF00504; chloroa_b-bind; 1.
Photosynthesis; Photosystem II; Chloroplast; Transit peptide;
                                                                                                                                       EMBL; U04336; AAA63649.1; -.
                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW
                                                                                                                                                                                                                                                                                                                                         Wallbraun M., Kim S., Green B.R., Piechulla B., Pichersky E.;
"Nucleotide sequence of a tomato psbS gene.";
Plant Physiol. 106:1703-1704(1994).

-!- FUNCTION: Seems to be involved in nonphotochemical quenching, a process maintains the balance between dissipation and utilization of light energy to minimize generation of oxidizing molecules, thereby protecting the plant against photo-oxidative damage (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core en Asteridae; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE ELIP/PSBS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95148755; PubMed=7846177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P54773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                     Thylakoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Photosystem
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                                                      TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBI_TaxID=4081;
                                                                                                                                                                                                                                                                                             similarity).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN;

THYLAKOID (By similarity).
                                                                                                                            T06331; T06331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 PPKQKREV 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Swiss Institute of Bioinformatics and the
                                                                    Transmembrane; Repeat
68
62
169
106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel.
(Rel.
(Rel.
II 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34, Createa,
34, Last sequence update)
40, Last annotation update)
kDa protein, chloroplast precursor (CP22).
276
168
276
126
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75.0%;
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                                           PHOTOSYSTEM
                                                        CHLOROPLAST
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                   moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                              There are no restrictions on ng as its content is in no
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                                           (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                   CHLOROPLAST
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                                                                                                                                                                                                                                                         collaboration
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                                                                                                                                                      RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Okazaki Y., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Corbani L.E., Cousins S.,
RA Baldarelli R., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Balda E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gansterland T., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marthionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Oshio T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yangi I., Yangi L.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yangi I., Yangi L.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Birnev R. Havashiraki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSD6Z1; QBBVL1; QBVDT2; Q99LT8; Q9CT15; 28-FEB-2003 (Rel. 41, Created) 15-SEP-2003 (Rel. 42, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation updat Nucleolar protein where 'Western's page 1975 (Necleolar protein where 'Western's page 1975)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01798; Nop; 1.
ProDom; PD004104; Nop; 1.
Hypothetical protein; Complete proteome.
DOMAIN 349 414 ASP/GLU/LYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; F64386; F64386.
TIGR; MJ0694; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U67516;
PIR; F64386; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleolar protein Nop56 (Nucleolar protein 5A)
NOL5A OR NOP56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J;
PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
TISSUE=Embryo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                 Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome
60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                             STRAIN=C57BL/6J,
PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G. Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., S
                                                                                                 60,770 full-length cDNAs
Nature 420:563-573(2002)
                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PPKKKKRK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPKKKKK 371
                                                               FROM
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                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rodentia;
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85.7%;
                                                 FVB/N-3;
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                                                 TISSUE=Mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Tongue;
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   Schuler
                                                                                                                                  annotation
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casawant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rakesley R.W., Touchman J.W., Skalska U., Smailus D.E.,
RA Rakesley R.W., Touchman J.W., Stalska U., Smailus D.E.,
RA Rakesley R.W., Touchman J.W., Stalska U., Smailus D.E.,
RA Rakesley R.W., Touchman J.W., Stalska U., Smailus D.E.,
RA Rakesley R.W., Schein J.E., Jones S.J.M., Marra M.A.,
RA Rakesley R.W., Schein J.E., Jones S.J.M., Marra M.A.,
RA Rakesley R.W., Schein J.E., Jones S.J.M., Marra M.A.,
RA Rakesley R.W., Schein J.E., Jones S.J.M., Marra M.A.,
RA Rakesley R.W., Schein J.E., Jones S.J.M., Marra M.A.,
RA Rakesley R.W., Schein J.E., Jones S.J.M., Marra M.A.,
RA RA
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                                                                            Query Match
Best Local S
Matches 7
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CONFLICT
CONFLICT
SEQUENCE
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EMBL; AK011481; BAB27647.2;
EMBL; AK077795; BAC37015.1;
EMBL; BC002231; AAH02231.1;
EMBL; BC022355; AAH21355.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Altschul S.F.,
                                                                                                                                                                                                                                        ProDom; PD004104; Nop
Ribosome biogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified
                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity)
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545
                                                                                                                                                                                                                                                                Pro; IPR002687; Nop. PF01798; Nop; 1. nop; 1.
                                      1 TPPKKKKK 8
                                                                            Similarity 7; Conserv
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TTPKKKRK 552
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182
436
580
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182
436
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87.5%;
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                                                                                                                                                                                 r protein.
Q -> K (]
I -> V (]
                                                                                 0,
                                                                                                    Score 36;
Pred. No.
                                                                                                                                                                Q -> K (IN REF. 1;
I -> V (IN REF. 1;
T -> A (IN REF. 2;
60AA1D43E349ADD7
                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                      54;
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                                                                                                                         DB 1;
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                                                                                                                         Length 580
                                                                                                                                                                BAC37015).
BAB27647).
AAH21355).
CRC64;
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RESULT 34
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SMF_HUMAN STANDARD; PRT; 1435 AA (012766; Q9UMF4; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation updat
                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                         SMF protein (Fra
SMF OR KIAA0194.
TISSUE=Bone marrow;
MEDLINE=96281124; Pu
Nagase T., Seki N.,
                                                    SEQUENCE FROM N.A.
                                                                                                                                                                            (Fragment).
 PubMed=8724849;
., Ishikawa K.-I.,
                                                                                                          Primates;
                                                                                                                         Chordata;
                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
Tanaka
                                                                                                                                                                                                 update)
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   A., Nomura
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S38742; AAB19293.1; -.

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RESULT
TLX1 M
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Best Local S
Matches 6
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EMBL; AF067443; AAG100
PIR; A40855; A40855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P43345;
01-NOV-1995
01-NOV-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                        MEDLINE=94203286; PubMed=7908720; Roberts C.W.M., Shutter J.R., Korsmeyer S.J.; "Hox11 controls the genesis of the spleen."; Nature 368:747-749(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                 "The optimal binding sequence of the Hox11 protein contains predicted recognition core motif."; Nucleic Acids Res. 23:1928-1935(1995).

-I- FUNCTION: CONTROLS THE GENESIS OF THE SPLEEN. BINDS TO 7 SEQUENCE 5-GGCGTDAGTGG-3.

-I- SUBCELLULAR LOCATION: Nuclear (Probable).

-I- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS EMBRYONIC TISSUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P14653; 1872.
TRANSFAC; T02054; -.
TRANSFAC; T02056; TLX1.
                                                                                                                                                                                                                      MEDLINE=95319935; PubMed=7596820; Tang S., Breitman M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94206842; PubMed=7908826; Raju K., Tang S., Dube I.D., Kamel-Reid S., Bryce D.M., Breitman M.L.; "Characterization and developmental expression of Tlx-1, the murine homolog of HOX11.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0007048; P:oncogenesis;
                                                                                                                                                                                                                                                                      DNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mech.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
AND SPLEEN.
SIMILARITY: Contains 1 homeobox domain
                                               INCLUDING BRANCHIAL ARCHES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR HOX11 OR TLX-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186770;
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AF067443; AAG10096.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria;
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330 /
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(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
smia homeobox protein 1 (Homeobox
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71
276
34365
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Rodentia;
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85.7%;
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Pred. No. 32;
1; Mismatches
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L -> R (IN REF. 4).
; 09A518FB5271F7ED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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RESULT
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4_METUA

7694 METUA

Q58105;

01-NOV-1997

01-NOV-1997

16-OCT-2001 (
                                                                                                                                                     STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Puhrmann J.L., Nguyen D.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
This SWISS-PROT entry is copyright. It is produble between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us entities requires a license agreement (See http
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homeobox; DNA-binding; NucTear protein; Developmental protein.
DNA_BIND 203 262 HOMEOBOX.
SEQUENCE 332 AA; 34644 MW; 79FC71EZE44E6F82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
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MGD; MGI:98769; Tlx1.
GO; GO:0007417; P:central nervous system development; IMP.
GO; GO:0030182; P:neuron differentiation; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; S70632; AAB30542.1; JOINED EMBL; S70756, AAB30542.1; JOINED EMBL; S70629; AAB30542.1; JOINED HSSP; P14653; 1B72.
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                                                                                                                 Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
MJ0694.
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                                                                                                                                              "Complete genome jannaschii.";
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
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85.7%;
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RESULT 29
TLX1_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
T-cell leukemia homeobox protein 1 (Homeobox protein Hox-11) (Homeobox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TXT
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MEDLINE=98315212; PubMed=9651221;
                                                                                                      DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no rest
use by non-profit institutions as great as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Neurosci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              connectivity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Logan C.C., Wingate R.J.T., McKay I.J., Lumsden A.; "Tlx-1 and Tlx-3 homeobox gene expression in cranial sensory and hindbrain of the chick embryo: markers of patterned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLX1 OR HOX11.
                                                                                                                                 PROSITE; PS00027; HÓMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
HOMEOBOX; DNA-binding; Nuclear protein;
DOMALN 167 170 POLY-LYS.
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                                                                                                                                                                                               ProDom;
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                                                                                                                                                                                                            PRINTS;
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InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                          Neurosci. 18:5389-5402(1998).
FUNCTION: SEEMS TO BE INVOLVED IN THE DEVELOPMENT SENSORY INNERVATION FROM PERIPHERAL GANGLIA.
SUBCELLULAR LOCATION: Nuclear (By similarity).
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 164
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6; Conserv
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                                                  Similarity 6; Conser
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297 i
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85.7%;
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Pred. No. 26;
1; Mismatches
                                                                Score 36;
Pred. No.
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26;
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                                                                                                                                             Developmental protein.
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RESULT 30

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TIX1 HUMAN STANDARD; PRT; 330 AA. 23134; O75699; O9HCAO; O1-JUL-1993 (Rel. 26, Created) O1-JUL-1993 (Rel. 26, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) T-cell leukemia homeobox protein 1 (Homeobox
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MEDLINE=92020958; PubMed=1681546;

Kennedy M.A., Gonzalez-Sarmiento R.,

Dear T.N., Boehm T., Rabbitts T.H.;

Dear T.N., bomenbox-containing T-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92319541; PubMed=1352396;
Lu M., Zhang N., Ho A.D.;
"Genomic organization of the putative human homeobox proto-oncogene "HOX-11 (TCL-3) and its endogenous expression in T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                    Watt P.M., Ranford P.R., Kees U. "HUG-1: a novel upsteam gene nei in a T-cell leukaemia cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91289163; PubMed=1676542;
Hatano M., Roberts C.W., Minden M.,
"Deregulation of a homeobox gene, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The tcl-3 proto-onco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc.
EMBL;
                                                                                                                     This
                                                                                                                                                                                                               MEDLINE=98449474; PubMed=9778044;
Brake R.L., Kees U.R., Watt P.M.;
"Multiple negative elements contribute
proto-oncogene.";
Oncogene 17:1787-1795(1998).

-i- FUNCTION: CONTROLS THE GENESIS OF T
DNA SEQUENCE 5-GGCGGTAAGTGG-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                              modified and this st
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                                                                                                        between
                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                      eukemia
                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                             SUBCELLULAR LOCATION: Nuclear (Probable)
DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL)
CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(10;14) (Q24;Q11)
WHICH INVOLVES HOX11 AND T-CELL RECEPTOR DELTA CHAIN (TCRD) GEI
SIMILARITY: Contains 1 homeobox domain.
M75952;
M62626;
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leukemia codes for a homeobox protein.";
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AAA58662.
AAA36719.
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Primates;
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ine.";
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Catarrhini;
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PERSON; PRO0600; Flu NS1; I.
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NODSTRUCTURAL PROTEIN; Alternative splicing.
NODSTRUCTURAL PROTEIN; Alternative splicing.
NODSTRUCTURAL PROTEIN; 398B4B5AF2FDE420 CRC64;
                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                 EMBL; M25374; AAA43557.1; -. PIR; G32662; MNIVA4. HSSP; P03495; INS1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Influenza A virus (strain A/Pintail/Alberta/119/79).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
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Pfam; PF00600; Flu NS1; 1.
ProDom; PD000613; Flu NS1; 1.
Nonstructural protein; Altern
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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitech E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Pallsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.";
RN Mature 415:871-880(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION.
MEDLINE=21881936; PubMed=11884590;
Ohi M.D., Link A.J., Ren L., Jenni
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cell cycle control protein cwf16.
CWF16 OR SPAC9.13C OR SPAPJ735.01C.
GeneDB_SPombe;
Pfam; PF04502;
                                     EMBL; AL163031; CAB86262.1; -.
EMBL; AL121764; CAB57431.1; -.
                                                                                                                                          use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                      the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                      FUNCTION: Involved in mRNA splicing where it associates with cdc5 and the other cwf proteins as part of the spliceosome. SUBUNIT: Interacts with cdc5.
SUBCELLULAR LOCATION: Nuclear (Probable).
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Pfam; PF00600; Flu NS1; 1.

ProDom; PD000613; Flu NS1; 1.

ProDom; PD0060613; PD006
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Ludwig S., Schultz U., Mandler J.,
"Phylogenetic relationship of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=81001890; PubMed=7407920;
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EMBL; V01101; CAA24286.1; -.
EMBL; V00199; AAA43139.1; ALT_SEQ.
HSSP; P03495; 1AIL
                                                                                                                                                                                                                                                                                                                          Influenza A virus (strain A/Mallard/New York/6750/78), and Influenza A virus (strain A/Anas acuta/Primorje/695/76). Viruses; SSRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A. NCBI_TaxID=11435, 11323;
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                          "The B allele of the NS gene of avian influenza buriuses, bu A allele, attenuates a human influenza A virus for squirrel monkeys.";
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                                                                                               STRAIN=A/Mallard/New York/6750/78;
MEDLINE=89299445; PubMed=2525836;
Treanor J.J., Snyder M.H., London W.T., Murphy B
"The B allele of the NS gene of avian influenza"
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l (NS) genes
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P13139;
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SEQUENCE FROM N.A.
STRAIN=A/Anas acuta/Primorje/695/76;
MEDLINE=91306439; PubMed=1830182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrate by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              influenza A viruses.";
Virology 183:566-577(1991).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000256; Flu NS1.
Pfam; PF00600; Flu NS1; I.
ProDom; PD0000613; Flu NS1; 1.
Nonstructural protein; Alternative splicing SEQUENCE 230 AA; 26083 MW; CF3C4AFE2B8B;
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EMBL; M60800; AAA43130.1; -.
PIR; C32662; MNIVA2.
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"Phylogenetic relationship of the nonstructural (NS) genes
This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                     Treanor J.J., Snyder M.H., London W.T., Murphy E "The B allele of the NS gene of avian influenza A allele, attenuates a human influenza A virus f
                                                                                                                                                                                                                                                                                                                                                                                                                         Influenza A virus
NCBI_TaxID=11436;
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA negative-strand viruses; Influenza A viruses; Influenzavirus A.
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                                                                                                                                                                                                             Virology 171:1-9(1989).
                                                                                                                                                                                                                                                             monkeys.";
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                                                                                                                                             IsoId=P13139-1; Sequence=Displayed;
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                                                                                              IsoId=P13147-1; Sequence=External;
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VNS1_IADU3
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P08270;
01-AUG-1988
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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InterPro; IPR000256; Flu NS1.
Pfam; PF00600; Flu NS1; 1.
ProDom; PD00613; Flu NS1; 1.
                                                                                                                                                                                                                                                                                                                                              Pfam; PF00600; Flu_NS1; 1.
ProDom; PD000613; Flu_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M16565; AAA43512.1; -. HSSP; P03495; 1NS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87236215; PubMed=2954302;
Nakajima K., Nobusawa E., Ogawa T.,
"Genetic divergence of the NS genes
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Best Local :
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21-JUL-1986
28-FEB-2003
                                                                                                                                                                                  VNS1_IAFPR
P03500;
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_IAFPR
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01-FEB-1996
28-FEB-2003
Proc.
         MEDIJINE=81054909; PubMed=6254054;
Porter A.G., Smith J.C., Emtage J.S.;
"Nucleotide sequence of influenza virus RNA segment coding regions for NS1 and NS2 proteins overlap.";
Proc. Natl. Acad. Sci. U.S.A. 77:5074-5078(1980).
                                                                                           Influenza A virus (strain A/Fowl plague virus/Rostock/34). Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virology
[2]
                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M16564;
HSSP; P03495;
                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (s or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakajima K., Nobusawa E., C
"Genetic divergence of the
Virology 158:465-468(1987).
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MEDLINE=87236215; PubMed=2954302;
MChiicawa E., Ogawa T.,
                                                                                   NCBI_TaxID=11383;
                                                                                                                                         Nonstructural
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Influenza A virus (strain A/Tern/South Africa/61).
Viruses; ssRNA negative-strand viruses; Orthomyxov
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ProDom; PD000613; Flu_NS1; 1.
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Nakajima K.;
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al protein
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of avian
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RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Glaser P., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautter L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Gautter L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Madueno E., Maitournam A., Schlueter T., Simoes N., Tierrez A.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Wazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RC Comparative genomics of Listeria species.";
Science 294:849-852(2001):
Science 294:849-852(2001):
Science 294:849-852(2001):
Science 294:849-852(2001):
RI Science 294:849-852(2001):
Science 294:849-852(2001):
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Best Local S
Matches 7
                                                                                                                                  VNS1_IACKJ STANDARD P08274; 01-AUG-1988 (Rel. 08, C 01-AUG-1988 (Rel. 08, L 28-FEB-2003 (Rel. 41, L Nonstructural protein N
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ListiList; LMOUZDOU,
HAMAP; ME 00357; -; 1.
Pfam; PFO5066; RNA pol_delta; 1.
Pfam; PFO5066; RNA polymerase; Transcription; Complete proteome.
DNA-directed RNA polymerase; Transcription; Complete proteome.
110 178
20640 MW; 241725288916148B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes;
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MEDLINE=21537279; PubMed=11679669;
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NCBI_TaxID=11340;
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                                             Viruses; ssRNA negative-strand
Influenza A viruses; Influenzav
                                                                                            Influenza A virus (strain
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Pred. No.
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                                                                    viruses; Orthomyxoviridae;
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Best Local Similarity
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Virology 158:465-468 (1997).
-!- ALTERNATIVE PRODUCTS:
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P08272;
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MEDLINE=87236215; PubMed=2954302;
                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                        "Genetic divergence of the NS genes
Virology 158:465-468 (1987).
-i- ALTERNATIVE PRODUCTS:
-Event=Alternative Transition
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Pfam; PF00600; Flu NS1; I.
ProDom; PD000613; Flu NS1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Influenza A virus (strain A/Duck/England/1/56). Viruses; ssRNA negative-strand viruses; Orthomy Influenza A viruses; Influenzavirus A.
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                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
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s of avian
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EMBL; M16563; AAA43510.1;

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Matches 6
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Q9MUT8;
16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                             PRODOM; PD001141; Ribosomal 123; 1
PROSITE; PS00050; RIBOSOMAL 123; FALSE NEG.
Ribosomal protein; Chloroplast; rRNA-binding;
SEQUENCE 92 AA; 10714 MW; A6BBADC44DC3DAX
                                                                                                                                                Pfam; PF00276; Ribosomal_L23;
                                                                                                                                                                          EMBL; AF166114; AAF43813.1; -.
                                                                                                                                                                                                                                                                                                              lemieux C., Otis C., Turmel M.;
"Ancestral chloroplast genome in Mesostigma viride reveals an
branch of green plant evolution.";
Nature 403:649-652(2000).
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=NIES-296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MESVI
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PRINTS; PR00418; TP12FAMILY.
PRODOM; PD000742; DNA_topoisoIV;
AMARTS SM00387; HATPase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20150907; PubMed=10688199; Lemieux C., Otis C., Turmel M.;
                                                                                                                                                             InterPro; IPR001014; Ribosomal_L23.
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=41882;
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Mesostigmatales; Mesostigmataceae; Mesostigma.
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NP_BIND 196
ACT_SITE 833
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SMART; SM00433; TOP2c; 1.
SMART; SM00434; TOP4c; 1.
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56
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                                                           Similarity
                       PPKKKKKKV 9
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(Rel. 40, Last annotation update)
50S ribosomal protein L23.
                                              Conservative
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omerase; DNA-bInding; ATP-binding; Phosphorylation;
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833
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75.0%;
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Pred. No.
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Pred. No.
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                                                                                              A6BBADC44DC3DA27
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Mismatches
                                                Mismatches
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CLEAVAGE (BY SIMILARITY).
E3A992F63474BD64 CRC64;
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RESULT 19
RPOE_LISMO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RA Glaser P., Frangeul I., Buchrieser C., Rusnick C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

RA Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Ra Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

Gautier I., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones I.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

Madueno E., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

"Comparative genomics of Listeria species.";

Science 294,849-952(2001).
                                                                                                                                                                       Matches
                                                                                                                                                                                       Query Match
Best Local (
RPOE LIS
                                                                                                                                                                                                                                                       ListiList; LIN02705; -...
HAMAP; MF 00357; -; 1.
Pfam; PF05066; RNA pol_delta;
DNA-directed RNA polymerase; 7
DOMAIN 110 178
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                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                            PIR; AC1770; AC1770
                                                                                                                                                                                                                                                                                                                                                            EMBL; AL596173; CAC97931.1; -.
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STRAIN=CLIP 11262 / Serovar 6a;
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
Probable DNA-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listeria innocua.
Bacteria, Firmicutes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPOE OR LIN2705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1642;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of transcription. In the presence of the delta subunit, RNAP displays an increased specificity of transcription, a decreased affinity for nucleic acids, and an increased efficiency of RNA synthesis because of enhanced recycling (By similarity). SUBUNIT: RNAP is composed of a core of 2 alpha, a beta and a beta' subunits. The core is associated with a delta subunit and one of several sigma factors (By similarity).

SIMILARITY: BELONGS TO THE RPOE FAMILY.
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                                                                                                                                                                       Similarity 7; Conserv
                                                                                                     TTPKKKKK 102
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87.5%;
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RNA polymerase delta su
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, D052246CCC16148A CRC64;
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Pred. No. 18;
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Pfam; PF00276; Ribosomal L23; 1.
ProDom; PD001141; Ribosomal L23; 1.
PROSITE; PS00050; RIBOSOMAL L23; 1.
PROSITE; PS00050; RIBOSOMAL L23; 1.
Ribosomal protein; Chloroplast; rRNA-binding
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01-FEB-1994 (Rel. 28, Last sequence upda
15-SEP-2003 (Rel. 42, Last annotation up
Transcription initiation factor RAP74)
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PIR; S73233; S73233.
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-!- FU
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                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                               Finkelstein A., Kostrub C.F., Li J., Chavez D.P., Wang B.Q., Fang S.M., Greenblatt J., Burton Z.F.;
"A cDNA encoding RAP74, a general initiation factor for transcription by RNA polymerase II.";
Nature 355:464-467(1992).
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE=92131136; PubMed=1734284;
                                                                                                                                                                                                                                                                                                                                                                                                                           Kitajima S., Weissman S.M., Yasuko "Characterization of cDNA for the initiation factor TFIIF.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aso T., Vasavada H.A., I
Kitajima S., Weissman S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., MEDLINE=92131135; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T2FA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                Nature 355:461-464(1992)
EMBL; X64037; CAA45408.1;
                               or send an
                                                                                                                                                                                     SUBUNIT: Heterodimer of an alpha SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                       PTM: PHOSPHORYLATED.
SIMILARITY: TO OTHER TRANSCRIPTION
                                                                                                                                                                                                                                                   FUNCTION: TFIIF IS A GENERAL TRANSCRIPTION INITIATION FACTOR BINDS TO RNA POLYMERASE II AND HELPS TO RECRUIT IT TO THE
                                                                                                                                                                                                                      TRANSCRIPTION ELONGATION.
                                                                                                                                                                                                                                    INITIATION COMPLEX IN COLLABORATION WITH
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                                                           non-profit institutions as long as its content and this statement is not removed. Usage by ar
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                               email to license@isb-sib.ch).
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75.0%;
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Pred. No. 7.5;
1; Mismatches
                                            agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             large subunit of the transcription
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alpha subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Germino F.J., i Y.;
                                                                                                                                                                                                     and a beta subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
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7.5;
                                                                                                                                                       FACTOR IIF, ALPHA SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae;
                                                                                                                                                                                                                                    TFIIB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ganguly S.,
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                                                                                                                                                                                                                                    HH
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RESULT 16
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Best Local S
Matches 6
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PDB; 1127; 07-MAR-01.

PDB; 1127; 30-JAN-03.

PDB; 1NHA; 25-FEB-03.

TRANSFAC; T02168; ...
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation; 3D-structure.
CONFLICT 231 231 V
CONFLICT 361 361 F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycot
Eurotiales; Trichocomaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9Y8G8;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X64002; CAA45404.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penicillium
                                                                                                                                                           EMBL; AB029613;
HSSP; P06786; 11
                                                                                                                          [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0005674; C:transcription factor TFIIF complex; TAS. GO:0016251; F:general RNA polymerase II transcription f. GO:0005515; F:protein binding activity; TAS. GO:0003711; F:transcription co-activator activity; TAS. GO:0003717; P:transcription initiation from Pol II prof. GO:0006367; P:transcription from Pol II prof. GO:0006367; P:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Nuclear
MISCELLANEOUS: BUKARYOTIC TOPOJSOMERASE I
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS
RELAX ONLY NEGATIVE SUPERCOILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: ATP of double-stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II MAKES DOUBLE-STRAND BREAKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189968;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TPPKKKRK 8
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                                                                                         5786; 1BGW.; IPR003594; IPR003957;
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517 AA;
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                                                                                                                                                                                         BAA82356.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39, Created)
39, Last sequence update)
39, Last annotation updat
II (EC 5.99.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ascomycota; Pezizomycotina; Eurotiomycetes; comaceae; mitosporic Trichocomaceae; Penicillium.
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75.0%;
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CBFA_NFYB_topis
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Pred. No.
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F -> L (IN REF. 2)
; FOD2BE44D2F3820F
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                                                                                                                                                                                                                                                                                   (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB
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m chrysogenum.";
/DDBJ databases.
TES OF DNA BY TRANSIEN
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                                                                                                                                                                                                                                                                                                                                                                                                                    outstation
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InterPro;

IPR001241; IPR002205;

DNA_topoisoII.

topoisoIV

the distribution of Adducin-like transcripts during

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A Amanatides P.G., Scheers S.E., Li P.W., Hoskins R.A., Galle R.F., A Galcerge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Worthand M.R., Yandell M.D., Zhang Q., Chen L.X., RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G., RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G., RA Barlow R.M., Danyak R.A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Barlow R.J., Bardwarews-Pfannkoch C., Beldwin D., RA Ballew R.M., Basu A., Barchael J., Bayraktaroglu L., Beasley E.M., RA Borkova D., Betchan M.R., Bouck J., Brokstein P., Bolshakov S., RA Borkova D., Betchan M.R., Bouck J., Brokstein P., Bolshakov S., RA Borkova D., Betchan M.R., Bouck J., Brokstein P., Bolshakov S., RA Borkova D., Betchan M.R., Bouck J., Brokstein P., Bolshakov S., Chandra I., Chang Y.J., Deng Z., Mays A.D., Davies P., RA Borkova D., Betchan M.R., Bouck J., Brokstein P., Brottler P., RA Borkova D., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Borkova D., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Bodson K.J., Evangeliste C.C., Ferraz C., Ferriars S., Fleischmann W., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K., RA Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris M.L., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Harris M.L., Lang Y., Lin X., Liang Y., Lin X., Liako P., Lei Y., Levitsky A.A., Li J., Li, Liang Y., Lin X., Liako P., Lei Y., Levitsky A.A., Li J., Li, Liang Y., Lin X., Liako P., Lei Y., Muznh P., Muznh D.M., Nelson D., RA Mount S.M., Wolf M., Muzhy B., Muzhy L., Muznh D.M., Nelson D.M., Nelson D.M., Nelson D.M., Nelson D.M., Nelson D.M., Nelson J.M., Welson M., Stupki M.P., Smith T., Ra Mount S.M., Wolf M., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
- FUNCTION: REQUIRED FOR ASSEMBLING ATT RING CANALS IN - DEVELOPING EGG CHAMBERS. PROBABLY INTERACTS WITH OTHER DEVELOPMENTAL PROTEINS INVOLVED IN NURSE CELL/OCCYTE TRANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Berkerey;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22426069; PubMed=12537572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M.D., Celn:
Amanatides P.G.,
Note=No experimental confirmation available;
DEVELOPMENTAL STAGE: OOGENESIS AND EARLY EMBRYOGENESIS.
MISCELLANEOUS: 'HU-LI TAI SHAO' MEANS 'TOO FROM
                                                                                                                                                                                                                                                Name=Long;
IsoId=Q02645-1;
                                                                                                                                                                                                                                                                                                                                                                               DEVELOPING EGG CHAMBERS, PROBABL DEVELOPMENTAL PROTEINS INVOLVED THROUGH THE RING CANALS.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                  Event=Alternative
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P.G., Scherer S.E.,
                                                                                                                                                                                                                                                             Sequence=Displayed;
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Plant Mol. Biol. Rep. 13:333-335(1995)
-!- SIMILARITY; BELONGS TO THE L23P FA
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Cytoskeleton; Membrane; Developmental protein; Alternative splicing.
Cytoskeleton; Membrane; Developmental protein; Alternative splicing.
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Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner
Wambutt R., Korn B., Klein M., Poustka A.;
"Towards a catalog of human genes and proteins: sequencing ar
analysis of 500 novel complete protein coding human cDNAs.";
Genome Res. 11:422-435(2001).
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Probable RNA-binding protein KIAA0682.
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Mammalia; Eutheria; Primates;
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MEDLINE=21154917;
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ACTIVITY OF THE ESC/E(Z) COMPLEX.
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ACTIVITY OF THE ESC/E(Z) COMPLEX.
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SMART; SM00360; RRM
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SWISS-2DPAGE; Q9Y4C8; HUMAN.
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                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE=93211992; PubMed=7681599;
Ding D., Parkhurst S.M., Lipshitz H.D.;
"Different genetic requirements for anterior RNA localization
                                                    Yue L., Spradling A.C.;
"hu-li tal shao, a gene required for rir
"hu-li tal shao, a gene required for rir
Drosophila oogenesis, encodes a homolog
Genes Dev. 6:2443-2454(1992).
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16-OCT-2001 (Rel. 40, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
                                                                                      MEDLINE=94040709; PubMed=1340461;
                                                                                                       SEQUENCE FROM N.A.
                                                                                                                       NCBI_TaxID=7227;
                          TISSUE=Embryo;
                                    SEQUENCE
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7; Conserve
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RA Abril J.F., Abgayani A., Anni-J., Andrews-Pfamikoch C.R., Malawin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktargglu L., Beasley E.M.,
RA Beleson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Harris D., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McBerson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yelon S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Gibbs R.A., Myers E.W., Rubni G.M., Venter J., Shu X., Smith H.O.,
RA Gibbs R.A., Nyers E.W., Rubnin G.M., Venter J., Shu X., Smith H.O.,
RN [3]
                                                                                               MEDLINE=98226554; PubMed=9566901;
Jones C.A., Ng J., Peterson A.J., Morg
"The Drosophila esc and E(z) proteins
group_mediated_repression.";
                                                                                                                                                                                                                                                                                                             MEDLINE=97164720; PubMed=9012527; Carrington E.A., Jones R.S.; "The Drosophila Enhancer of zeste examination of wild-type and mutar Development 122:4073-4083(1996).
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
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"A Drosophila full-length cDNA resource.";
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MEDLINE=20196006; PubMed=10731132;
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Jones R.S., Gelbart w.m.,
"The Drosophila Polycomb-group gene
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MEDLINE=94019309; PubMed=8413234;
Jones R.S., Gelbart W.M.;
IDENTIFICATION IN A COMPLEX WITH RPD3;
                                                                                                                                                                                                                                                  INTERACTION
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forming multiprotein complexes, which are required to maintain the transcriptionally repressive state of homeotic genes throughout development. PGG proteins are not required to initiate repression, but to maintain it during later stages of development. They probably act via the methylation of histones, rendering chromatin heritably changed in its expressibility. Component of the Esc/Ez) complex, which methylates Lys-9 and Lys-27 residues of histone H3. Although not sufficient to methylate histone H3 by itself, it probably represents the catalytic subunit of the Esc/Ez) complex. The Esc/Ez) complex, which may recruited to DNA by Pho, is necessary but not sufficient to recruit a functional PG repressive complex that represses target genes, suggesting that the recruitment of the distinct PRC1 complex is also required to allow a subsequent represses target genes, suggesting that the recruitment of the Esc/Ez) complex is also required to Su(z)12, Rpd3, Caf1 and probably Pho. This complex is distinct from the PRC1 complex, which contains many other PcG proteins like interact together during the first 3 hours of development to establish PcG silencing.

-I- SUMILARITY: Contains 1 SANT domain.

SIMILARITY: Contains 1 SANT domain.
                                        EMBL; U00180; AAC46462.1; --
EMBL; AE003547; AAF50149.1;
EMBL; AY051785; AAK93209.1;
                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
             FlyBase; FBgn0000629; E(z).
GO; GO:0005634; C:nucleus; IDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Czermin B., Melfi R., McCabe D., Seit: "Drosophila Enhancer of zeste/ESC commethyltransferase activity that marks
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Cell 111:197-208(2002).
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METHYLTRANSFERASE ACTIVITY OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22296674;
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                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel
16-OCT-2001 (Rel
Large T antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P24597;
01-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear protein; Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF04935; SURF6; 1.
                                           ZN_FING
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                 polyomavirus, Kilham strain.";
Virology 181:469-480(1991)
-i- SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                               Pfam; PF00226; DnaJ; 1.
Pfam; PF02217; T Ag DNA bind; 1.
SMART; SM00271; DnaJ; 1.
                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                              Mayer M.,
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91196237; PubMed=1849675;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10638;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse polyomavirus (strain Viruses; dsDNA viruses, no
                                                                                               PROSITE; PS00636; DNAJ_1; FALSE_NEG.
PROSITE; PS50076; DNAJ_2; FALSE_NEG.
BEATLY protein; Nuclear protein; ATP-binding; DNA-binding;
                                                                                                                                                                                         EMBL; M55904; AAA46551.1; -.
                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 J domain.
                                                                                                                                                                 InterPro; IPR001623; DnaJ_N.
InterPro; IPR003133; T_Ag_DN
                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequence and genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0005730; C:nucleolus; 1
GO:0003723; F:RNA binding
                                                                                     replication; Zinc-finger.
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7; Conser
Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361
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                                            648
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77.8%;
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                                            MW;
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/FTId=VAR 0.14532.

T -> M (IN dbSNP:886089).

/FTId=VAR 0.14533.

T -> M (IN dbSNP:1800867).

/FTId=VAR_0.14533.
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Score 39; DB Pred. No. 18; 1; Mismatches
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Pred. No.
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                                           J-DOMAIN.
C2H2-TYPE (ATYPICAL) (BY
ATP (POTENTIAL)
, 6F7FEF95A8AB255A CRC64;
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-> N (IN REF. 1).
34F63992E3E82797 CRC64;
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                                                                                     u1-NOV-1995 (Rel. 32, Created)
15-SEP-2003 (Rel. 42, Last seque
15-SEP-2003 (Rel. 42, Last annot
Polycomb protein E(Z) (Enhancer of
E(Z) OR CG6502.
                                                                                                                                                              EZ DROME
P42124; Q9VT
01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Origin recognition
                                                                                                                                                                                                                                                                                                                                                                                                              DNA replication; Nuclear SEQUENCE 252 AA; 28106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS.
-1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: BELONGS TO THE ORC6 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1999)
-!- FUNCTION: COMPONI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Dean F.B., O'Donnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GK; Q9Y5N6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF139658; AAD32666.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
            Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
                                                Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA cloning of a homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

NUCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAN BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOWAL REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION IN AN ATP-DEPENDENT MANNER.
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                                                                                                                                                                                                                                                                                                                                             Similarity 5; Conserv
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55.6%;
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                                                                                                                 (Enhancer of zeste
                                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                  protein; DNA-binding.
6 MW; 78840387605F45FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                              Score 38;
Pred. No.
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01-NOV-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vande Waa E.A., O'Leary K.A., Kessler M.A., Scnuter L.A., Goes A.M., Mandal C., Doughty B.L., Tracy J.W.; Submitted (XXX-1995) to the EMBL/GenBank/DBBJ databases.
-!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
-!- SIMILARITY: NONE TO THE GST SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GT6_SCHMA
P46435;
                                                                                                                                                                                     EMBL; L06180; AAA29887.2; -. InterPro; IPR006958; Mak16. Pfam, PF04874; Mak16; 1.
                                                                                                                                                                                                                                                                           entities requires a license agreement (So or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Schistosomatoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schistosoma mansoni (Blood fluke).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glutathione
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00633; BROMODOMAIN 1; 2.
PROSITE; PS50014; BROMODOMAIN 2; 2.
Bromodomain; Nuclear protein; DNA-binding;
Transcription regulation; Phosphorylation;
DOMAIN 157 165 PRO-RICH.
                                                                                                                                                  Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6183;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: STRONG,
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TPPKKKRKV
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                                                                                                                           236 AA;
                                          Conservative
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
S-transferase 6 (EC 2.5.1.18) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Platyhelminthes;
Schistosomatidae;
                                                                                                                              28286
                                                             81.2%;
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87.5%;
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                                                                                                                           MW;
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RX MEDLINE=2238857; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F. Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rolas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P. H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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SUR6 HUMAN STANDARD,
SUR6 HUMAN STANDARD,
SUR6 HUMAN STANDARD,
O75683; Q9BRK9; Q9BTZ5; Q9UK24;
15-UL-1999 (Rel. 38, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                Angiolillo A., Russo G., Porcellini A., Smaldone S., Scognamiglio D'Alessandro F., Pietropaolo C.T.;
D'Alessandro F., Pietropaolo C.T.;
"The human homologue of the mouse Surf-5 gene encodes multiple alternatively spliced transcripts.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN A NUCLECLAR FUNCTION (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
-!- SIMILARITY: BELONGS TO THE SURF6 FAMILY.
                               EMBL; AF186772; AAD56587.1;
EMBL; BC003001; AAH033001.1;
EMBL; BC006197; AAH06197.1;
EMBL; BC014878; AAH14878.1;
EMBL; AJ224639; CAA12054.1;
                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as not removed. entities requires a license agreement (See
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Mammalia; Eutheria;
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InterPro; IPR003593; AAA ATI
InterPro; IPR007109; Brix.
InterPro; IPR001270; Chaprn:
Pfam; PF04427; Brix; 1.
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SEQUENCE
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Pfam; PF00226; DnaJ; 1.

SMART; SM00271; Tag DNA bind; 1.

SMART; SM00271; DnaJ; 1.

PROSITE; PS00636; DNAJ 1; FALSE NEG.

PROSITE; PS0076; DNAJ 2; 1.

PROSITE; PS50076; DNAJ 2; 1.

Barly protein; Nuclear protein; ATP-binding; DNA-binding; DNA replication; Zino-finger.

DNA replication; Zino-finger.

DOMAIN 12 75

J-DOMAIN 12 75

J-DOMAIN 12 75

J-DOMAIN 12 75

J-DOMAIN 12 75
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01-OCT-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Hypothetical protein F44G4.1 in chromosome
F44G4.1.
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         Durbin R.;
Submitted (JUL-2001) to
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-1996)
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SEQUENCE 384 AA;
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Pred. No. 7
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ATP (POTENTIAL).
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T2D1_HUMAN STANDARD; PRT; 18/2 AA
P21675;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Transcription initiation factor TFIID 250 k
(TAFFII250) (TBP-associated factor 250 kDa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The p250 subunit of native TATA box-binding cell-cycle regulatory protein CCG1.";
Nature 362:179-181(1993).
                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Nuclear.
-!- PTM: PHOSPHORYLATED BY CASEIN KINASE II
-!- SIMILARITY: Contains 2 bromodomains.
-!- SIMILARITY: Contains 1 HMG box domain.
-!- SIMILARITY: TO DROSOPHILA TAFII-230. SOW
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MEDLLINE=93196704; PubMed=7680771;
Ruppert S., Wang E.H., Tjian R.;
"Cloning and expression of human TAFII250: a TBP-associated factor
implicated in cell-cycle regulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY SEQUENCE FROM N.A.
MEDLINE=8905056; PubMed=3169001;
Sekiguchi T., Miyata T., Nishimoto T.;
Sekiguchi T., Myata T., Nishimoto T.;
"Molecular cloning of the cDNA of human X chromosomal gene (CCG1)
which complements the temperature-sensitive G1 mutants, tsBN462 au
ts13, of the BHX cell line.";
EMBO J. 7:1683-1687(1988).
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Mammalia; Eutheria; Primates;
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TAF1 OR TAF2A
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Hisatake K., Hasegawa S., Takada R.,
                                                  EMBL; D90359; BAA14374.1; EMBL; X07024; CAA30073.1;
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MEDLINE=91246200; PubMed=2038334;
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                       A40262; A40262
                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El European Bioinformatics Institute. There are no rest:
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un email to license@isb-sib.ch).
07-JUN-00.
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Catarrhini; Hominidae;
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kDa) (P250) (Cell cycle gen
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TO THREODINE 124.";

NITO TO THE SHOT ON THE VIRAL ORIGIN OF REPLICATION VIA ELABORATE INTERACTIONS WITH THE VIRAL ORIGIN OF REPLICATION. BINDS TWO ADJACENT SITES IN THE SV40 ORIGIN OF REPLICATION. BINDS TWO ADJACENT SITES IN THE SV40 ORIGIN OF REPLICATION. BINDS TWO CO. INTERACTIONS EXEMITAL FOR THE ASSEMBLY OF ATP.

C. I- SUBUNIT: FORMS HOWOHEXAMERS IN THE PRESENCE OF ATP.

C. INTERACTIONS ESSENTIAL FOR THE ASSEMBLY OF STABLE T-ANTIGEN HEXAMERS AT THE ORIGIN OF REPLICATION AND HEXAMERS ARE NEEDED FOR SUBSEQUENT ALTERATIONS IN THE STRUCTURE OF ORIGIN DNA.

C. PHOSPHORYLATED ON SER-120 AND SER-123 THREONINE RESIDUES.

PHOSPHORYLATION ON SER-120 AND SER-123 THREONINE RESIDUES.

WHILE THAT ON THREONINE-124 ENHANCES REPLICATION BY ACTIVATING THE
     InterPro; IPR001623; DnaJ N.
InterPro; IPR003133; T_Ag_DNA_bind.
Pfam; PF00226; DnaJ; 1.
Pfam; PF02217; T_Ag_DNA_bind; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS00636; DNAJ_1; FALSE_NEG.
PROSITE; PS50076; DNAJ_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as longers at its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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MCDLINE=91172186; PubMed=1848686;
MCDLINE=911721866; PubMed=1848686;
MCDLINE=911721866; PubMed=1848686;
MCDLINE=911721866; PubMed=1848666; PubMed=1848666; PubMed=1848666; PubMe
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J. Virol. 65:2098-2101(1991).
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Scheidtmann K.H., Virshup D.M., Kelly T.J.;
"Protein phosphatase 2A dephosphorylates simian virus 40 large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphorylation.";
Cell 61:735-738(1990)
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McVey D., Woelker B., Tegtmeyer P.;
Mechanisms of Bimian virus 40 T-antigen activation by phosphorylation
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MISCELLANEOUS: THE INITIAL 82 RESIDUES OF THE LARGE T AND SMALL ANTIGENS FROM SV40 ARE CODED BY THE SAME NUCLEOTIDE SEQUENCE.
SIMILARITY: Contains 1 J domain.
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SFAC; T00788; -.
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1GH6; 15-NOV-01.
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DNAJ_1; FALSE_NEG
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SEQUENCE
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                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                              Frisque R.J., Bream G.L., Cannella M.T "Human polyomavirus JC virus genome.", J. Virol. 51:458-469(1984).
                                                                                                                                                                                                                                         Polyomavirus JC.
Viruses; dsDNA viruses,
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P03072;
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                      EMBL; J02226; AAA82102.1; -. PIR; A03609; TVVPTJ.
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ATP-binding; DNA-binding; DNA replication; Zinc-finger; 3D-st
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F -> Y /TV
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REPLICATION ACTIVATION.
S->A: ENHANCED DNA REPLIC
, CB81306EF9E4E2C0 CRC64;
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A -> P (IN STRAIN 776).
Y -> P (IN STRAIN 776).
T->A: 200-FOLD REDUCTION
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BINDING TO HOST P53 PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "BK virus DNA sequence coding for the t and T antigens and evaluation of methods for determining sequence homology.";
J. Virol. 34:416-430(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Dunlop;
MEDLINE=80090082; PubMed=229976;
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Viruses; dsDNA viruses,
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21-JUL-1986
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    -!- SUBCELLULAR LOCATION: Nuclear

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang R.C.A., Wu R.; "BK virus DNA: complete nucleotide sequence of a human tumor virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=80058557;
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SMART; SM00271; DnaJ; 1.
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InterPro; IPR003133; T_Ag_DN
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genome of human papovavirus BKV.";
18:963-977(1979).
                                                                                                                                                                                               replication;
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C2H2-TYPE (ATYPICAL) (BY SIMILARITY).

ATP (POTENTIAL).

MISSING (IN STRAIN MM).

S -> N (IN STRAIN MM).

O -> K (IN STRAIN MM).

S -> V (IN STRAIN MM).
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RESULT 3
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Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                               MEDLINE=88265851; PubMed=2838952;
Graesser F.A., Scheidmann K.H., The
"In vitro phosphorylation of SV40
Virology 165:13-22(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Decaprio J.A., Ludlow J.W., Figge J., Shew J.-Y., Fige W.-H., Marsilio E., Paucha E., Livingston D.M.; "SV40 large tumor antigen forms a specific complex the retinoblastoma susceptibility gene."; Cell 54:275-283(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The finger domain of simian virus DNA-binding specificity.";
J. Virol. 64:6291-6296(1990).
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Kalderon D., Roberts B.L., Richardson W.D., Smith A.E.;
"A short amino acid sequence able to specify nuclear location.";
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"Complete nucleotide sequence of S
Nature 273:113-120(1978).
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Hoess A., Moarefi I.F., Fanning E
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Science 200:494-502(1978).
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Pan J., Ghosh P.K., Celma M.L.,
                         IN VITRO ACTIVATION OF DNA REPLICATION BY MEDLINE=90059993; PubMed=2555176;
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                                                                                                                                                                           McVey D., Brizuela L., Mohr "Phosphorylation of large to
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IN VITRO PHOSPHORYLATION
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hexamer assembly and origin melting.";
Virol. 65:3167-3174(1991).
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Herreweghe J., Volckaert G., Ysebaert M.;
quence of SV40 DNA.";
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P03070 simian viru
P03072 polyomaviru
P54073 caenorhabdi
P21675 homo sapien
P46435 schistrosoma
075683 homo sapien
P24597 mouse polyo
09y5n6 homo sapien
P42124 drosophila
094468 homo sapien
Q9p7c5
093366
P31314
P43345
Q58105
Q9d6z1
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Q9mut8
Q927t3
Q927t3
Q8y494
P08277
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RESULT 2 TALA_POVBK

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C; Genetics:

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C;Accession: F64386

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A. rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser; C.M.; Smith, H.O.; Woese, (A;Reference number: A64300; MUID:96337999; PMID:8688087

A;Accession: F64386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein MJ0694 - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C;Accession: F64386 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann R D. Suitton C
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A;Map position: 10q24/unknown
C;Keywords: homeobox; fusion protein
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                                                                                                                                                                                                                                                                      A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: C70474
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-422 <AQF>
                                                                                                                                                 A;Gene:
                                                                                                                                                                                                                                                                                                                                                              Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                   R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: garden pea SAR DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: GB:U67516; GB:L77117; NID:g2826307; PIDN:AAB98689.1; PID:g1591409;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Aquifex aeolicus
Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999;
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R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heion, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
                                                                                                                                                                                                A;Cross-references: GB.AE005672; PIDN:AAK75466.1; PID:gl4972853; GSPDB:GN00164; A;Experimental source: strain TIGR4 C;Genetics:
                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-424 <KUR>
                                                                                                                                                                                                                                                                                                                                 A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus A; Reference number: A95000; MUID:21357209; PMID:11463916 A; Accession: A95159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 C;Accession: A95159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         psr protein [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
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TIGR:SP4

S.; Heid

Search completed: December Job time : 16.12 secs 11, 2003, 09:58:51

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Cre recombinase protein - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C;Accession: JC7213
R;Koresawa, Y:; Miyagawa, S:; Ikawa, M.; Matsunami, K.; Yamada, M.; Shirakura,
J. Biochem. 127, 367-372, 2000
                                           A;Title: Synthesis of a new Cre recombinase gene based on A;Reference number: JC7213; MUID:20198248; PMID:10731707 A;Accession: JC7213
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R;Raju, K.; Tang, S.; Dube, I.D.; Kamel-Reid, S.; Bryce, D.M.; Breitman, M.L. Mech. Dev. 44, 51-64, 1993
A;Title: Charactérization and developmental expression of Tlx-1, the murine h A;Reference number: I57032; MUID:94206842; PMID:7908826
A;Accession: I57032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene Tlx-1 protein -
C;Species: M:--
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A;Residues: 1-275,'L',277-330 <LUM>
A;Cross-references: EMBL:M62626; NID:g339199; PIDN:AAA36719.1; PID:g387683
A;Cross-references: Ganzalez-Sarmiento, R.; Kees, U.R.; Lampert, F.; Dear, N.; Boehm,
  A; Molecule type: mRNA
A; Residues: 1-350 < KOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns: 192/1; 259/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: Tlx-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-332 < RES>
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C;Superfamily: unassigned homeobox proteins;
C;Keywords: DNA binding; homeobox; leukemia;
F;202-258/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated
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A;Title: HOX11, a homeobox-containing T-cell oncogene on human chromosome 10q24.
A;Reference number: A41224; MUID:92020958; PMID:1681546
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A;Residues: 1-189,'VALSPFTVTRRI',190-275,'L',277-330 <KEN>
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GB:S70632; NID:g546379; PIDN:AAB30542.1; PID:g546380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;202-258/Domain: homeobox homology <HOX>
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Pred. No. 1e+02;
1; Mismatches
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Pred. No.
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A;Cross-references: GB:X16734; NID:g525225
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RESULT 37
A61181
A; Molecule type: mRNA
A; Residues: 1-405 < DUB>
                                                         A; Reference number: A61181; A; Accession: A61181
                                                                                   A; Title: A novel human homeobox gene lies at the chromosome 10 A; Reference number: A61181; MUID: 92063028; PMID: 1683261
                                                                                                                           Blood 78, 2996-3003, 1991
                                                                                                                                          C;Accession: A61181
R;Dube, I.D.; Kamel-Reid, S.; Yuan, C.C.; Lu, M.; Wu, X.; Corpus, G.; Raimondi, S.C.;
                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 10-Mar-1994 #sequence_revision 09-May-1996 #text_change 13-Aug-1999
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A;Description: The sequence of C. elegans cosmid C45E5.
A;Reference number: Z21484
A;Accession: T34170
                                         A; Status: not compared with
                                                                                                                                                                                                                                     homeotic protein HOX11-derived mutant fusion protein - human
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A;Cross-references: EMBL:U61950; PIDN:AAC24290.1; GSPDB:GN00022; CESP:C45E5.
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A; Residues: 215-393 <ED2>
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A;Experimental source: strain Bristol N2; clone H35B03
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A;Residues: 1-393 <EDW>
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RESULT 29
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                                                                                                                                                                                                                                                                        Virology 171, 1-9, 1989

A; Title: The B allele of the NS gene of avian influenza viruses, A; Reference number: A32662; MUID:89299445; PMID:2525836

A; Molecule type: genomic RNA
A; Residues: 1-230 < TRE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: BLIGHT NO. C; Superfamily: influenza virus no C; Keywords: alternative splicing
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                 MNIVA3
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Proc. Natl. Acad. Sci. U.S.A. 77, 5074-5078, 1980
A;Title: Nucleotide sequence of influenza virus RNA segment A;Reference number: A93858; MUID:81054909; PMID:6254054
A;Accession: A04091
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C;Superfamily: influenza virus nonstructural protein NS1
C;Keywords: alternative splicing; nonstructural protein
                                                                                                                                                                                                                                                                                                                                                                                   nonstructural protein NS1 - influenza A virus (strain A/mallard/New York/6750/78)
C;Species: influenza A virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 08-Apr-1994
C;Accession: C32662
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C;Species: influenza A virus
C;Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 30-Sep-1993
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 nonstructural
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                                    J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
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6; Conserv
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                                                                                                         PPKKKRKV 9
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                                                                           PPKOKRKM 222
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influenza A virus (strain A/mallard/New York/6874/78)
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Pred. No.
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2; Mismatches
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C;Genetics:
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A; Residues: 1-330 < HAT >
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75.0%;
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R;Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R. Virology 171, 1-9, 1989
A;Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, A;Reference number: A32662; MUID:89299445; PMID:2525836
A;Accession: G32662
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A;Title: The B allele of the NS gene of avian influenza viruses, A;Reference number: A32662; MUID:89299445; PMID:2525836
A;Accession: E32662
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C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 08-Apr-1994
C;Accession: E32662
A;Cross-references: GB:S38742; NID:g232582; PIDN:AAB19293.1; PID:g23258 R;Lu, M.; Gong, Z.; Shen, W.; Ho, A.D.
EMBO J. 10, 2905-2910, 1991
A;Title: The tcl-3 proto-oncogene altered by chromosomal translocation A;Reference number: S17311; MUID:92007734; PMID:1717256
                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Peb-1992 #sequence revision 28-Peb-1992 #text_change 24-Sep-1999
C;Accession: A4085; S17311; Ā41224
R;Hatano, M.; Roberts, C.W.M.; Minden, M.; Crist, W.M.; Korsmeyer, S.J.
Science 253, 79-82, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: segment 8
C;Superfamily: influenza virus nonstructural protein NS:
C;Keywords: alternative splicing; nonstructural protein
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C;Superfamily: influenza virus nonstructural
C;Keywords: alternative splicing; nonstructu
                                                                                                                                                                                                                     A;Title: Deregulation of a homeobox gene, HOX11, by the t(10;14) in T cell leukemia A;Reference number: A40855; MUID:91289163; PMID:1676542 A;Accession: A40855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: influenza A virus
C;Date: 31-Mar_1991 #sequence_revision 31-Mar-1991 #text_change 08-Apr-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: tcl-3 proto-oncogene
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Pred. No.
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A; Map position: segment 8
A; Map position: segment 8
C; Superfamily: influenza virus nonstructural protein NS1
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1394
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A; Gene: lin2705
C; Superfamily:
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AH1394
C;Accession: AH1
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A;Title: Genetic divergence of the NS genes of avian influenza viruses.
A;Reference number: A94361; MUID:87236215; PMID:2954302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999 C;Accession: A27846
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C;Species: influenza A virus
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A;Experimental source: strain EGD
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A; Residues: 1-227 < NAK>
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A; Residues: 1-178 < GLA>
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Best Local S
Matches 6
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Best Local S
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Best Local S
Matches 7
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PPKQKRKM 219
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Fsihi, H.
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A; Molecule type: genomic A; Residues: 1-227 < NAK>
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A;Title: Genetic divergence of the NS genes of avian influenza A;Reference number: A94361; MUID:87236215; PMID:2954302
                                                                                             nonstructural protein NS1 - influenza A virus (strain A/Duck/Ukraine/63 [H3N8]) (fragmen C;Species: influenza A virus (Strain A/Duck/Ukraine/63 [H3N8]) (fragmen C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999 C;Accession: G27846
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: segment 8
C;Superfamily: influenza virus nonstructural protein NS1
C;Keywords: alternative splicing; nonstructural protein
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, Virology 158, 465-468, 1987
A;Title: Genetic divergence of the NS genes of avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nonstructural protein NS1 - influenza A virus (strain A/Tern/South Africa/61 [H5N3]) (fr C;Species: influenza A virus C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999 C;Accession: E27846
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C; Superfamily: influenza virus nor
C; Keywords: alternative splicing;
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A;Cross-references: GB:M16563;
C;Genetics:
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C;Date: 30-Sep-1989 #seque
C;Accession: C27846
R;Nakajima, K.; Nobusawa,
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                                      Virology 158, 465-468, 1987
A; Title: Genetic divergence
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A; Residues: 1-227 < NAK>
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A;Title: Genetic divergence of the NS genes of avian influenza A;Reference number: A94361; MUID:87236215; PMID:2954302
                                                                            R; Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima,
                                                                                                                                                                                     MNI VX7
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A; Residues: 1-227 < NAK>
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C;Species: influenza A virus
A; Accession: G27846
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hypothetical protein C33G3.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C;Accession: T19690
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A;Introns: 57/3; 72/3; 95/1; 143/3; 240/3; 285/3; 336/3; 419/3; 585/2; 658/3; 690/3; 75
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A;Experimental source: clone C33G3
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A;Reference number: Z19163
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A; Accession: T49709
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N;Alternate names: protein B23L21.220
hypothetical protein A233R - Chlorella virus PBCV-1 C;Species: Chlorella virus PBCV-1 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 C;Accession: T17724
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A;Experimental source: BAC clone B23L21; strain OR74A
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A; Residues: 1-863 <SCH>
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                                                                  RESULT 21
T17724
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Accession: T19690
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Sequence Database,
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75.0%;
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Pred. No. 1.4e+02;
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Pred. No. 1.6e+02;
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                15-Oct-1999 #text_change 04-Mar-2000
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1e+02;
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, G.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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C;Superfamily: Chlorella virus PBCV-1 hypothetical protein A233R
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A;Residues: 1-112 <GRA>
A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96601.1
A;Experimental source: specific host Chlorella strain NC64A
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Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AC1770
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-178 <GLA>
A; Rosidues: 1-178 <GLA>
A; Experimental source: strain Clip11262
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C;Accession: AC1770
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Ar
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A;Molecule type: DNA
A;Residues: 1-162 <HEI>
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C;Accession: F82493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein VCA0173 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae
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                                                                                                                                                                                                                                                                                                   B. subtilis RNA polymerase delta chain homolog lin2705 [imported] - Listeria C;Species: Listeria innocua C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Date: 27-Nov-2001
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A; Experimental source:
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Best Local S
Matches 7
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D.; Jones, L.M.; Karst, U.
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7; Conserva
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ce: serogroup
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87.5%;
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Pred. No. 54;
1; Mismatches
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Durand, L.; D
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Dussurget, O.;
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                           GSPDB:GN00178
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Fsihi, H
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ribosomal protein L23 - red alga (Porphyra purpurea) chloroplast (;Species: chloroplast Porphyra purpurea (;Species: chloroplast Porphyra purpurea (;Date: 23-Oct-1998 #sequence_revision 23-Oct-1998 #text_change 22-Jun-1999 (;Date: 23-Oct-1998 #text_change 22-Jun-1999 (;Accession: S73233 R;Reith, M.; Munholland, J. Plant Mol. Biol. Rep. 13, 333-335, 1995 Plant Mol. Biol. Rep. 13, 335-335 Plant Mol. Biol. Rep. 
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A;Note: sequence extracted from NCBI backbone (NCBIN:128
R;Yue, L.; Spradling, A.C.
Genes Dev. 6, 2443-2454, 1992
A;Title: hu-li tai shao, a gene required for ring canal
A;Reference number: A46392; MUID:94040709; PMID:1340461
A;Accession: A46392
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A;Experimental source: egg C;Comment: This protein is required for assembling actin at ring canals in developing C;Comment: This protein is required for assembling actin at ring canals in developing
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Proc. Natl. Acad. Sci. U.S.A. 90, 2512-2516, 1193
A;Title: Different genetic requirements for anterior RNA localization revealed by A;Reference number: A47397; MUID:93211992; PMID:7681599
A;Accession: A47397
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A;Note: DKFZp586F1023.1
C;Superfamily: unassigned ribonucleoprotein repeat-conta:
                                                                                                                                                                                     A; Reference number: S73108
A; Accession: S73233
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A;Cross-references: FlyBase:FBgn0004873
A;Cross-references: EMBL:U38804; NID:g1276652; PIDN:AAC08198.1; PID:g1276778
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
                                                                           A; Residues: 1-110 < REI>
                                                                                                                                                       A;Status: nucleic
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                                                                                                             A; Molecule type: DNA
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Matches 6
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Best Local (
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                                                                                                                                                   acid sequence not shown; translation
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87.5%;
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                              Porphyra purpurea chloroplast genome.
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                                     DNA binding; transcription
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A; Molecule type: protein
A; Residues: 35-45;50-68;90-100;154-163;383-394;426-434 <FIN2>
                                             A;Molecule type: mRNA
A;Residues: 1-230,'I',232-360,'L',362-517 <FIN1>
A;Cross-references: EMBL:X64002; NID:g35870; PIDN:CAA45404.1;
A;Accession: S25403
                                                                                                                                                                          A, Title: A cDNA encoding RAP74, a general initiation factor A, Reference number: S20589; MUID:92131136; PMID:1734284
                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 27-40;91-97;445-460;505-517 < ASO2>
R; Finkelstein, A.; Kostrub, C.F.; Li, J.; Chavez, D.P.;
Nature 355, 464-467, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Characterization of cDNA for the large subunit of the transcription initiation A;Reference number: S20248; MUID:92131135; PMID:1734283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Aso, T.; Vasavada, H.A.; Kawaguchi, T.; Germino, F.J.; Ganguly, S.; Kitajima, S.; Nature 355, 461-464, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change C;Accession: S20248; S25402; S20589; S25403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription factor TFIIF large chain - human
N;Alternate names: ATP-dependent DNA helicase RAP30/74 chain RAP74; RNA polymerase II-as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Primary structure of the alcelaphine herpesvirus 1 genome A;Reference number: Z14840; MUID:97404659; PMID:9261371 A;Accession: T03131 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T03131
R;Ensser, A.; Pflanz, R.; Fleckenstein,
J. Virol. 71, 6517-6525, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alkaline exonuclease (EC 3.1.11.-) - alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
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A;Genome: chloroplast
A;Genome: chloroplast
C;Superfamily: Escherichia coli ribosomal protein L23
C;Keywords: chloroplast; protein biosynthesis; ribosom
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X64037; NID:g35868; PIDN:CAA45408.1; PID:g35869
A;Accession: S25402
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A; Residues: 1-517 < ASO1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AF005370; NID:g2337967; PIDN:AAC58083.1; C;Superfamily: human cytomegalovirus alkaline exonuclease
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A; Residues: 1-485 < ENS>
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|PPKRKRKL 317
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Pred. No.
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                                                                                                                                                                                                                                                       Wang,
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                                                                          PID:g35871
                                                                                                                                                                                                                                                       B.Q.; Fang, S.M.; Greenbla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-Nov-1999
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A;Map position: Xq13.1-Xq13.1
C;Superfamily: transcription initiation factor IID 250K chain; bromodomain homology; HMG C;Superfamily: transcription initiation factor IID 250K chain; duplication; phosphop F;I-1893/Product: transcription initiation factor IID 250K chain splice form 1 #status F;I-1893/Product: transcription initiation factor IID 250K chain splice form 2 #F;I-17,199-1893/Product: transcription initiation factor IID 250K chain splice form 2 #F;I-17,199-1893/Product: transcription initiation factor IID 250K chain splice form 2 #F;I-17,199-1893/Product: transcription initiation factor IID 250K chain splice form 2 #F;I-17,199-1893/Product: transcription signal F;I-1995/Domain: HMG box homology <HRO1>
F;1379/Region: nuclear location signal F;1426-1481/Domain: bromodomain homology <HRO1>
F;1549-1604/Domain: bromodomain homology <HRO2>
F;1549-1604/Domain: bromodomain homology <HRO2>
F;137,1740,1751,1847,187/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #sf;678,1054,1684/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #sf;1020,1361/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #sf;1020,1361/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #sf;1020,1361/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #sf;1020,1361/Binding site: phosphate (Thr)
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Nature 362, 175-179, 1993
A;Title: Cloning and expression of human TAF(II)250: a TBP-associated factor A;Reference number: S32352; MUID:93196704; PMID:7680771
                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: A37945
R;Mayer, M.; Doerries, K.
Virology 181, 469-480, 1991
A;Title: Nucleotide sequence and genome organization of A;Reference number: A37945; MUID:91196237; PMID:1849675
A;Accession: A37945
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R;Hisatake, K.; Hasegawa, S.; Takada, R.; Nakatani,
Nature 362, 179-181, 1993
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A;Cross-references: GDB:120573; OMIN:313650
A;Map position: Xq13.1-Xq13.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1372-1379;1386-1604,'DNE','CSSKANDIVCLIQYCSSQIEELRF'
A;Cross-references: EMBL:X07024
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C, Superfamily: large T antigen;
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A; Residues: 1-649 < MAY>
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Species: Polyomavirus muris (mouse polyomavirus)
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Residues: 'P';587-595;1009-1022;1351-1355;1357-1360 <HIS>
Note: 1351-Val, 1353-Lys, and 1354-Glu were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 12-Dec-1997
Accession: A37945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
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                                                                                                                        Matches
                                                                                                                                                                                  Query Match
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140
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                                                                                                                 Similarity 7; Conserv
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   TPPKKKAKM 148
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                                                          TPPKKKRKV 9
                                                                                                                                                                                                                                                dnaJ amino-terminal homology
                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                              protein
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                                                                                                                                                  81.2%;
                                                                                                                                                                                                                                                                                                        dnaJ amino-terminal homology
                                                                                                                                                     Score 39;
Pred. No.
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Pred. No. 1e+02;
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                                                                                                                        Mismatches
                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                             #status atypical <DNJ>
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                                                                                                                                                                               Length 649,
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RESULT 12

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protein F01D4.5 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: G88012
R;Accession: G88812
R;Anonymous, The C: elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Fittle: Genome sequence of the nematode C. elegans: a platform for investigating biolog.
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans.
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
G88812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, October 1996 A;Reference number: Z19278 A;Accession: T20460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Wild,
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A;Residues: 1-195 <STO>
A;Cross-references: GB:chr_IV; PIDN:CAB02880.1; PID:g3875478; GSPDB:GN00022; CESP:F01D4.
A;Note: predicted using Gemefinder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns: 36/1; 97/3; 109/3; 183/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z81054; PIDN:CAB02880.2; GSPDB:GN00022; CESP:F01D4.5
                                                                                                                            R; Ansorge, W.; Wirkner, U.; Mewes, submitted to the Protein Sequence I
                                                                                                                                                                     C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000 C;Accession: T17297
                                                                                                                                                                                                                  hypothetical protein DKFZp586F1023.1 - C;Species: Homo sapiens (man)
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                    A; Molecule type: mRNA
A; Residues: 1-960 < ANS
                                                               A;Status: preliminary
                                                                                 A; Reference number: Z18729
A; Accession: T17297
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Best Local
Cross-references: EMBL:AL117547
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                   16 SPPKKRRRV
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                                                                                                                              Sequence Database,
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Pred. No. 29;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38;
Pred. No.
                                                                                                                                                     H.W.; Gassenhuber, J.; Wiemann,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                         human
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                                                                                                                              September
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R; anonymous, The C. elegans Sequencing Consortium.

R; anonymous, The C. elegans Sequencing Consortium.

Rcience 282, 2012-2018, 1998

A; Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A; Reference number: A75000; MUID:99069613; PMID:9851916

A; Note: see websites genome. wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C ele

A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A; Accession: B88252
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                                                                                                                                                                                                                                                                                                                                                                               protein F44G4.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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A; Residues: 1-754 < STO>
                                                                                                                                                                                        A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                            C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, June 1995
A;Reference number: Z19530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:Z70034; PIDN:CAA93858.2; GSPDB:GN00020; CESP:F44G4.1
A;Experimental source: clone C18E9
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Best Local S
Matches 7
Best Loc
Matches
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Best Local
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                                     Query Match
                                                                                              Gene:
                                                                                                                Genetics:
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                 Local
                                                                                                F44G4.1
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Similarity 7; Conserv
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                                                                                                                             GB:chr_II;
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                 83.3%;
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87.5%;
                                                                                                                                 PIDN: CAA90124.1;
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Pred. No.
                 Pred. No.
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Pred. No.
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41;
                 46;
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                                     Length 754;
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Indels
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Gaps
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A; Molecule type: mRNA
A; Residues: 1-177,1993 <SEK>
A; Cross-references: GB:D90359; NID:g559319; PIDN:l
A; Note: nucleotide sequence not complete
R; Sekiguchi, T.; Miyata, T.; Nishimoto, T.
submitted to the EMBL Data Library, February 1988
A; Reference number: S03005
A; Accession: S03005
EMBO J. 7, 1683-1687, 1988

A;Title: Molecular cloning of the cDNA of human X chrom A;Reference number: S00830; MUID:89005056; PMID:3169001 A;Accession: S00830
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A40262
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A;Cross-references: GB:D26114; NID:g439485; PIDN:BAA05110.1; PID:g474971
A;Cross-references: GB:D26114; NID:g439485; PIDN:BAA05110.1; PID:g474971
C;Superfamily: transcription initiation factor IID 250K chain; bromodomain homology; HMG
C;Keywords: alternative splicing; cell cycle control; DNA binding; duplication; phosphop
F;1190-1269/Domain: HMG box homology <HMG1>
F;1190-1269/Domain: bromodomain homology <HRG1>
F;1346-1353/Region: nuclear location signal
F;1400-1455/Domain: bromodomain homology <HRG2>
F;1523-1578/Domain: bromodomain homology <HRG2>
F;1523-1578/Domain: bromodomain homology <HRG2>
F;1513-1714,1725,1821,1843/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase
F;994,1335/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase)
F;994,1335/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase)
F;1511,1714,1725,1821,1843/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase)
F;994,1335/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase)
                                                                                                                                                              A; Molecule type: mRNA
A; Residues: "Mr. (60-17,199-1604, 'DNECSSKANDIVCLIQYCSSQIEELRF'
A; Cross-references: EMBL:X07024; NID:g29732; PIDN:CAA30073.1; PI
A; Note: this sequence has been revised in reference A40262
A; Note: this sequence has been revised in reference A40262
R; Sekiguchi, T.; Miyata, T.; Nishimoto, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A40262; MUID:91246200; PMID:2038334 A;Accession: A40262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Jun-2000
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A40262; 803005; 800830; 832352; 832353
C;Accession: A40262; 803005; 800830; 832352; 832353
R;Sekiguchi, T, Nohiro, Y, Nakamura, Y; Hisamoto, N.; Nishimoto, T.
Mol. Cell. Biol. 11, 3317-3325, 1991
A;Title: The human CCG1 gene, essential for progression of the G-1 phase, es
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: 210K nu N;Contains: transcription
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A;Title: The CCG1/TAFFI250 gene is mutated in thermosensitive G1 mutants of the BHK21
A;Reference number: I48155; MUID:94215915; PMID:8163200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: I48155
R;Hayashida, T.; Sekiguchi, T.; Noguchi, E.; Sunamoto, H.; Ohba,
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C;Date: 10-Sep_1999 #sequence_revision 10-Sep-1999 #text_change 15-Oct-1999
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Similarity 87.5%;
7; Conservation
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Pred. No. 1e+02;
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                                                                                           chromosomal
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                                                                                           gene (CCG1) which compleme
                                                                                                                                                                                                                                                          PID:g29733
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acid sequence not

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A;Experimental source: strain MM
R;Yang, R.C.A.; Young, A.; Wu, R.
J. Virol. 34, 416-430, 1980
A;Title: BK virus DNA sequence coding for the t and T antigens and A;Title: BK virus DNA sequence coding for the t and T antigens and A;Reference number: A92981; MUID:80185151; PMID:6246273
A;Reference number: A92981; MUID:80185151; PMID:6246273
A;Recsion: A92981
A;Recsion: A92981
A;Residues: 1-695 < YA2>
A;Experimental source: strain MM
A;Experimental source: strain MM
C;Superfamily: large T antigen; dnaJ amino-terminal homology
C;Keywords: early protein; 9lycoprotein
F;12-62/Domain: dnaJ amino-terminal homology #status atypical <DNJ:F;155/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 1-33,35-
A; Cross-references:
RESULT 4
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R;Fiers, W.; Contrerss, R.; Haegeman, G.; Rogiers, R.;
Nature 273, 113-120, 1978
A;Title: Complete nucleotide sequence of SV40 DNA.
A;Reference number: A36763; MUID:78156432; PMID:205802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The genome of simian virus 40. A;Reference number: A03631; MUID:78159686; PMID:205947 A;Accession: B03631
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Science 200, 494-502,
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A;Experimental source: strain 776
C;Comment: The initial 82 residues of the large T and small t antigens C;Cuperfamily: large T antigen; dnaJ amino-terminal homology
C;Superfamily: large T antigen; dnaJ amino-terminal homology
C;Kupwords: acetylated amino end
F;12-62/Domain: dnaJ amino-terminal homology #status atypical <DNJ>
F;1/Modified site: acetylated amino end (Met) #status experimental
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Best Local S
Matches 9
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Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 12-Dec-1997
Accession: B03631; B36763; A03607
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Cross-references: GB:V01109; GB:J02039; NID:g60851; PIDN:CAA24302.1; PID:g60852
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Best Local
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100.0%; Pred. No. 2;
tive 0; Mismatches
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                                                                                                     (polyomavirus JC)
(bion 25-Feb-1985 #text_change 16-Jul-1999
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Pred. No. 2.1;
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      PMID:6086957
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A; Decure type: DNA
A; Rolecule type: DNA
A; Residues: 1-286 <STO>
A: Cross-references: GB: AE002093; NID: g4512650; PIDN: AAD21705.1; GSPDB: GN00139
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A; Residues: 1-688 <FRI>
A; Cross-references: GB:J02226; GB:J02227; EMBL:V01118; NID:g1083524;
C; Superfamily: large T antigen; dnaJ amino-terminal homology
E;12-62/Domain: dnaJ amino-terminal homology #status atypical <DNJ>
                                                                                                                                                                                                                                                                                                                                                                        R;Johnson, D.; Stellyes, L.
R;Johnson, D.; Stellyes, L.
submitted to the EMBL Data Library, Decemb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein At2g20620 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F33D4.6b - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 01-Dec-2000 C;Accession: T32557; T32558
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A;Map position: 2
C;Superfamily: Ar
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Nature 402, 761-768,
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                                                                                                                A;Molecule type: DNA
A;Residues: 1-404,'VTFCFMHF' <JO2>
A;Cross-references: EMBL:AF036702; PIDN:AABB8378.1; GSPDB:GN00022; CESP:F33D4.6a
                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                        A;Accession: T32557
                                                                                                                                                                                                                                                                                                                                                        A; Reference number: Z21190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Map position: 4
A;Introns: 131/3; 164/2; 215/2; 237/2; 276/3; 293/3; 380/3; 404/3
                                                A; Gene: CESP:F33D4.6b; CESP:F33D4.6a
                                                                                           A; Experimental source: strain Bristol
                                                                                                                                                                                                     A; Accession: T32558
                                                                                                                                                                                                                       A; Experimental source: strain Bristol
                                                                                                                                                                                                                                            A; Residues: 1-672 < JOH>
A; Cross-references: EMB1
                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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se: strain Bristol N2; clone F33D4
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: pir1:*
2: pir2:*
3: pir3:*
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Match Length DB
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Gapop 10.0 , Gapext 0.
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Sequence 11, Application US/10006760
Publication No. US20030186385A1
GENERAL INFORMATION:
APPLICANT: Koide, Shohei
TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND
TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF
FILE REFERENCE: 176/60901
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; OTHER INFORMATION: plasmid sequence
US-10-314-669-12
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PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/376,053
PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR FILING DATE: 2002-88-05
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Matches 8
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Best Local Similarity 100.0%; Pred. No.
Matches 8; Conservative 0; Mismatci
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
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CURRENT APPLICATION NUMBER: US/10/314,669
CURRENT FILING DATE: 2002-12-09
                                                                                                                                                                                            NAME/KEY: UNSURE
LOCATION: (199)..(205)
OTHER INFORMATION: Xaa at positions 199, 200,
OTHER INFORMATION: 205 can be any amino acid
                                                                                                                                                                                                                                                                                              NAME/KEY: UNSURE
LOCATION: (147)..(151)
OTHER INFORMATION: Xaa at positions 147, 148, 149, 150, and 151 can
OTHER INFORMATION: be any amino acid
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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PPKKKRKV 28
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                                                                                                      89.6%; Score 43; DB 12; Length 215; 100.0%; Pred. No. 20;
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Search completed: December 11, 2003, 10:13:38 Job time : $33.4 \ \text{secs}$

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PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 266
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 221
LENCTH: 210
TYPE: PRT
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PRIOR FILING DATE: 2001-12-07
PRIOR PPLICATION NUMBER: US 60/376,053
PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR FILING DATE: 2002-08-02
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CURRENT APPLICATION NUMBER: US/10/314,669
CURRENT FILING DATE: 2002-12-09
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PRIOR APPLICATION NUMBER: US 60/338,441
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/376,053
PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR FILING DATE: 2002-08-02
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CURRENT APPLICATION NUMBER: US/10/314,669
CURRENT FILING DATE: 2002-12-09
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ORGANISM: Artificial Sequence
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Lee, Dong-Ki
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Lee, Yangsoon
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Lee, Seong-il
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Lee, Yangsoon
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100.0%;
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Pred. No.
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20;
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NUMBER OF SEQ ID NOS: 266
SOFTWARE: FASCSEQ for Windows Version 4.0
SEQ ID NO 264
LENGTH: 211
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
OTHER INFORMATION: plasmid sequence
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                                                                                                       RESULT 39
US-10-314-669-12
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CURRENT APPLICATION NUMBER: US/10/314,669
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/338,441
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/376,053
PRIOR APPLICATION NUMBER: US 60/400,904
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Best Local
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                                                                        Sequence 12, A
Publication No
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                           GENERAL
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PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR FILING DATE: 2002-08-05
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APPLICANT:
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                                             APPLICANT:
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Lee, Yangsoon
                                                                        Application US/10314669 No. US20030194727A1
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Lee, Dong-Ki
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5. US20030194727A1
            Park, Kyung-Soon
Lee, Dong-Ki
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ilarity 100.0%;
Conservative
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                                             Jin-Soo
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2279-007001
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Wongi
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20;
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Yang, Hy-Tee, Yangsoon

Young-Soon Hyo-Young

Seong-il Horim

100.0%;

Pred. No. 17;

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APPLICANT: Seol, Wongi
APPLICANT: Lee, Seong-il
APPLICANT: Lee, Seong-il
APPLICANT: Yang, Hyo-Young
APPLICANT: Yang, Hyo-Young
APPLICANT: Jang, Young-Soon
APPLICANT: Jang, Young-Soon
TITLE OF INVENTION: PHENOTYPIC SCREEN OF CHIMERIC PROTEINS
FILE REFERENCE: 12279-007001
CURRENT APPLICATION NUMBER: US/10/314,669
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/338,441
PRIOR FILING DATE: 2001-12-07
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Publication No.
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 266
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
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Publication No. US20030194727A1
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Matches 8; Conserva
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PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/401,089
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CURRENT APPLICATION NUMBER: US/10/314,669
CURRENT FILING DATE: 2002-12-09
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APPLICANT: Park, Kyung
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PRIOR FILING DATE: 2001-12-07
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OTHER INFORMATION: plasmid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 209
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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Lee, Dong-Ki
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Lee, Yangsoon
Jang, Young-Soon
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Lee, Dong-Ki
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APPLICANT: Jang, YOUNG-SOON
TITLE OF INVENTION: PHENOTYPIC SCREEN OF CHIMERIC PROTEINS
FILE REFERENCE: 12279-007001
CURRENT APPLICATION NUMBER: US/10/314,669
CURRENT FILING DATE: 2002-12-09
FRIOR APPLICATION NUMBER: US 60/338,441
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/376,053
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR FILING DATE: 2002-04-26
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR FILING DATE: 2002-08-05
PRIOR FILING DATE: 2002-08-05
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US-10-314-669-16
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SEQ ID NO 14
LENGTH: 209
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 209
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Matches
                                                                   Matches
                                                                                                   Query Match
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PRIOR FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 266
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PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR FILING DATE: 2002-08-02
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                                                                                                                                                      OTHER INFORMATION: plasmid sequence
                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                             TYPE: PRT
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                                                                                     Local Similarity
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14 PPKKKRKV 21
                           2 PPKKKRKV 9
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Lee, Seong-il
Yang, Hyo-Young
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Lee, Dong-Ki
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Lee, Yangsoon
                                                                   Conservative
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                                                                                     100.0%;
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100.0%; Pred. No.
tive 0; Mismatc!
                                                                                                   89.6%;
                                                                   0; Mismatches
                                                                                     Score 43; ; Pred. No.
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                                                                                                     DB 12; Length 209;
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                                                                   Indels
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RESULT 36 US-10-314-669-260 ; Sequence 260, Ap

Application US/10314669

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; OTHER INFORMATION: plasmid sequence US-10-314-669-231
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US-10-314-669-229
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PRIOR APPLICATION NUMBER: US 60/338,441
PRIOR TILING DATE: 2001-12-07
PRIOR PELICATION NUMBER: US 60/376,053
PRIOR PILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR FILING DATE: 2002-08-05
PRIOR FILING DATE: 2002-08-05
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 231
LENGTH: 130
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Best Local Similarity
Matches 8; Conserv
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SEQ ID NO 228
LENGTH: 158
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                                                    GENERAL INFORMATION:
                                                                    Sequence 229, Application US/10314669 Publication No. US20030194727A1
                                                                                                                                                                                                                                             Matches
APPLICANT: Kim, Jin-Soo
APPLICANT: Park, Kyung-
APPLICANT: Lee, Dong-Ki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jang, Young-Soon
APPLICANT: Jang, Young-Soon
TITLE OF INVENTION: PHENOTYPIC SCREEN OF CHIMERIC PROTEINS
FILE REFERENCE: 12279-007001
FILE REFERENCE: 12279-007001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                            FEATURE: OTHER INFORMATION: plasmid sequence
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                           Local Similarity
les 8; Conserv
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: Lee, Horim
: Lee, Seong-il
: Tang, Hyo-Young
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Lee, Yangsoon
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                   Kyung-Soon
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100.0%; Pred. No.
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100.0%; Pred. No.
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APPLICANT: Yang, Hyo-Young
APPLICANT: Lee, Yangsoon
APPLICANT: Lee, Yangsoon
APPLICANT: Lang, Young-Soon
TITLE OF INVENTION: PHENOTYPIC SCREEN OF CHIMERIC PROTEINS
FILE REFERENCE: 12279-007001
CURRENT APPLICATION NUMBER: US/10/314,669
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/338,441
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2001-04-26
PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR FILING DATE: 2002-08-05
PRIOR FILING DATE: 2002-08-05
PRIOR FILING DATE: 2002-08-05
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US-10-314-669-262
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PRIOR APPLICATION NUMBER: US 60/338,441
PRIOR FILING DATE: 2001-12-07
PRIOR PRILING DATE: 2001-12-07
PRIOR PILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR FILING DATE: 2002-08-02
PRIOR PILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR APPLICATION NUMBER: US 60/401,089
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 229
LENGTH: 158
                                                                                                                        SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 262
LENGTH: 181
TYPE: PRT
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Best Local
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Query Match
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CURRENT APPLICATION NUMBER: US/10/314,669
CURRENT FILING DATE: 2002-12-09
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                                                           ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: plasmid sequence
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les 8; Conservative
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Lee, Dong-Ki
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Lee, Yangsoon
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Yang, Hyo-Young
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5. US20030194727A1
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100.0%; Pred. No.
  89.6%;
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  Score 43;
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    DB 12;
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  Length 181;
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                                                                                                                                                LENGTH: 102
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-965-703-52
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                                                                          Query Match
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Matches 8
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 79
                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 52
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Best Local :
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APPLICANT: Thomas, Wayne
APPLICANT: Hopkine, Richard
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: diverse expression libraries
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/965,703
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/191,355
PRIOR FILING DATE: 2000-03-22
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CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/568,229
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,711
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/269,799
PRIOR TILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: PCT/US01/09050
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kápitskaya, Marianna Zinovjevna
APPLICANT: Cress, Dean Ervín
TITLE OF INVENTION: NO. US20020119521Alel Ecdysone Receptor-Based Inducible Gene Exp.
FILE REFERENCE: A01020B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rohm and Haas Company APPLICANT: Palli, Subba Reddy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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8; Conserv
PPKKKRKV 11
                          PPKKKRKV 9
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                                                                      89.6%; Score 43; ilarity 100.0%; Pred. No. Conservative 0; Mismatcl
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APPLICANT: Jang, Young-Soon
ITILE OF INVENTION: PHENOTYPIC SCREEN OF CHIMERIC PROTEINS
FILE REFERENCE: 12279-007001
CURRENT APPLICATION NUMBER: US/10/314,669
CURRENT FILING DATE: 2002-12-09
FRIOR APPLICATION NUMBER: US 60/338,441
PRIOR TILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/376,053
PRIOR APPLICATION NUMBER: US 60/376,053
PRIOR FILING DATE: 2002-04-26
PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR APPLICATION NUMBER: US 60/401,089
PRIOR APPLICATION NUMBER: US 60/401,089
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US-10-314-669-231
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US-10-314-669-230
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PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/376,053
PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/400,904
PRIOR APPLICATION NUMBER: US 60/401,089
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Best Local Similarity
Matches 8; Conserv
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SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 230
LENGTH: 130
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APPLICANT: Kim, Jin-Soo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 230, Publication No.
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/314,669
CURRENT FILING DATE: 2002-12-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Lee, Yangsoon
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Lee, Dong-Ki
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Lee, Yangsoon
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o. US20030194727A1
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Lee, Dong-Ki
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Pred. No.
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US-10-372-003A-63
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PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,711
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71
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APPLICANT: Watt, Paul
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Best Local :
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APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: diverse expression libraries
FILE REFERENCE: FBRIC40.001CP1
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thomas, Wayne
APPLICANT: Hopkins, Richard
ITILE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: diverse expression libraries
FILE REFERENCE: FBRIC40.001CP1
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/568,229
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,711
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NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
                                                                                                                                                                        OTHER INFORMATION: synthetic clone BGF05 with first open reading OTHER INFORMATION: frame
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; OTHER INFORMATION: synthetic clone BGF06 with first open reading ; OTHER INFORMATION: frame US-10-372-003A-67
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US-10-372-003A-67
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 75
LENGTH: 57
TYPE: PRT
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APPLICANT: Watt, Paul
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LENGTH: 55
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Best Local Similarity
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APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: diverse expression libraries
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APPLICANT: Thomas, Wayne
APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: diverse expression libraries
FILE REFERENCE: FBRIC40.001CP1
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PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,711
PRIOR FILING DATE: 1999-05-05
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CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/568,229
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SOFTWARE: FastSEQ for Windows Version 4.0
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21 PPKKKRKV 28
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No. US20030215846A1
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100.0%; Pr
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Pred. No.
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Pred. No.
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US-09-883-649A-16
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PRIOR APPLICATION NUMBER: 08/486,549
PRIOR APPLICATION NUMBER: 08/486,549
PRIOR APPLICATION NUMBER: 08/486,549
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Word/No. US20020136708A1epad, saving as .txt file, modifying Patentin Ver.
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PRIOR
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                                                                                                 TELEPHONE: 617-832-100
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE: USA
COUNTRY: USA
2109-2170
20109-2170
20109-2170
20109-2170
MOLECULE TYPE:
                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-069.03
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,572
PILING DATE: 29-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gyuris, Jeno
APPLICANT: Lamphere, Lou
APPLICANT: Lamphere, Lou
APPLICANT: Beach, David H.
TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
TITLE OF INVENTION: RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                              LENGTH: 24 amino acid
TYPE: amino acid
STRANDEDNESS:
                       TOPOLOGY:
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APPLICATION NUMBER: 08/080,727
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100.0%; Pred. No.
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GENERAL INFORMATION:
APPLICANT: Howley, Peter M.
APPLICANT: Howley, John
APPLICANT: Kasukawa, Hiroaki
TITLE OF INVENTION: COMPOSITIONS AND METHODS FO!
FILTE OF INVENTION: PAPILLOMAVIRUS-INFECTED CE:
FILE REFERENCE: HMV-041.01
CURRENT APPLICATION NUMBER: US/10/161,499
CURRENT APPLICATION NUMBER: US/09/347,504
PRIOR APPLICATION NUMBER: US/09/347,504
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 79
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US-10-161-499-8
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US-09-862-179A-37
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PATENT NO. US20020147306A1
GENERAL INFORMATION:
APPLICANT: Lin, Danny
APPLICANT: Pawson, Anthony
                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENCTH: 24
TYPE: PRT
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SEQ ID NO 37
LENGTH: 24
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                                                                   Matches
                                                                                 Query Match
Best Local Similarity
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Publication No. US20030044427A1
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CURRENT APPLICATION NUMBER: US/09/862,179A
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PAWSON, ARTHORY
TITLE OF INVENTION: PEPTIDES THAT MODULATE THE INTERACTION OF B CLASS EPHRINS
TITLE OF INVENTION: AND PDZ DOMAINS
                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Simian Virus 40
                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: RGD/SV40 OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 PPKKKRKV 21
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14 PPKKKRKV 21
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                     PPKKKRKV 9
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                                                                                 89.6%; Score 43;
100.0%; Pred. No.
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; OTHER INFORMATION: Protein localization sequence US-09-967-772-8
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US-10-133-973-106
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NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: No. US20030199009Aleborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/10083849B Publication No. US20030199009A1
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Best Local Similarity
                                                                        SOFTWARE: PatentIn version 3.1 SEQ ID NO 20
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TITLE OF INVENTION: METHODS AND COMPOSITIONS COMPRISING RENILLA GFP
FILE REFERENCE: A-68531-3/RMS/CYO
CURRENT APPLICATION NUMBER: US/10/133,973
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US/60/290,287
PRIOR APPLICATION NUMBER: US/60/290,287
                                                                                                                                                                FILE REFERENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
                                                                                                                                                                                                                          APPLICANT: Mumberg, Dominik
APPLICANT: Donner, Peter
TITLE OF INVENTION: Modifications of Apoptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/710,058 PRIOR FILING DATE: 2000-11-10
                                                                                                                            PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-20
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                                                                                                            NUMBER OF SEQ ID NOS: 20
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ORGANISM: Artificial sequence
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FEATURE:
              ORGANISM: Chicken anemia virus
                                  TYPE: PRT
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; Pred. No. 6.1e+05;
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RESULT 17
US-10-335-517-8
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CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US/09/967,772
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 09/459,956
PRIOR FILING DATE: 1999-12-13
PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: US 08/765,860
PRIOR FILING DATE: 1996-12-19
PRIOR FILING DATE: 1996-12-19
PRIOR FILING DATE: 1996-10-16
PRIOR FILING DATE: 1996-10-6
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LENGTH: 8
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Publication No.
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APPLICANT: Graham, Frank L.
APPLICANT: Ng, Philip
APPLICANT: Parks, Robin J.
APPLICANT: Parks, Robin J.
APPLICANT: Bacchetti, Silvia
APPLICANT: Anglana, Mauro
TITLE OF INVENTION: A SYSTEM FOR PRODUCTION OF HELPER DEPENDENT ADENOVIRUS VECTORS
TITLE OF INVENTION: USE OF ENDONUCLEASES
FILE REFERENCE: AdVec11CA
CURRENT APPLICATION NUMBER: US/09/883,649A
CURRENT FILING DATE: 2001-06-19
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 1999-12-30
                                                                                                                                                                                                                                                                                           Sequence 16, Application US/09883649A Patent No. US20020136708A1
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Matches 8; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GONZALEZ, Jesus
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS
FILE REFERENCE: REGEN1290-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA APPLICANT: TSIEN, ROGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MISC_FEATURE OTHER INFORMATION: amino acid sequence encoding the SV40-Large T nuclear localizatic OTHER INFORMATION: n signal
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No.
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5. 6.1e+05;
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Sequence 5, Application US/10006760

Publication No. US20030186385A1

GENERAL INFORMATION:
APPLICANT: Koide, Shohei

TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND
TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF
FILE REFERENCE: 176/60901

CURRENT APPLICATION NUMBER: US/10/006,760

CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER 60/249,756

PRIOR APPLICATION NUMBER: US/10/006,760

COURRENT FILING DATE: 2000-11-17

NUMBER OF SEQ ID NOS: 73

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 201
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Best Local Similarity
Thes 9; Conserva
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NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 290, Applic Publication No. US20 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1-Endogenous; Constitutively Activated Human G
TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Behan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US/09/170,496
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: B42-FNfn10 fusion protein
                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:Human/murine OTHER INFORMATION: chimeric single chain binding polypeptide OTHER INFORMATION: (C6ML3-98Fv'-L2-nls)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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9; Conserv
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o. US20030105292A1
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ilarity 100.0%;
Conservative 0
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100.0%; Pred. No. 4.5;
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Pred. No. 18;
0; Mismatches
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RESULT 14
US-09-967-772-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09967772
Patent No. US20020164577A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1 SEQ ID NO 7
                                             APPLICANT: TSIEN, ROGER
APPLICANT: GONZALEZ, Jesus
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS
FILE REFERENCE: REGEN1290-5
CURRENT APPLICATION NUMBER: US/09/967,772
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 09/459,956
PRIOR FILING DATE: 1999-12-13
PRIOR PELICATION NUMBER: US 08/765,860
PRIOR PELICATION NUMBER: US 08/765,860
PRIOR PELICATION NUMBER: US 08/765,860
PRIOR FILING DATE: 1996-12-19
PRIOR PELICATION NUMBER: US 08/765,860
PRIOR PELICATION NUMBER: US 08/765,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/949,780 CURRENT FILING DATE: 2001-09-10 PRIOR APPLICATION NUMBER: US 60/236,117 PRIOR FILING DATE: 2000-09-28 NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhang, Ying-Hui
APPLICANT: Leliveld, Sirik R.
TITLE OF INVENTION: A Delivery Method
TITLE OF INVENTION: Apoptin
FILE REFERENCE: 2906-5001.1US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: No. US20020061296Aleborn, Mathieu H.M. APPLICANT: Voorhoeve, Pieter M.
                                                                                                                                                                                                                                                                          APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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LOCATION: (90)...(96)
OTHER INFORMATION: Xaa at any position can be any
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OTHER INFORMATION: Xaa at any position can be any amino acid FEATURE:
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Local Similarity 88.9%;
les 8; Conservative
APPLICATION NUMBER: US 08/481,977
                   APPLICATION NUMBER: PCT/ US96/09652 FILING DATE: 1996-06-06
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Pred. No.
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13;
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Publication No. US20030069173A1 GENERAL INFORMATION:

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RESULT 9
US-10-200-879-95
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NAME: SULLIVAN, SALLY A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 32-95D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
TELEPHANE: (303)499-8080
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 48; DB 11; Length 40; Best Local Similarity 100.0%; Pred. No. 0.71; Matches 9; Conservative 0: Micmarche.
                                                                                                                                                                                                                                            Sequence 95, Application US/10200879 Publication No. US20030144230A1 GENERAL INFORMATION:
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SCHIFFERLI, KEVIN P.

GEBEYEHU, GULILAT
TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
NUMBER OF SEQUENCES: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/911,569

FILING DATE: 23-Jul-2001

CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/039,780
FILING DATE: 16-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
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CORRESPONDENCE ADDRESS:

ADDRESSEE: GREENLEE, WINNER & SULLIVAN
STREET: 5370 MANHATTAN CIRCLE, SUITE 201
                                                              SHIH, POJEN
JESSE, JOEL A.
SCHIFFERLI, KEVIN P.
SCHIFFERLI, GULILAT
TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
NUMBER OF SEQUENCES: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 95:
                                                                                                                                                                                                                        APPLICANT: HAWLEY-NELSON, PAMELA
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ZIP: 80303
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                                                                                                                                                                                                                                                                                                                                                                                               TPPKKKRKV 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAN, JIANQING
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                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Huston, James S.
APPLICANT: Wile, Pierre
APPLICANT: Zhu, Quan
APPLICANT: Laurent, Olivier
APPLICANT: Marasco, Wayne A
APPLICANT: Scherman, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: SULLIVAN, SALLY A.

REGISTRATION NUMBER: 32-9-
REFERENCE/DOCKET NUMBER: 32-9-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
TELEPAX: (303)499-8080
TELEPAX: (303)499-8089
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
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                                                             APPLICANT: Laurent, Olivier
APPLICANT: Marasco, Wayne A.
APPLICANT: Scherman, Daniel
TITLE OF INVENTION: BIOENGINEBRED VEHICLES FOR TARGETED NUCLEIC ACID
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 23611-A USA
CURRENT APPLICATION NUMBER: US/09/888,721
CURRENT APPLICATION NUMBER: US/09/888,721
CURRENT ETLING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/213,653
PRIOR FILING DATE: 2000-06-23
NUMBER: 05 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055 15 055
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NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2
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FILING DATE: 23-JUL-2001

• APPLICATION NUMBER: US 09/039,780
FILING DATE: 16-MAR-1998
APPLICATION NUMBER: US 08/818,200
FILING DATE: 14-MAR-1997
APPLICATION NUMBER: US 08/658,130
FILING DATE: 04-JUN-1996
APPLICATION NUMBER: US 08/477,354
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: not relevant TOPOLOGY: linear
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                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 33
                                                                                        Query Match
Best Local
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Best Local S
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CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 09/242,131
PRIOR FILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: PCT/JP96/03861
PRIOR FILING DATE: 1996-12-27
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Takeda, Katsuo
APPLICANT: Hasegawa, Mamoru
TITLE OF INVENTION: PHAGE WITH NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nakanishi, Mahito
APPLICANT: Nagoshi, Emi
APPLICANT: Akuta, Teruo
APPLICANT: Takeda, Katsuo
                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 50026/015001
                                                                                                                                                                TYPE: PRT
ORGANISM: Simian virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 94:
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NAME: SULLIVAN, SALLY A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 32-95E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                    1 TPPKKKRKV 9
                                                                       Similarity
9; Conserv
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TPPKKKRKV 21
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FILING DATE: 23-JUL-2001
APPLICATION NUMBER: US 09/039,780
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TELEFAX: (303)499-8089
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                                                                                        100.0%; Score 48; DB
100.0%; Pred. No. 0.6;
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                                                                       Mismatches
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                                                                                                                                               ; ORGANISM: Simian Virus US-09-844-813-8
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US-09-876-904A-24
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                                                                                                                                                                                 SEQ ID NO 8
LENGTH: 35
TYPE: PRT
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Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTICE TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
NUMBER OF SEQ ID NOS: 629
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SEQ ID NO 24
LENGTH: 34
                                                                       Matches
                                                                                                         Query Match
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Best Local :
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APPLICANT: Hasegawa, Mamoru
TITLE OP INVENTION: PHAGE WITH NUCLEAR LOCALIZATION SIGNAL
FILE REFERENCE: 50026/015001
CURRENT APPLICATION NUMBER: US/09/844,813
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 09/242,131
PRIOR FILING DATE: 2000-07-06
PRIOR FILING DATE: 2000-07-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nakanishi, Mahito
APPLICANT: Nagoshi, Emi
APPLICANT: Akuta, Teruo
                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1996-12-27
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/JP96/03861
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                                                                       Local Similarity hes 9; Conserv
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                  1 TPPKKKKRKV
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Pred. No. 0.63;
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Pred. No. 0.61;
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RESULT 8 US-09-911-569-95 ; Sequence 95, Application US/09911569

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GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
                                                                                                                                                                                                            Sequence 94, Application US/09911569
Publication No. US20030069173A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/584,043
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 217/189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/805,301
FILING DATE: 12-Max:-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                  JESSE, JOEL A.
SCHIFFERLI, KEVIN P.
GEBEYEHU, GULILAT
TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
NUMBER OF SEQUENCES: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 83:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREENLEE, WINNER & SULLIVAN
STREET: 5370 MANHATTAN CIRCLE, SUITE 201
                                                                                                                                                                        APPLICANT: HAWLEY-NELSON, PAMELA LAN, JIANQING
                                                                                                                                                                                                                                                                                                                                                                                       1 TPPKKKRKV 9
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 90071-2066
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Mims, Martha P.
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/200,879
FILING DATE: 23-0u1-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: SULLIVAN, SALLY A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 32-95D
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             GEBEYEHU, GULILAT
TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HAWLEY-NELSON,
LAN, JIANQING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/911,569 FILING DATE: 23-Jul-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                     ADDRESSEE: GREENLEE, WINNER & SULLIVAN
STREET: 5370 MANHATTAN CIRCLE, SUITE 201
CITY: BOULDER
STATE: CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (303)499-8080
TELEFAX: (303)499-8089
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No. US20030144230A1
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JESSE, JOEL A.
SCHIFFERLI, KEV
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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seq length: 2000000000
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/ cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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9 US-09-844-813-8
11 US-09-911-569-95
12 US-10-200-879-95
10 US-09-888-721-44
15 US-10-251-386-290
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US-09-805-301-83
US-09-911-569-94
12 US-10-200-879-94
US-09-844-813-2
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         Sequence 30, Appl
Sequence 94, Appl
Sequence 94, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 7, Appli
                                                                                                                                                                                                                                                                                                     Description
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43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43
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-10-	-10-314-669-22	-10-006-760-	0-006-760-	-10-006-760-1	-10-006-760-	-10-314-669-1	14-66	-10-314-669-2	-10-314-669-2	-10-314-669-1	-10 - 31	-10-314-669-1	14-669-	-10-314-669-	14-669-22	14-669-	-10-314-	-09-965-703-5	-10-372-003A-7	US-10-372-003A-75	72-003A-6	0-372-003A-	-10-	-10-161-	62-179	US-08-902-572-10	-09-883-6	0-335-51	US-10-083-849B-20
e 22	equence 222	e 14,	e 8,	e 17,	e 11,	e 12,	e 264	e 221	e 260	e 16,	e 14,	e 10,	e 262	e 229	e 228	e 231	e 23(e 52,	e 79,	e 75,	e 67,	e 63,	e 71,	е 8,	ce 37,	10,	e 16,	е 8,	Sequence 20, Appl

ALIGNMENTS

RESULT 1

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Sequence 30, Application US/09888721

Patent No. US20020132990A1

GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Wils, Pierre
APPLICANT: Zhu, Quan
APPLICANT: Zhu, Quan
APPLICANT: Zhu, Olivier
APPLICANT: Zhu, Olivier
APPLICANT: Scherman, Daniel
ITILE OF INVENTION: BIOENGIMEERED VEHICLES FOR
ITILE OF INVENTION: DELIVERY
FILLE REFERENCE: 23611-A USA
CURRENT APPLICATION NUMBER: US/09/888,721
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/213,653
PRIOR APPLICATION NUMBER: 60/213,653
PRIOR FILLNG DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN VET. 2.0

SEQ ID NO 30
LENGTH: 9
TYPE: PRI
COZANISM: Simiar virus 40
TYPE: PRI
COZANISM: Simiar virus 40
RESULT 2
US-09-805-301-83
; Sequence 83, Application US/09805301
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                                                                                                                                                                                                         Query Match 100.0%; Score 48; DB 10; Best Local Similarity 100.0%; Pred. No. 6.1e+05; Matches 9; Conservative 0; Mismatches 0;
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SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TOPOLOGY: linear
TOPOLOGY:
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/969,038 FILING DATE: October 30, 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/370,225
FILING DATE: January 9, 1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Interaction Trap System for Isolating TITLE OF INVENTION: No. 5786169el Proteins NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                      NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                     APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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CITY: Boston
STATE: Massac
                                                 ADDITION OF THE STREET: STREET: SOSTON MASSAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08 FILING DATE: June 5, 1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                 COUNTRY: U.S.A. ZIP: 02110-2804
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                                                   Massachusetts
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Golemis, Erica
                                                                                         225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.6%; Score 43; DB 1; I
100.0%; Pred. No. 2.5e+05;
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US-08-853-733B-27
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Matches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY/AGENT INFORMATION:
NAME: PAUL T. CLARK
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/160001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,733B
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/625,209
APPLICATION NUMBER: US 08/625,209
APPLICATION NUMBER: US 08/625,209
APPLICATION NUMBER: 32,503
APPLICATION NUMBER: 32,503
APPLICATION NUMBER: 32,503
APPLICATION NUMBER: 32,503
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  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0 SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,498
REFERENCE/DOCKET NUMBER: 32,503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)832-7000
FORMATION FOR CEO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lamphere, Lou
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: Cdc37 Cell-Cycle Regulatory Protein,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag, & Eliot, LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gyuris, Jeno
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CITY: B
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                                                                                                                                                                                  US 08/625,209
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                                                                                                                                                                                                                                                                                         Version #1.25
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US-08-370-225-5
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                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/969,038

PILING DATE: 10/30/92

ATTONNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: Brent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM 52" Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Interaction Trap System for Isolating TITLE OF INVENTION: No. 5580736el Proteins NUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson
                                    REFERENCE/DOCKET NUMBER: 00786/143001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEPHAX: (617) 542-8906
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REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: US
FILING DATE: 29 JAN 19
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APPLICANT: Golemis, Erica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Paul T. Clark
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STRANDEDNESS: N/A
TOPOLOGY: linear
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nes 8; Conservative (
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                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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100.0%; Pred. No.
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                                                             Query Match
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/464,05:
PILING DATE: 05 JUN 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                            TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INVERACTING PROTEINS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
CITY: E
                                                                                                                                         TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: linear
                                                                                                                                                                                                                                                 TELEPHONE: (617) 542-8906
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                                                                                                                                                                                            LENGTH:
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                       2 PPKKKRKV 9
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                                                                              89.6%;
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100.0%; Pred. No. 2.5
cive 0; Mismatches
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                                                             Score 43; DB 1; L; Pred. No. 2.5e+05; 0; Mismatches 0;
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RESULT 38 US-08-461-859-5 ; Sequence 5, Ap

Application US/08461859

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Best Local Similarity
                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMEER: US 08/588,201
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UFLA:062\KITTELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Zolotu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
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FILING DATE: 01/18/1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara 8.
REGISTRATION NUMBER: 33,92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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APPLICANT:
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                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White
STREET: P. O. Box 4433
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Houston
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Hauswirth, William W.
Muzyczka, Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                   (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (512) 418-3100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.6%; Score 43; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White & Durkee
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                                                                                                                                                                                                                                                    US/08/893,327
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ARR: UFLA:039\KIT
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US-09-459-956-8
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CURRENT FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: 08/765,860
PRIOR FILING DATE: 1999-05-08
PRIOR APPLICATION NUMBER: 08/481,977
PRIOR APPLICATION NUMBER: 08/481,977
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1996-06-06
NUMBER OF SEQ ID NOS: 22
PRIOR FILING DATE: 1996-06-06
                                                                                                                                                                                                                                                                                                                 US-08-011-398B-5
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LENGTH: 8
TYPE: PRT
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                                                                                                                                                                                                                                                                           Sequence 5, Application US/08011398B Patent No. 5512473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tsien, Roger Y.
APPLICANT: Gonzalez, III, Jesus E.
APPLICANT: GONZALEZ, III, JESUS E.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS
TITLE OF INVENTION: OPTICAL METHODS
                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Roger Bren
APPLICANT: Antonis S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Eukaryote
FEATURE:
NAME/KEY: VARIANT
LOCATION: (0)...(0)
OTHER INFORMATION: Nuclear (import) protein targeting sequence
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED TITLE OF INVENTION: MOLECULES AND METHODS
                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                    COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                       STATE:
                                                                                                                      STREET:
                                                                                                                                          ADDRESSEE:
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8; Conservative
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                                                                   Massachusetts
                                                                                                                        225 Franklin Street
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                                                                                                                                                                                                                                            Roger Brent
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                                                                                                                                          Fish & Richardson
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100.0%;
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pred. No.
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SEQ ID NO 290
LENGTH: 1310
TYPE: PRT
ORGANISM: Homo sapiens
US-09-170-496D-290
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                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: Receptors
FILE REPERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 290, Application US/09170496D Patent No. 6555339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 9; Conserv
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APPLICATION NUMBER: 60/036,28
PILING DATE: 27-JAN-1997
ATTORNEY,AGENT INFORMATION:
NAME: Seide, Rochelle K
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: AP30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-705-5000
TELEPHONE: 212-705-5020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFORMATION FOR SEQ ID NO:
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LENGTH: 136 amino acid
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OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 50 STREET: 50 YORK CITY: New York TATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Baker & Botts, L.L.P. STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
120
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                               1 TPPKKKRKV 9
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                                                                 Similarity 9; Conserv
TPPKKKKKV 128
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                                                                 Conservative
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                                                                               100.0%; Score 48; DB 4; Length 1310; 100.0%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 48; DB 3
100.0%; Pred. No. 0.59;
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                                                               Mismatches
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RESULT 32
US-09-169-605-6
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US-08-588-201-6
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: ZOLOTUKTH, William W.
APPLICANT: Muzyczka, Nicholas
TITLE OF INVENTION: Humanized Gree:
TITLE OF INVENTION: Humanized Gree:
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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Best Local Similarity
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COUNTRY: USA
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                      Sequence
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COMPUTER READABLE FORM:
MEDIUM TYPB: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,201
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 3,928
REFERENCE/DOCKET NUMBER: UFLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zolotukhin, Sergei APPLICANT: Hauswitth, William W APPLICANT: Muzyczka, Nicholas TITLE OF INVENTION: Humanized G TITLE OF INVENTION: and Methods NUMBER OF SEQUENCES: 14
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                                                                                                                  STATE:
                                                                                                                                                    ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
77210-4433
                                                                                                                                     CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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STREET: P.
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                                                                                                                                                                                                                                                                                                                                      6, Application US/09169605
o. 5968750
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Conservative
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                                                                                                                                                                                                                                           Humanized Green Fluorescent Protein Genes
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100.0%; Pred. No. 2.5
cive 0; Mismatches
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William W.
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US-09-039-780A-95
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SEQ ID NO 1
LENGTH: 39
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6376248
GENERAL INFORMATION:
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Best Local Similarity
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Patent No. 60937
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APPLICANT: Wolff, Jon A.

TITLE OF INVENTION: A METHOD FOR COVALENT ATTACHMENT OF COMPOUNDS TO GENES FILE REFERENCE: COVALENT ALEACHMENT to Genes
CURRENT APPLICATION NUMBER: US/08/990,015A
CURRENT FILING DATE: 1997-12-12
EARLIER APPLICATION NUMBER: 60/050842
EARLIER FILING DATE: 1997-05-26
RARLIER FILING DATE: 1997-05-26
NUMBER OF SEQ ID NOS: 11
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APPLICANT: Budker, Vladimir
APPLICANT: Hagstrom, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: CONTAINS OTHER INFORMATION: SEQUENCES FROM THE SV40 GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
         COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/039,780A

FILING DATE: 16-Max-1998

CLASSIFICATION: CURKNOWN>

ATTORNEY/AGENT INFORMATION:

NAME: SULLIVAN, SALLY A.

REGISTRATION NUMBER: 32,064

REGISTRATION NUMBER: 32,064
                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   GEBEYEHU, GULILAT
TITLE OF INVENTION: PERTIDE-ENHANCED TRANSFECTIONS
NUMBER OF SEQUENCES: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
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                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: GREENLEE, WINNER & SULLIVAN STREET: 5370 MANHATTAN CIRCLE, SUITE 20
                                                                                                                                                                                                                                                                                                                           STATE: CO
                                                                                                                                                                                                                                                                                                                                               CITY: BOULDER
REFERENCE/DOCKET NUMBER: 32-95C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAWLEY-NELSON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JESSE, JOEL A.
SCHIFFERLI, KEVIN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHIH, POJEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAN, JIANQING
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APPLICANT: Christine, Rainer
TITLE OF INVENTION: USE OF CELLULAR TRANSPORT SYSTEMS FOR
TITLE OF INVENTION: THROUGH THE NUCLEAR ENVELOPE
FILE REFERENCE: 30430.1USWO
CURRENT APPLICATION NUMBER: US/09/869,875
CURRENT APPLICATION NUMBER: US/09/869,875
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: PCT/DE00/00061
PRIOR APPLICATION NUMBER: DE 199 00 513.3
PRIOR FILING DATE: 1099-01-08
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: DE 199 33 939.2
PRIOR APPLICATION NUMBER: DE 199 33 939.2
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US-09-869-875-7
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US-09-014-438-2
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                            Sequence 2, Application US/09014438
Patent No. 6168929
GENERAL INFORMATION:
APPLICANT: Bloas, James M.
APPLICANT: Brodsky, Jeffrey L.
TITLE OF INVENTION: METHOD OF IDENTIFYING AGENTS
TITLE OF INVENTION: THAT DISRUPT THE INTERACTION OF SV40 T ANTIGEN WITH
TITLE OF INVENTION: DNAK HOMOLOGUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1 SEQ ID NO 7
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-07-20 NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Siebenkotten, APPLICANT: Christine, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 95: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: PNA-NLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 67
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                       57 TPPKKKRKV 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (303)499-8080
TELEFAX: (303)499-8089
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; TYPE: PRT
; ORGANISM: Simian virus
US-09-615-283-2
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US-09-615-283-2
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                                    US-09-242-131A-8
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                    SOFTWARE:
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Best Local (
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 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
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Patent No. 6235521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                       APPLICANT: Nakanishi, Mahito
APPLICANT: Nagoshi, Emi
APPLICANT: Akuta, Teruo
APPLICANT: Takeda, Katsuo
APPLICANT: Hasegawa, Mamoru
TITLE OF INVENTION: PHAGE WITH NUCLEAR LOCALIZATION SIGNAL
FILE REFERENCE: 50026/015001
                                                                                                                                      PRIOR FILING DATE: 1996-08-09
PRIOR APPLICATION NUMBER: PCT/JP96/03861
PRIOR FILING DATE: 1996-12-27
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/242,131A
CURRENT FILING DATE: 199-09-10
PRIOR APPLICATION NUMBER: 8/227787 JP
PRIOR FILING DATE: 1996-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/242,131
PRIOR FILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: PCT/JP96/03861
PRIOR FILING DATE: 1996-12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 50026/015001
CURRENT APPLICATION NUMBER: US/09/615,283
CURRENT FILING DATE: 2000-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nakanishi, Mal
APPLICANT: Nagoshi, Emi
APPLICANT: Akuta, Teruo
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TITLE OF INVENTION: PHAGE WITH NUCLEAR LOCALIZATION SIGNAL
                                                  LENGTH: 35
TYPE: PRT
ORGANISM: Simion Virus 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 9; Conserv
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                                                                                                                         FastSEQ for Windows Version 4.0
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 100.0%;
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 Score 48;
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Length 35;
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; SEQ ID NO 8; LENGTH: 35; TYPE: PRT; ORGANISM: Simian Virus 40 US-09-615-283-8
                                                                                US-08-990-015-2
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                                                                                                                                                                            NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 37
TYPE: PRT
Best Local Similarity Matches 9; Conserv
                                    Query Match
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Best Local (
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                                                                                                                                                                                                                                                                          TITLE OF INVENTION: A METHOD FOR COVALENT ATTACHMENT OF COMPOUNDS TO GENES FILE REFERENCE: COVALENT Attachment to Genes CURRENT APPLICATION NUMBER: 1097-12-12
EARLIER APPLICATION NUMBER: 60/050842
EARLIER FILING DATE: 1997-05-26
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Budker, Vladimir
APPLICANT: Hagstrom, James E.
APPLICANT: Sebestyen, Magdolna G.
APPLICANT: Wolff, Jon A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hasegawa, Mamoru
TITLE OF INVENTION: PHAGE WITH NUCLEAR LOCALIZATION SIGNAL
FILE REFERENCE: 50026/015001
CURRENT APPLICATION NUMBER: US/09/615,283
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/242,131
PRIOR PILING DATE: 2000-07-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nakanishi, Mahito
APPLICANT: Nagoshi, Emi
APPLICANT: Akuta, Teruo
APPLICANT: Takeda, Katsuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/JP96/03861 PRIOR FILING DATE: 1996-12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 12
                                                                                                FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CONTAINS
OTHER INFORMATION: SEQUENCES FROM THE SV40 GENOME
                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 TPPKKKRKV 22
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  Conservative
                    100.0%; Score 48; DB 3; Length 37; 100.0%; Pred. No. 0.19;
<u>,</u>
Mismatches
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  Indels
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Gaps
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Query Match
Best Local Similarity
Matches 9; Conserve
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              CURRENT APPLICATION NUMBER: US/08/969,137A
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 25
                                                                                                                                                                                       Patent No. GENERAL INFORMATION:
GENERAL INFORMATION:
KANDEL, ERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 94,
                                                                                                                                                                                                                               Patent No. 650919
                                                                                                           APPLICANT: KANDEL, ERIC
APPLICANT: MAYFORD, MARK
TITLE OF INVENTION: DNA REGULATORY ELEMENT FOR THE EXPRESSION OF TRANSGENES IN NEURON
TITLE OF INVENTION: MOUSE FOREBRAIN
FILE REFERENCE: 0575/52776
FILE REFERENCE: 0575/52776
FILE REFERENCE: 0575/52776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/039,780A
FILING DATE: 16-Mar-1998
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: SULLIVAN, SALLY A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 32-95C
TELECOMMINICATION INFORMATION:
TELEPHONE: (303)499-8080
TELEFAX: (303)499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JESSE, JOEL A.
SCHIFFERLI, KEVIN P.
GEBEYLEHU, GULILAT
TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                       14 TPPKKKRKV 22
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                                                                                                                                                                                                                                              Application US/08969137A
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Pred. No.
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US-09-869-875-2
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US-09-242-131A-2
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Matches 9; Conserv
SOPTWARE: FASTSEQ for Winds SEQ ID NO 2
LENGTH: 33
TYPE: PRT
ORGANISM: Simian virus 40
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APPLICANT: Nagoshi, Emi
APPLICANT: Akuta, Teruo
APPLICANT: Takeda, Katsuo
APPLICANT: Takeda, Katsuo
APPLICANT: Hasegawa, Mamoru
TITLE OF INVENTION: PHAGE WITH NUCLEAR LOCALIZATION SIGNAL
FILE REFERENCE: 50026/015001
CURRENT APPLICATION NUMBER: US/09/242,131A
CURRENT FILING DATE: 199-09-10
PRIOR APPLICATION NUMBER: 8/227787 JP
PRIOR APPLICATION NUMBER: 8/227787
PRIOR FILING DATE: 1996-12-27
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: SIMIAN VIRUS 40 US-08-969-137A-1
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CURRENT APPLICATION NUMBER: US/09/869,875
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: PCT/DE00/00061
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: DE 19 00 513.3
PRIOR APPLICATION NUMBER: DE 19 33 939.2
PRIOR APPLICATION NUMBER: DE 19 33 939.2
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
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SEQ ID NO 2
LENGTH: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Siebenkotten, Gregor
APPLICANT: Christine, Rainer
TITLE OF INVENTION: USE OF CELLULAR TRANSPORT SYSTEMS FOR THE TRANSFER OF NUCLEIC ACI
TITLE OF INVENTION: THROUGH THE NUCLEAR ENVELOPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 100.0%;
Local Similarity 100.0%;
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FastSEQ for Windows Version 4.0
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Pred. No. 0.14;
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Pred. No. 0.13;
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; OTHER INFORMATION: SV21
US-09-869-875-1
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Best Local :
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Patent No. 6521456
                                                                                        ATTOKNESS.

NAME: SAXE, Bernhard D.

REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 1873:
REFERENCE/DOCKET NUMBER: 1873:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1702-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: DE 199 33 939.2
PRIOR FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/DE00/00061
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: DE 199 00 513.3
PRIOR FILING DATE: 1999-01-08
PRIOR FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/869,875
CURRENT FILING DATE: 2001-07-06
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TITLE OF INVENTION: USE OF CELLULAR TRANSPORT SYSTEMS FOR THE TRANSFER OF NUCLEIC ACI
TITLE OF INVENTION: THROUGH THE NUCLEAR ENVELOPE
FILE REFERENCE: 30430.1USWO
                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
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APPLICANT: Christine, Rainer
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                 SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                 FILING DATE: 18-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,103
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                           TELEPHONE: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
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3000 K Street, N.W., Suite 500
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Pred. No. 0
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RESULT 18
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Best Local (
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                                                                                                                                                                                                                                                                                                  LENGTH:
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TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-584-043A-83
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US-08-584-043A-83
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                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/584,043A FILING DATE: January 8, 1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: LIPOPHILIC PEPTIDES FO TITLE OF INVENTION: MACROMOLECULE DELIVERY NUMBER OF SEQUENCES: 139
                                                                                                                                                                                                                                      TELEFAX: (21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: sir
                                                                                                                                                                                                                                                       TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y MACCH 100.0%;
Local Similarity 100.0%;
nes 9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 83, ...
No. 6344436
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                                                           Similarity 9; Conserv
                                                                                                                                                                                   amino acids
TPPKKKRKV 11
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                           TPPKKKRKV 9
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Mims, Martha P
                                                           100.0%;
ilarity 100.0%;
Conservative (
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linear
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                                                           Score 48; DB 4
Pred. No. 0.13;
Mismatches
                                                                                          DB 4; Length 24;
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APPLICATION NUMBER:

08/167,641

December 14, 1993 UMBER: 07/855,389 March 20, 1992

PCT/US93/02725 19, 1993

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                                                     RESULT 13
US-09-869-875-9
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                                                                                                                                                                                                                                                                                      US-09-029-228-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Reiss, Bernd
APPLICANT: Kosak, Hans
APPLICANT: Kosak, Hans
APPLICANT: Klelmm, Manfred
APPLICANT: Schell, Jeff
TITLE OF INVENTION: Stimulation of homologous recombination in eukaryotic
TITLE OF INVENTION: organisms or cells by recombination promoting enzymes
TITLE REFERENCE: 147-170P
CURRENT APPLICATION NUMBER: US/09/029,228
CURRENT FILING DATE: 1998-04-28
EARLIER APPLICATION WIMBER: PCT/EP96/03824
EARLIER FILING DATE: 1996-08-30
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09029228 Patent No. 6583336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 9; Conserv
Sequence 9, Application US/09869875 Patent No. 6521456 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: nuclear OTHER INFORMATION: targeting sequence
                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/8
FILING DATE: March 20, 1
APPLICATION NUMBER: PCT/
FILING DATE: March 19, 1
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600 TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: SIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                         100.0%; Score 48; DB 4; Length 15; 100.0%; Pred. No. 0.085; tive 0; Mismatches 0; Indels
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RESULT 15 US-09-869-875-1

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APPLICANT: Reiss, Bernd
APPLICANT: Kosak, Hans
APPLICANT: Kosak, Hans
APPLICANT: Schell, Jeff
TITLE OF INVENTION: Stimulation of homologous recombination in eukaryotic
TITLE OF INVENTION: organisms or cells by recombination promoting enzymes
FILE REFERENCE: 147-170P
CURRENT APPLICATION NUMBER: US/09/029,228
CURRENT FILING DATE: 1998-04-28
CURRENT FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: POT/EP96/03824
EARLIER FILING DATE: 1996-08-30
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 17
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CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: PCT/DE00/00061
PRIOR TELING DATE: 2000-01-03
PRIOR PPLICATION NUMBER: DE 199 00 513.3
PRIOR PILING DATE: 1999-01-08
PRIOR PPLICATION NUMBER: DE 199 33 939.2
PRIOR PILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-029-228-8
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OTHER INFORMATION: Sequence corresponds to a neutral hybrid consisting of the SV40 N
Patent No. 6521456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09029228 Patent No. 6583336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                           Query Match
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TITLE OF INVENTION: USE OF CELLULAR TRANSPORT SYSTEMS FOR THE TRANSFER OF
TITLE OF INVENTION: THROUGH THE NUCLEAR ENVELOPE
FILE REFERENCE: 30430.1USWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Siebenkotten, Gregor APPLICANT: Christine, Rainer
                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: LS and the N-terminal flanking region of the NLS from polyoma viroTHER INFORMATION: us \mathtt{VP2} protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: artificial OTHER INFORMATION: ribosome binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 16
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Local Similarity 100.0%;
                                                                              Local Similarity les 9; Conserv
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  9 TPPKKKRKV 17
                                        1 TPPKKKKRKV 9
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                                                                                Conservative
                                                                                                    100.0%; Score 48; DB 4; 100.0%; Pred. No. 0.095;
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                                                                                       Mismatches
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                                                                                                                           Length 17;
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CORRESPONDENCE ADDRESS:

65

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California

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RESULT 10
US-08-462-040-27
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Best Local Similarity 100
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Woo, Savio L.C.

APPLICANT: Smith, Louis C.

APPLICANT: Cristiano, Richard J.

APPLICANT: Gottchalk, Stephen

TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND

TITLE OF INVENTION: METHODS OF USE

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,971A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/063
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS LENGTH: 15 amino acid:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRANKESEQ for Windows 2.0
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                      ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: WOO, Sar
APPLICANT: Smith,
APPLICANT: Cristia:
APPLICANT: Gottcha
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066.
ZIP: 90071-2066.
COMPUTER REALDABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 617755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COmpatible
ODERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/167,641
APPLICATION NUMBER: 08/167,641
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: 07/853/302725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERNCE/DOCKET NUMBER: 212/078
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth S
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NUCLEIC ACID TO TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%; Score 48; DB 3; Local Similarity 100.0%; Pred. No. 0.085; nes 9; Conservative 0; Mismatches
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Gottchalk, Stephen
WENTION: NUCLEIC ACID
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Smith, Louis C.
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US-08-167-641C-33
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Best Local Similarity
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                                                                                                                                                                                                                TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.(
SOFTWARE: FastSQ for Windows 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
                                                                                                                                       TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Woo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                    TYPE: amino acids
                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/167, FILING DATE: December 14, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND THE OF INVENTION: METHODS OF USE
                                                                            Local
                                                                                                                                                                   STRANDEDNESS:
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                                                             Similarity 9; Conser
                             TPPKKKRKV 9
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TPPKKKRKV 12
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                                                             Conservative
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                                                                                                                                                                     single
                                                                        100.0%;
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                                                           Score 48; DB 3;
Pred. No. 0.085;
; Mismatches
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RESULT 8

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US-08-460-971A-27; Sequence 27, Application US/08460971A; Patent No. 6150168
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                                                                                                                 Sequence 33, Patent No. 6
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Best Local ?
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION UNMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION UNMBER: PCT/US93/02725
FILING DATE: March 19, 1993
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                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FASTSEQ for WINDOWS 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/460,971A FILING DATE: June 5, 1995 CIASSTIFICATION. 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3:5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID
TITLE OF INVENTION: METHODS OF U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (213) 489-161
TELEFAX: (213) 955-0440
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9; Conserv
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                                                             Woo, Savio L.C.
Smith, Louis C.
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                                                                                  Savio L.C.
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 NUCLEIC ACID TRANSPORTER SYSTEMS METHODS OF USE
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PRIOR APPLICATION DATA:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY_AGENT INFORMATION:
NAME: Warburg Pinkers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 12-10 TELEFAX: 67-3510
                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon Liyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.0%;
nes 9; Conservativo
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/066
                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08 FILING DATE: December
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TPPKKKKRKV 9
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Pred. No. 0.085;
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US-08-167-641C-27
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                                                                                                                                             APPLICATION NUMBER: US/08/167,641C FILING DATE: December 14, 1993 CLASSIFICATION: 435 PRIOR APPLICATION: 435 PRIOR APPLICATION DATE: 07/855,389 PILING DATE: March 20, 1992 APPLICATION NUMBER: 07/8593/02725 APPLICATION NUMBER: PCT/US93/02725 PILING DATE: March 19, 1993 ATTORNEY/AGENT INFORMATION: NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327 REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 205/012 TELECOMMUNICATION INFORMATION: TELEPAX: (213) 489-1600 TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                   TELEX: 67-3510 INO:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION: (213) 489-1600
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 90071-2066
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                     STRANDEDNESS: single TOPOLOGY: linear
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peptide
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US-08-257-307-1
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; Sequence 1, Application US/C; Patent No. 5674977; GENERAL INFORMATION: GARIEPY, JEAN TITLE OF INVENTION: BRAINUMBER OF SEQUENCES: BRAINUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                  Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1in MOLECULE TYPE: HYPOTHETICAL: 1
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APPLICATION NUMBER: US 07/991,199
FILING DATE: 15-DEC-1992
ATTORNEY/AGENT INFORMATION:

NAME: Szekeres, Gabor L.

REGISTRATION NUMBER: 28,675
REGISTRATION NUMBER: 28,675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Meyer Jr., Rich B.
APPLICANT: Gall, Alexander A.
APPLICANT: Reed, Michael W.
TITLE OF INVENTION: Peptide Linkers For Improved
TITLE OF INVENTION: Oligonucleotide Delivery
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acida STRANDENESS: **
TOPOLOGY
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: ORIGINAL SOURCE:
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LENGTH: 10 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 854-5502
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CITY: Irvine
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                                                                                                       Application US/08257307
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                                                   GARIEPY, JEAN
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15-DEC-1993
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                                  BRANCHED SYNTHETIC PEPTIDE CONJUGATE
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Best Local
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APPLICATION NUMBER: US/08/014,180
FILING DATE: 5-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: ONTCA/39C/1494
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHNE: (416) 868-1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: WS-DOS 6.0
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,307
FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (416) 868-14
TELEPAX: (416) 362-0823
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: 3.5" Diskette, 1.44 ME
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEO for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                          STATE: C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single st
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ZIP: M5H 2J7
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STATE: Ontario
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
APPLICATION NUMBER: US/08/460,890A FILING DATE: June 5, 1995 CLASSIFICATION: 435
                                                                                                                                                                             ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TPPKKKRKV 9
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Gottchalk, Stephen
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Post-processing: Minimum Match 0%
Maximum Match 10
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seq length: 2000000000
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1: /cgm2_6/ptodata/1.
2: /cgm2_6/ptodata/1.
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4: /cgm2_6/ptodata/1.
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6: /cgm2_6/ptodata/1.
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Match
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     GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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PCT-US93-12246-3
US-08-257-307-2
US-08-460-890A-27
US-08-460-890A-33
US-08-167-641C-27
US-08-460-971A-27
US-08-460-971A-33
US-08-460-971A-33
US-08-462-040-33
US-08-462-040-33
US-08-462-040-33
US-08-462-040-33
US-09-029-228-6
US-09-029-228-6
US-09-0869-875-9
US-09-869-875-1
PCT-US95-11405-16
US-08-584-043A-83
US-09-08-584-03A-83
US-09-08-584-03A-83
US-09-08-583-8
US-09-615-283-8
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Sequence
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                                                                           ; ORGANISM:
US-07-991-199D-3
                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Szekeres, Gabor L.
REGISTRATION UNUBER: 28,675
REFERENCE/DOCKET NUMBER: 491-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 854-4897
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
US-07-991-199D-3
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative 0
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APPLICANT: Meyer Jr., Rich B.

APPLICANT: Gall, Alexander A.

APPLICANT: Reed, Michael W.

TITLE OF INVENTION: Deptide Linkers For Improved TITLE OF INVENTION: Oligonucleotide Delivery NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,199D
FILING DATE: 15-DEC-1992
                                                                                                                 FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                    MOLECULE TYPE: PORTICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92715
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Klein & Szekeres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 4199 Campus Drive, Suite CITY: Irvine STATE: CA COUNTRY: U.S.A.
                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA
v. U.S.A.
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                                                                                                                                                                                            linear
                                                                                                                                  internal
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US-09-1014-438-2
US-09-110-496D-290
US-08-588-201-6
US-09-1169-605-6
US-09-149-956-8
US-08-833-327-6
US-08-813-388-5
US-08-461-859-5
US-08-461-859-5
US-08-462-498-5
US-08-853-7338-27
US-08-853-7338-27
US-08-853-7338-27
US-08-853-7338-27
US-08-953-7338-361-8
US-09-359-361-8
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Score 48; DB 1; Length 10; Pred. No. 0.06; Mismatches 0; Indels
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Score

Minimum DB Maximum DB

Scoring table:

Title: Perfect score:

Run on:

Database :

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RESULT 40
AAB35920
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Best Local Similarity
Matches 9; Conserve
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AAB60061
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Matches 9; Conserv
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29-NOV-1999;
21-DEC-1999;
                                                                                                                                                                                                                                          drug
                                                                                                                                                                                                                                                                                                                     Delivering nucleic acids to a cell, useful for delivering and releasing compounds or drugs to cells, e.g. tumor cells, by employing pH-sensitive delivery systems, comprising labile linkages and membrane-coring compounds.
Epitope identification; display system; gene delivery; bacteriophage {\tt T7}.
                             Nuclear localisation signal peptide #2.
                                                  26-FEB-2001
                                                                     AAB35920;
                                                                                        AAB35920 standard;
                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                    The present invention provides a method for delivering a nucleic acid ( a cell, involving the introduction of a solution comprising a membrane active compound and the nucleic acid to a cell. This method is useful :
                                                                                                                                                                                                                                                                                          Disclosure; Page 34; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-091200/10.
                                                                                                                                                                                                                                                                                                                                                                                    Wolff JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-2000; 2000WO-US15651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-DEC-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhesus macaque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SV40; nuclear localisation signal; drug delivery; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SV40 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAR-2001
                                                                                                                                                                                                                                                                                                              membrane-active compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB60061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB60061 standard; peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        (MIRU-) MIRUS
                                                                                                                                                                                                                                            delivery and gene therapy.
                                                                                                                                          17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen
                                                                                                                                                      TPPKKKKKKV
                                                                                                                                          TPPKKKRKV
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                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0137859.
99US-0167836.
99US-0172809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyoma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nuclear localising signal #4.
                                                                                       peptide; 39
                                                                                                                                          25
                                                                                                                                                             9
                                                  entry)
                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                0;
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                                                                                                                                                                                          Score 48; I
Pred. No. 0
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                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                   DB .
າ.78;
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                                                                                                                                                                                                   Length 37;
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         drug
          delivery;
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Search completed: December 11, Job time: 49.96 secs.
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                                                                                                                                                                      Query Match
Best Local S
Matches 9
                                                                                                                                                                                                        This invention relates to a process comprising exposing an epitope display system to blood products to identify useful epitopes. The process is useful for identifying new peptide ligands that protect the display system e.g. phage, which delivers drugs and genes in vivo. The delivery system may be inhibited through binding to complement, the process reveals peptides which may be used to protect the system from this inhibition. The present sequence represents a nuclear localisation signal
                                                                                                                                                                    Sequence
                                                                                                                                                                                               peptide, used in examples illustrating the invention.
                                                                                                                                                                                                                                                                                                                                                  Identifying new peptide ligands that protect phage which delivers drugs and genes in vivo, by binding to blood proteins, comprises exposing an epitope display system to blood products -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-APR-1999;
07-JUN-1999;
                                                                                                                                                                                                                                                                                                                        Disclosure; Page 50; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-687379/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Wolff JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200065350-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR-2000; 2000WO-US11270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MIRU-) MIRUS
                                                        19
                                                                                                            9; Conserv
                                                                            TPPKKKRKV 9
                                                        TPPKKKRKV
                                                                                                                                                                     39 AA;
                                                                                                            100.0%;
ilarity 100.0%;
Conservative 0
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99US-0139431.
                                                        27
               2003, 09:55:19
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                                                                                                            Score 48; DB 21;
Pred. No. 0.82;
; Mismatches 0;
                                                                                                               0
                                                                                                                                        Length 39;
                                                                                                               Indels
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RESULT 37
AAU03182
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an alkylating agent (such as a mustard or a cyclopropa-pyrrolo-indol moiety), which is in turn attached to the DNA. The covalent attachement does not involve biotinylated DNA, and does not prevent expression of the gene. The method is useful for enhancing gene delivery to a cell via the gene of the cell's internal localisation mechanisms, and does not the cell of the cell's internal localisation mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of enhancing gene delivery to a cell for expression. The method comprises covalently attaching a cellular transport signal such as a nuclear localisation signal (NLS) to the nucleic acid to direct the nucleic acid to a target location. The signal sequence is not directly attached to the DNA; instead, it is attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enhancing gene delivery to a cell for expression comprises covalently attaching a cellular transport-enhancing signal to the nucleic acid through an alkylating molecule, e.g. cyclopropapyrroloindole -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sebestyen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with prior art methods which rely on non-covalent complex formation between the DNA and the targetting moiety. Sequences AAB30981-B20987 are nuclear localisation signals which may be used in the method of the invention. These sequences all contain an N-terminal cysteine residue to facilitate attachment to the alkylating agent. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MIRU-) MIRUS
                                                                                                                                                                                                                                                                        SV40; T-antigen; nuclear localising signal; NLS; drug delivery; amphiphile binding agent; ABA; polymer delivery; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      affect with gene expression. Covalent attachment of a cellular transport signal to the gene is a more efficient means of gene delivery compared
                            WPI; 2001-432579/46
                                                                                                                     29-NOV-1999;
                                                                                                                                                    29-NOV-2000; 2000WO-US32612
                                                                                                                                                                                  31-MAY-2001
                                                                                                                                                                                                                WO200137665-A1
                                                                                                                                                                                                                                             Rhesus
                                                                                                                                                                                                                                                                                                                      Long nuclear localising signal (NLS)
                                                                                                                                                                                                                                                                                                                                                   24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                   AAU03182
                                                                                                                                                                                                                                                                                                                                                                                                                AAU03182 standard; peptide;
                                                                                         (MIRU-) MIRUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 9; Conserva
                                                                                                                                                                                                                                           macaque polyoma virus
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                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                      peptide #2 of SV40 T-antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .78;
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Expressing desired compounds

e.g.

nucleic acids in cells,

by forming

Query Match

100.0%;

Score

48;

DB

22;

Length

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RESULT 38
AAB68672
ID AAB68
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                described in an invention relating to methods of days delivery using amphiphile binding molecules. Methods of days delivery expression product by delivering a polynucleotide in vitro or in vivo, comprises forming a complex by associating an amphiphile binding agent (ABA), an amphiphile and a polynucleotide, delivering the complex to a cell and expressing the polynucleotide. The method is useful for delivering polyners, nucleic acids, drugs and genes to cells. The delivering polynucleotides or genetic material produce a change in the cell that can be therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence representing long nuclear localising signal (NLS) peptide #2 of SV40 T-antigen is 1 of several peptides (AAU03179-AAU03187)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complex with amphiphile binding agent, delivering the complex to the cell and
                                      The present invention relates to a method for delivery of modified nucleic acids to a cell. The method may be used for gene delivery and gene therapy. Polynucleotides are modified to contain specific signals enhance e.g. cellular uptake, cytoplasmic transport, nuclear localisation, gene expression, or chromosomal integration. The present sequence is a nuclear localisation signal which was used in the present
                                                                                                                                                                                                                            Wolff
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SV40 T antigen long nuclear localisation signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB68672 standard; peptide;
                                                                                                                                                                                                                                                                               02-AUG-1999;
02-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                    Rhesus macaque
                                                                                                                                                                                                                                                                                                                                                                                                                             Gene delivery; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB68672;
                                                                                                                                                                        Covalently modifying polynucleotides for use
                                                                                                                                                                                                   WPI; 2001-191426/19
                                                                                                                                                                                                                                                                                                                       02-AUG-2000; 2000WO-US21067
                                                                                                                                                                                                                                                                                                                                                                           WO200108710-A1
Sequence
                                                                                                                                Disclosure; Page 17;
                                                                                                                                                          therapy
                           invention.
                                                                                                                                                                                                                                                       (MIRU-) MIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPPKKKRKV
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 37
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ilarity 100.0%;
Conservative
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2000US-0146824.
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  AA;
                                                                                                                                                                                                                                                                                                                                                                                                    polyoma virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54pp;
                                                                                                                                  45pp; English.
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Pred. No. 0.78;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               nuclear localisation signal; SV40 T antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amphiphile and a polynucleotide, expressing the polynucleotide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                          in gene delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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RESULT 34
AAW24457
ID AAW24
XX AAW24
XX AAW24
XX Nucle
XX Nucle
XX Nucle
KW JTS-1
XX Synth
XX JTS-1
XX Synth
XX
                                                                                                                     RESULT 35
AAB35921
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Best Local Similarity
Matches 9; Conserva
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW24434-W24459 are nucleic acid (NA) binding peptides, capable of both condensing and stabilising a NA. The peptides can be conjugated to a lytic peptide to form a nucleic acid transporter system. The lysis agent forms an alpha-helical structure. The transporter system is used to deliver nucleic acid to a cell and for treating humans by gene therapy. By taking advantage of the characteristics of both the lysis agents and the binding molecules, delivery of the nucleic acid is enhanced. Specific lysis agents are capable of releasing the nucleic acid into the cellular interior from the endosome. Release is efficient without endosomal/lysosomal degradation. Once released the binding complexes help target the nucleic acid to the nucleus.
26-FEB-2001
                                                AAB35921;
                                                                                              AAB35921 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 50; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid transporter useful in gene therapy - contains binding complex associated with surface and nuclear ligands and lysis agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-052345/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid transporter; gene therapy; binding complex; lysis agent; JTS-1; K8; alpha helix; endosome; lysosome; nucleus targeting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BAYU ) BAYLOR COLLEGE MEDICINE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a process comprising exposing an epitope display system to blood products to identify useful epitopes. The process is useful for identifying new peptide ligands that protect the display system e.g. phage, which delivers drugs and genes in vivo. The delivery system may be inhibited through binding to complement, the process reveals peptides which may be used to protect the system from this inhibition. The present sequence represents a nuclear localisation signal peptide, used in examples illustrating the invention.
                                                                                                                               Nuclear localisation covalent attachment; large T antigen.
26-JUN-1997;
                                                                                              Synthetic
                                                                                                          Rhesus macaque polyoma virus
                                                                                                                                                                               SV40 large T antigen nuclear localisation signal,
                                                                                                                                                                                                                                                       AAB20982 standard; peptide; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                      12-DEC-1997;
                                               25-JUL-2000
                                                                       US6093701-A.
                                                                                                                                                                                                          11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 50; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying new peptide ligands that protect phage which delivers drugs and genes in vivo, by binding to blood proteins, comprises exposing an epitope display system to blood products -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1999;
07-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Epitope identification; display system; gene delivery; drug delivery; bacteriophage T7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wolff JA;
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97US-0050842
                      97US-0990015.
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99US-0139431.
                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                            signal; NLS; cellular targetting; gene delivery; alkylating agent; SV40; simian virus 40;
                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB 2
Pred. No. 0.78;
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                                                                                                                                                                               SEQ
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Disclosure; Page 50; 125pp; English

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Query Match
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The present sequence represents a nuclear location signal (NLS) peptide. The present invention describes a phage (such as a lambda-phage) having a NLS peptide fused to the phage head region protein (e.g. gpp protein). This enables the phage to locate itself more efficiently at the nucleus of an infected cell. The phage obtained can package lambda-phage DNA of 80% or 100% genomic size. Also described is DNA coding for the fused NLS/phage head region protein; vectors containing this DNA; cells (such as Escherichia coll) transformed by these vectors, and kits for production of phage incorporating the NLS, which include these transformed cells. The phage bearing the NLS protein fused to the phage head region efficiently transports phage DNA to the cell nucleus (e.g. in mammalian cells). It is therefore useful for insertion of foreign genes into the cell nucleus for gene therapy and for research purposes.
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                                                                                                                                                                                                                                                                                                             Phage with improved location specificity nuclear location signal peptide fused to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phage; nuclear location signal; NLS; cell nucleus; gene therapy; head region. \cdot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhesus macaque
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                                                                                                                                                                                                                                                                       Page 16; 27pp; Japanese
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Pred. No.
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the phage gpD head prote
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                                                       The present invention describes a method for producing micelles with CC entrapped therapeutic agents. The method comprises: (1) combining consistively charged agent with a cationic lipid in a ratio where 30-90 % cC of the negatively charged atoms are neutralised by positive charges on CC lipid molecules to form an electrostatic micelle complex in 20-80 % cc thanol; and (2) combining the micelle complex of (a) with fusogenic-cx axyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing cmicelles with entrapped therapeutic agents. Also described is a method cc for delivering a therapeutic agent in vivo, comprising the administration of the micelle. ABB74256 to ABB74858 represent specifically claimed conclear localisation signal (NLS) peptides for use in the method as the CC diseases. The invention relates to the field of gene therapy and is CC diseases. The invention relates to the field of gene therapy and is CC diseases. The invention relates to the field of gene therapy and is CC diseases suitable for delivery of polymocleotides. The encapsulated complexes suitable for delivery of polymocleotides.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with nuclear localization signal/fusogenic peptide conjugates into targeted
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liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simple nuclear localisation signal peptide SEQ ID NO:24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 54; 107pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
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Pred. No. 0.71;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Sequence

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RESULT 30
AAW12916
ID AAW12
XX AAW12
XX AAW12
XX Octo
XX Octo
XX CTS
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              branched; conjugate; polylysine; scaffold; nuclear localisation signal; NLS; cytoplasmic translocation signal; CTS; domain; junction; octopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Octopeptide breast-2, a branched synthetic peptide conjugate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic probes.
The present sequence peptide breast-3, of
                                                                           09-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unit is 8, such structures being referred to as octopeptides. The conjugate is a relatively small molecule of flexible design having a branched structure for systematically incorporating a desired number of cytotoxic functions, peptide-based localisation signals or
                                                                                                                                                                                14-DEC-1995
                                                                                                                                                                                                                                      WO9533766-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW12916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW12916 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                           (ONTA-) ONTARIO CANCER INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TPPKKKRKV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPPKKKKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.
nilarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
F
                                                                           94US-0257307
                                                                                                                               94WO-CA00405
                                                                                                                                                                                                                                                                            /label= PHMFGFTSS
/note= "Peptide that binds to Human
Milk Fat Globule Protein Tumour-Specific Site.
This is probably an acronym rather than a
peptide sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "nuclear localisation signal of SV40
  large T antigen"
23...31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "the longest progressive chain from a branched polylysine of formula (Lys)4(Lys)2Lys providing eight amino terminal sites (including alphaand omega-amino groups), there being a cisplatin_KKKK-GG- peptide chain attached to each cisplatin_KKKK-GG- peptide chain attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "the N-terminal has a cisplatin molecule
    attached to it as a cytotoxic agent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "cytoplasmic translocation signal'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label= NLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= junctional_segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= branched_polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents a specific conjugate designated Octo-
formula (Acr-NLS-CTS-Gly-Gly)8-BP-PHMFGFPTSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   °.
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RESULT 31
AAW24456
ID AAW2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      designed to bind to a target cell surface receptor to penetrate into target cells and to deliver a diagnostic probe or cytotoxic functionality to a desired site of action.

The conjugate may be described as a series of peptide and chemical domains which may be separated by junctions. Each domain performs a particular cell trargetting or a cellular function. Junctional segments are spacer regions that may in some cases allow the incorporation of chemically active moieties or markers. These domains and junctions are assembled on a branched polymer (BP) scaffold. The branching of the peptide is preferrably provided by a polylysine construct having free alpha and epsilon amino groups to which linear series of domains and junctions can be attached. A preferred number of branches for the BP unit is 8, such structures being referred to as octopeptides.

The conjugate is a relatively small molecule of flexible design having a branched structure for systematically incorporating a desired charge of cyrotoxic functions, peptide-based localisation signals or diagnostic probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 9
Nucleic acid transporter useful in gene therapy - contains binding complex associated with surface and nuclear ligands and lysis agent
                                               WPI; 1997-052345/05
                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                   Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                  30-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New branched synthetic peptide conjugate - can be designed to bind to a tablet cell surface receptor or to deliver a diagnostic probe or cytotoxic functionality
                                                                                                                                           07-JUN-1995;
                                                                                                                                                                          23-APR-1996;
                                                                                                                                                                                                         19-DEC-1996
                                                                                                                                                                                                                                        WO9640958-A1
                                                                                                                                                                                                                                                                                                    JTS-1; K8; alpha
                                                                                                                                                                                                                                                                                                                   Nucleic acid transporter;
                                                                                                                                                                                                                                                                                                                                                                                                               AAW24456;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW24456 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 27; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide breast-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A branched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-040185/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gariepy J;
                                                                                                            (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents a specific conjugate designated Octo-
ide breast-2, of formula (cisplatin-CTS-Gly-Gly)8-BP-NLS-PHMFGFPTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TPPKKKRKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPPKKKKKV
                                                                              Sparrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic peptide conjugate is provided whi
o bind to a target cell surface receptor to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                (NA) binding peptide used in NA delivery to cells.
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,
                                                                                                                                           95US-0484777.
                                                                                                                                                                          96WO-US05679.
                                                                                                                                                                                                                                                                                                    helix;
                                                                              JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                    endosome;
                                                                               Woo
                                                                                                                                                                                                                                                                                                                   gene therapy; binding complex; lysis agent;
                                                                              SL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB
Pred. No. 0.6
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                    lysosome; nucleus targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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23-MAY-1997

(first entry)

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RXB
                                       RESULT 29
AAW12917
                                                                                                                                                                                                                                                the nucleus of eukaryotic cells, comprising applying an electrical pulse of field strength 2-10 kV/cm; duration at least 10 micro s and current at least 1 Amp. The transfected cells are used for diagnosis and for gene therapy, after ex vivo preparation. The method delivers DNA and/or other biological agents to the nucleus of cells of higher eukaryotes, regardless of whether they are resting or dividing, and with very low comortality. The time between transfection and analysis can be reduced to as little as 2 hours and pulse parameters are optimised for maximum cc as little as 2 hours and pulse parameters are optimised for maximum cc nuclear localisation. The high voltage gradient creates pores in both cc irreversible damage. The present sequence is that of a peptide nucleic acid (PNA) comprising a nucleotide sequence is that of a peptide cc sequence given in the current record. The PNA, on successful transfection of the target cell, provides a repressor for a reporter compliance and the reporter gene cassette and inhibiting gene expression. While the comprises a sequence specific for reporter gene repression, while
                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide nucleic acid 2 peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM48793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUN-2001; 2001WO-EP07348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200200871-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Siebenkotten G, Poppenborg S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUN-2000; 2000DE-1031179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Introducing active molecules into the nucleus of eukaryotic cells, useful for transfection and gene therapy, by applying controlled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-139917/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to introducing a biologically active molecule into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Page 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       electrical pulse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMAX-) AMAXA GMBH
                                                                                                                                                                                                             Sequence
                            AAW12917 standard;
AAW12917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide nucleic acid; transfection; diagnosis; gene therapy;
                                                                                                                                                                                                                                        comprises a nonspecific sequence.
                                                                                                 17
                                                                                                                          1 TPPKKKRKV
                                                                                                                                                      9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                     Similarity
                                                                                                 TPPKKKKKKV
                                                                                                                                                                                                             27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression.
                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Riemen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Christine R,
                                                                                                 25
                            peptide;
                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-terminus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rothmann
                            31
                                                                                                                                                        0
                                                                                                                                                      Score 48; DB 2
Pred. No. 0.6;
0; Mismatches
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hmann K, T
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Thiel C;
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                                                                                                                                                        0,
                                                                                                                                                                                 Length 27;
                                                                                                                                                         Indels
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Octopeptide breast-3, a branched synthetic
A branched synthetic peptide conjugate is provided which can be designed to bind to a target cell surface receptor to penetrate into target cells and to deliver a diagnostic probe or cytotoxic functionality to a desired site of action.

The conjugate may be described as a series of peptide and chemical domains which may be separated by junctions. Each domain performs a particular cell targetting or a cellular function. Junctional segments particular regions that may in some cases allow the incorporation of chemically active moieties or markers. These domains and junctions are assembled on a branched polymer (BP) scaffold. The branching of the peptide is preferably provided by a polylysine construct having free alpha and epsilon amino groups to which linear series of domains and junctions can be attached. A preferred number of branches for the BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTS; domain; junction; octopeptide.
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                                                                                                                                                                                                                                                                             New branched synthetic peptide conjugate - can be designed to bind to a tablet cell surface receptor or to deliver a diagnostic probe
                                                                                                                                                                                                                                                                                                                                                            Gariepy
                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9533766-A1
                                                                                                                                                                                                                              Disclosure; Page 27; 55pp; English.
                                                                                                                                                                                                                                                                or cytotoxic functionality
                                                                                                                                                                                                                                                                                                                                WPI; 1996-040185/04.
                                                                                                                                                                                                                                                                                                                                                                                              (ONTA-) ONTARIO CANCER INST
                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0257307
                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-CA00405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "the longest progressive chain from a branched polylysine of formula (Lys)4 (Lys)2Lys providing eight amino terminal sites (including alpha-and omega-amino groups), there being an hor-TPPKKKRKVEDP-KKKKK-GG- peptide chain attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "the N-terminal has an acridine molecule condensed onto it to act as a DNA intercalator having fluorescence properties to allow visualisation inside cells by fluoresence microscopy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Peptide that binds to Human Milk Fat Globu Protein Tumour-Specific Site. This is probably an acronym rather than a peptide sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "nuclear localisation signal of SV40 large T antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "cytoplasmic translocation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          each amino group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= branched_polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= junctional_segment
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Length 25;

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ID AAB;
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                                                                                                                delivery vehicle comprises a nucleic acid uptake and release fusion comprises a nucleic acid uptake and release fusion protein, itself comprising an influenza virus haemagglutinin (HA) cendosomolytic peptide covalently attached via an amide linkage to a receptor ligand protein such as adenovirus penton base protein, epidermal creceptor ligand protein as adenovirus penton base protein, epidermal protein may additionally be joined to peptides which provide additional protein may additionally be joined to peptides which provide additional celes of nucleic acid attachment, and may also be joined to a nuclear cocalisation signal (NLS). The invention also encompasses a DNA construct encoding the nucleic acid uptake and release protein of the invention. The nucleic acid delivery vehicle is used for the intracellular delivery of specific nucleic acid sequences, for gene therapy of cancer, genetic diseases and viral infections. The present sequence represents the SV40 large T antigen NLS which was incorporated into certain nucleic acid uptake/release proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 26
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Best Local S
Matches 9
                                              Query Match
Best Local :
                              Matches
                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      Novel vehicle comprising delivering nucleic acids and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SV40 large T antigen; NLS; nuclear localisation signal; nucleic acid delivery vehicle; nucleic acid uptake and release protein; influenza virus haemagglutinin; HA; endosomolytic peptide; receptor ligand protein; cancer; genetic disease; viral infection; gene therapy vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aurelian L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-1999;
                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel nucleic acid delivery vehicle. The
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 4; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-2000; 2000WO-US03074.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SV40 large T antigen nuclear localisation signal (NLS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYMA-) UNIV MARYLAND BALTIMORE.
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                                            Local
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DB; AAA90236.
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9; Conserv
                            Similarity 9; Conserv
 TPPKKKKKKV 9
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                              Conservative
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                                            100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   hemagglutinin-ligand fusion peptide useful for to treat viral infections, genetic diseases
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                                              Score 48;
Pred. No.
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Pred. No. 0.56;
                 Mismatches
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                                           0.56;
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RESULT 28 AAM48793 ID AAM48 XX

AAM48793 standard; peptide;

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RESULT 27
AAB10436
ID AAB10
XX AAB10
XX AAB10
XX VAO
XX DE199
XX DE199
XX OB-J#
XX OB-J#
XX VAO
PF 20-JI
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PF 13-JI
PF 20-JI
XX VAO
PF 10-Cal
PF Nucli
CC This
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PS Exam
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                                                                                                                                                                                                                                                                                                 This invention describes a novel nuclear transport system (I) which comprises (i) a module (A) that binds specifically to DNA and can not form a complex with more than one DNA molecule; and (ii) a module (B) chat includes a nuclear localization signal (NLS) or a non-NLS signal chart does not bind non-specifically to DNA. (I) is used to deliver nucleic acid to cells, especially for gene therapy of cancer, viral infections, diseases of the nervous system, transplant rejection and mono- or poly-genic inherited disorders. (I) provide efficient transfer of DNA to resting cells or cells with very low mitotic activity, i.e. primary cells, so eliminate the need to induce cell division for transfer, but can also be used with established cell lines. (I) does not transfer, but can also be used with established cell lines. (I) does not transport machinery, both features which improve transfer efficiency. It can be formulated as part of a virus-free gene transfer vehicle that is easy and inexpensive to prepare and easier to manipulate than known viral systems (and lacks the inherent risks of viral systems). This sequence crepresents the SV21 peptide described in the method of the invention.
                                                                                                                                                  Best
                                                                                                                           Matches
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear transport system, particularly for resting clocalization signal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Christine R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear transport system; nuclear localization system; NLS; cancer; gene therapy; viral infection; nervous system disease; virus-free; transplant rejection; mono-genic inherited disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 6; 10pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-499930/45
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poly-genic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE19933939-A1
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                                                                                                                                                     Local
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                                                             \vdash
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                                                                                                                        Similarity 9; Conserv
                                TPPKKKKRKV
TPPKKKRKV
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                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMBH C/O DEUT RHEUMA-FORSCHUNGSZEN
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                                                                                                                     100.0%; §
100.0%; I
ntive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful as part of gene therapy system, cells, comprises DNA binding region and
                                                                                                                                                     Score 48; DB;
Pred. No. 0.6;
                                                                                                                        Mismatches
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RESULT 24
AAY14143
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; neurological disorder; amnesia; Alzheimer's disease; Parkinson's disease; Huntington's disease; Pick's disease; retardation; amyotrophic lateral sclerosis; cerebral senility; learning disability; chronic peripheral neuropathy; Down's syndrome; duillain-Barre syndrome; Turret's syndrome; dyslexia; electric shock-induced amnesia; hippocampus; memory deficiency; mental illness; dementia; forebrain gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calcium-calmodulin dependent kinase II alpha; gene therapy; neurological disorder; amnesia;
                                                                                                                              This sequence represents the SV40 nuclear localisation signal sequence. The invention relates to a recombinant nucleic acid (I), that comprises region of a calcium-calmodulin dependent kinase II alpha (CaMKII alpha) promoter (A), linked to a gene (II) of interest. (I) are used in gene therapy to treat neurological disorders, specifically; amnesia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-337692/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1997;
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                             Alzheimer's, Parkinson's, Huntington's or Pick's diseases; amyotrophic lateral sclerosis; brain injury; cerebral senility; chronic peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant nucleic acid containing forebrain specific promoter
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brain injury; o
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                                      The present invention describes a nucleic acid uptake and release vehicle (UTARVE) comprising a fused ligand and endosmolytic peptide for the intracellular delivery of nucleic acid or oligonucleotides or modified analogues. The UTARVE can be used for intracellular delivery of gene sequences or oligonucleotides especially for gene therapy. Disease or disorder treated is dependent on the nucleic acid attached to the UTARVE, especially mentioned are the use of UTARVE-nucleic acid complexes as anti-viral or anti-cancer agents or for the treatment of genetic diseases e.g. diabetes, cystic fibrosis, haemophilia or adenosine deaminase defiency. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid uptake; release vehicle; adenovirus; influenza penton base protein; haemagglutinin endosomolytic peptide; d polylysylleucyl peptide; intracellular delivery; anti-viral; anti-cancer; genetic disease; cystic fibrosis; haemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                            Novel nucleic acid uptake and release vehicle - c ligand and endosmolytic peptide for intracellular nucleic acids, especially for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                     16-JAN-1998;
07-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                               Disclosure; Page 5;
                                                                                                                                                                                                                                                                                                           WPI; 1999-167357/14.
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                                                                                                              The invention relates to a peptide comprising Tat sequence linked to nucleic acid-binding group. Peptides of the invention are used as components of a cell transfection system particularly for gene therapy (especially of cancer). The present sequence is nuclear localisation signal (NLS) phosphorylation site peptide from simian virus 40 (SV40) used for transfection enhancement. This sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agricultural purposes. The complex is capable of transporting the macromolecule in a stable and condensed state and releasing the molecule into the cellular interior. The complex can bind with a cell surface receptor, lyse an endosome and target the nucleus of the cell.
                                                                                   Sequence
                                                                                                       exemplification of the invention.
                                                                                                                                                                                                                         New peptide comprising Tat sequence linked to nucleic acid-binding group, useful, e.g. in gene therapy, for improving cell-transfection
                                                                                                                                                                                                                                                                                                                                     14-MAR-1997;
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                                                                                                                                                                                         Example 1; Column 163-164; 108pp; English
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                                                                                                                                                                                                                                                                                           Hawley-Nelson P,
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                                                                                                                                                                                                                                                                                                                                                                                                                        Rhesus macaque
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide used
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RESULT

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The conjugate may be described as a series of peptide and chemical domains which may be separated by junctions. Each domain performs a particular cell targetting or a cellular function. Junctional segments
                                                                          A branched synthetic peptide conjugate is provided which designed to bind to a target cell surface receptor to per target cells and to deliver a diagnostic probe or cytotox functionality to a desired site of action.
                                                                                                                                                                                                        Disclosure; Pages 12,
                                                                                                                                                                                                                                                        New branched synthetic peptide conjugate to a tablet cell surface receptor or to or cytotoxic functionality
                                                                                                                                                                                                                                                                                                                                                                                                                 Gariepy J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ONTARIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 or 5, a branched synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0257307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-CA00405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CANCER INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= branched_polymer
/note= "the longest progressive chain from a
/note= "the longest progressive chain from a
/noted polylysine of formula (Lys)4(Lys)2Lys
providing eight amino terminal sites (including
and omega-amino groups), there being a
TPPKKKRKVEDP-KKKKK-GG- peptide chain attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "cytoplasmic translocation signal"
18..19
/label= junctional_segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= C-terminal_arm
/note= "used in analyt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "nuclear localisation signal of SV40 large T antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= NLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    construct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= bAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     morecure condensed onto it to act as a DNA intercalate having fluorescence properties to allow visualisation inside cells by fluoresence microscopy. In Octopeptide 4, the acridine molecule is absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                                                                                     13; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "in Octopeptide 5 the N-terminal ule condensed onto it to act as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIS
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                                                                                                                                                                                                                                                                                   to deliver
                                                                                                                                                                                                                                                                                can be designed to bind
liver a diagnostic probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         evaluation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translocation signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        has an acridine DNA intercalator
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RESULT 20
AAR25137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stable and efficient foreign protein prodn. transfection with recombinant contg. T7 poly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-016675/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lieber A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
05-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                    AAR25137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-)
                                                                   Maximising foreign protein expression in animal cells - by transfecting with viral replication gene, RNA polymerase g coupled to nucleus localisation sequence and vector contg.
                                                                                                                                                                                      29-SEP-1988;
                                                                                                                                                                                                                                   13-FEB-1992
                                                                                                                                                                                                                                                          DD298269-A5
                                                                                                                                                                                                                                                                                 Simian virus
                                                                                                                                                                                                                                                                                                      foreign gene
                                                                                                                                                                                                                                                                                                                   Simian Virus
                                                                                                                                                                                                                                                                                                                                          SV40 large T-antigen nuclear localisation sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                          AAR25137 standard; peptide; 23
DNA encding the SV40 T-antigen nuclear localisation preferred sequence for use in the construction of a
                                                                                                                                     Kiessling U,
                                                                                                                                                                                                            29-SEP-1988;
                                                         required
                                                                                                                                                              (MOLE-) ZENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 1; 10pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPPKKKKKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPPKKKRKV 9
                                                         protein gene
                                 Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strauss M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
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llarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                      expression;
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(first en
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                                                                                                                                                               INST MOLEKULARBIOLOGIE
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                                  Spp;
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                                   German.
                                                                                                                                         Platzer M,
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                                                                                                                                                                                                                                                                                                       polymerase gene; polyoma virus.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                         Strauss M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               odn. in animal cells - by polymerase gene localised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 23;
                                                                                                                                          Waehlte
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signal is the recombinant
                                                                               gene
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preferred sequence

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RESULT 21
AAW38769
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peptide-macromolecule complex of the invention. The peptide-macromolecule complex of the invention is for delivering a macromolecule into a cell and comprises a non-exchangeable lipophilic peptide (LP) comprising a delivery peptide associated with a lipid moiety, where the delivery peptide portion of the LP is complexed to the macromolecule. The complexes can be used for the delivery of macromolecules such as nucle acids, proteins, oligonucleotides, lipids or carbohydrates. They can bused to treat diseases by enhancing delivery of specific nucleic acid the appropriate targeted cells. They can also be used to create transformed cells as well as transgenic animals for assessing human disease in an animal model. They can also be used for livestock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence, a selection gene, a prokaryotic promoter homologous to the RNA polymerase and (under the control of this promoter), a gene encoding foreign protein. Cells with the highest synthesis of foreign protein are selected and fermented with addition of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clones with nucleus-localised polymerase are selected. Finally, expression vector is introduced for production of a foreign protein. The construct comprises a viral replication start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delivery peptide; peptide-macromolecule complex; macromolecule delivery; non-exchangeable lipophilic peptide; disease therapy; cell targeting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW38769;
                                                                                                                                                                                                                                                              New lipophilic peptide-macromolecule complexes - used delivery of macromolecules to cells, particularly for
                                                                                                                                                                                                                                                                                                                                                 Hauer J, Mims MP,
                                                                                                                                                                                                                                                                                                                                                                                                                     08-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9725070-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delivery peptide used in peptide macromolecule complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW38769 standard;
                                                                                                                                                                                                                            Claim 3; Page 96; 106pp; English.
                                                                                                                                                                                                                                                                                                                  WPI; 1997-372622/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Updated
                                                                                                                                                                                         This sequence represents a delivery peptide that can be used in the
                                                                                                                                                                                                                                                                                                                                                                                   (BAYU ) BAYLOR
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide;
                                                                                                                                                                                                                                                                                                                                                   Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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Pred. No. 0.52;
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                                                                                                                                                                                                                                                                                                                                                   Sparrow JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                             invention. The peptide-macromolecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                            ecule into a cell,
                                                                                                                                                                                                                                                                                    for the
                                                                                                                                                                                                                                                                 gene therapy
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                                                                                            as nucleic
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RESULT 18
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Matches 9; Conserv
                                                                                                                                                                               The specification describes compositions for delivering compounds into cells. These compositions comprise an organic halide, a targeting ligand, and a nuclear localization sequence in combination with the compound to be delivered. The compositions are used to deliver compounds into cells, particularly for the treatment of autoimmune disorders and inflammatory conditions such as rheumatoid arthritis. They may also be used to deliver pharmaceuticals, drugs, diagnostic agents, synthetic organic molecules, peptides, proteins, vitamins, teroids, genetic materials and other bioactive agents. AhB30402-26 represent nuclear localisation sequences. They are used to enhance import of compounds into the nucleus, in compositions of the invention.
                                                                                                                                                                                                                                                                                                                    Compositions to deliver compounds into cells e.g. to treat rheumatoid arthritis, comprise organic halide, targeting ligand and nuclear localization sequence in combination with compound and carrier -
 06-MAR-2001
                    AAB30409
                                      AAB30409 standard; peptide; 22 AA
                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                              Unger EC,
                                                                                                                                                                                                                                                                                                  Claim 23; Page 48; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disorder; inflammatory condition; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Targeting ligand; nuclear localization sequence; cell delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear localisation sequence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                  19-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB30405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB30405 standard; peptide; 22
                                                                                                                                                                                                                                                                                                                                                                                                (IMAR-) IMARX PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-2000; 2000EP-0303249
                                                                                                                                    Local Similarity
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                                                                                                       TPPKKKKRKV 9
                                                                                     TPPKKKRKV 22
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                                                                                                                                                                                                                                                                                                                                                                             McCreery T, Sadewasser DA;
                                                                                                                                                                22 AA;
                                                                                                                          Conservative
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                                                                                                                                  100.0%;
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                                                                                                                                  Score 48; DB Pred. No. 0.5;
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                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           import of compounds into nucleus.
                                                                                                                                            DB 21;
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                                                                                                                                           Length 22;
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 RESULT 19
AAR20076
                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                 片
                                                                                                                                                                                                                                                                                                            PXPXPXXXXXXXXXX
         29-SEP-1988;
                            14-AUG-1991.
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Query Match
Best Local S
Matches 9
                                                   Expression vector; nucleus localisation; T7 promoter.
                                                                                                                          signal.
                                                                                                                                                     Sequence of modified T7 poylmerase contg. nucleus localisation
                                                                                                                                                                                                            13-APR-1992
                                                                                                                                                                                                                                                             AAR20076;
                                                                                                                                                                                                                                                                                                                   AAR20076 standard; Protein; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used to deliver pharmaceuticals, drugs, diagnostic agents, synthetic organic molecules, peptides, proteins, vitamins, steroids, genetic materials and other bioactive agents. AAB30402-26 represent nuclear localisation sequences. They are used to enhance import of compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           compound to be delivered. The compositions are used to deliver compounds into cells, particularly for the treatment of autoimmune disorders and inflammatory conditions such as rheumatoid arthritis. They may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes compositions for delivering compounds into cells. These compositions comprise an organic halide, a targeting ligand, and a nuclear localization sequence in combination with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compositions to deliver compounds into cells e.g. to treat rheumatoid arthritis, comprise organic halide, targeting ligand and nuclear localization sequence in combination with compound and carrier -
Bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 23; Page 48; 78pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-681105/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-APR-2000; 2000EP-0303249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear localisation sequence for import of compounds into nucleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                into the nucleus, in compositions of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMAR-) IMARX PHARM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TPPKKKRKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                      (first entry)
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Pred. No. 0.5;
0; Mismatches
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88DD-0320251

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RESULT 15
AAB10435
ID AAB10
This invention describes a novel nuclear transport system (I) which CC comprises (i) a module (A) that binds specifically to DNA and can not form a complex with more than one DNA molecule; and (ii) a module (B) CC that includes a nuclear localization signal (NLS) or a non-NLS signal CC that does not bind non-specifically to DNA. (I) is used to deliver CC nucleic acid to cells, especially for gene therapy of cancer, viral CC infections, diseases of the nervous system, transplant rejection and CC mono- or poly-genic inherited disorders. (I) provide efficient transfer CC primary cells, so eliminate the need to induce cell division for transfer, but can also be used with established cell lines. (I) does not transport machinery, both features which improve transfer reficiency. It can be formulated as part of a virus-free gene transfer reficiency. It can be formulated as part of a virus-free gene transfer reficient that is casy and inexpensive to prepare and easier to manipulate than known viral complex with established of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a specific conjugate designated Octopeptide 2, of formula (Acr-NLS-Gly-Gly)8-BP-Tyr-Gly-bAla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostic probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         number of cytotoxic functions, peptide-based localisation signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear transport system; nuclear localization syste gene therapy; viral infection; nervous system diseas transplant rejection; mono-genic inherited disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB10435 standard; peptide; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SV40 nuclear localization peptide SV21 fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhesus macaque polyoma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                poly-genic inherited disorder.
                                                                                                                                                                                                                                                                                                                                                                                      Nuclear transport system, useful as part of gene therapy system, particularly for resting cells, comprises DNA binding region and
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-499930/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Christine R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                       Example 1; Page 6; 10pp; German.
                                                                                                                                                                                                                                                                                                                                                                        localization signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Siebenkotten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GMBH C/O DEUT RHEUMA-FORSCHUNGSZEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nuclear localization system; tion; nervous system disease;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLS; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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Sequence

21

B

Query Match

100.0%;

Score 48;

В

23;

Length

21;

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                       CC the nucleus of eukaryotic cells, comprising applying an electrical pulse co field strength 2-10 kV/cm; duration at least 10 micro s and current at cleast 1 Amp. The transfected cells are used for diagnosis and for gene chargay, after ex vivo preparation. The method delivers DNA and/or other biological agents to the nucleus of cells of higher eukaryotes, comprisity. The time between transfection and analysis can be reduced to as little as 2 hours and pulse parameters are optimised for maximum conclear localisation. The high voltage gradient creates pores in both commissiones surrounding the nucleus but its short duration avoids conversible damage. The present sequence is that of a peptide nucleic concerning a nucleotide sequence (ABA97765) and a peptide corresponder of the target cell, provides a repressor for a reporter prasmit already present in the cells, binding to a sequence between the corresponder and the reporter gene cassette and inhibiting gene expression. CC PNA2 comprises a sequence specific for reporter gene repression, while corresponder and comprises a nonspecific sequence.
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                                                                                                                                                                                                                                                                                                                                                                useful for electrical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PNA; peptide nucleic acid; transfection; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Siebenkotten G,
Poppenborg S, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                            Introducing active molecules into the nucleus of eukaryotic useful for transfection and gene therapy, by applying contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUN-2000; 2000DE-1031179
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Sequence
                                                                                                                                                                                                                                                                                            The invention relates to introducing a biologically active molecule into the nucleus of eukaryotic cells, comprising applying an electrical pulse
                                                                                                                                                                                                                                                                                                                                     Example 10; Page 16; 30pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMAX-) AMAXA GMBH
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 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Riemen G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Christine R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rothmann K,
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Pred. No. 0.48;
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mann K, Thiel C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
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                                                                                                                                                                                                                                                                                                                                                                               ryotic cells, controlled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lenz
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RESULT 14
AAW12913
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ABR39214
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Matches
AAW12913;
                    AAW12913 standard; peptide; 20 AA.
                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                 The present invention relates to isolated peptides comprising an amino acid sequence of a nuclear localization signal (NLS), thought to be cytostatic and virucidal in their action. The peptides are useful for screening anti-viral agents, as regulatory elements in
                                                                                                                                                                                                                                                                                                                New isolated peptides, useful for screening anti-viral agents, as regulatory elements in gene therapy and other in vivo regulatory functions, as probes for diagnostic purposes and research, or for treating viral infection or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAY-2001; 2001US-289084P.
24-OCT-2001; 2001US-344706P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                           Claim 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-2002; 2002WO-US14372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-viral agent; gene therapy; viral infection; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200290377-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuclear localization signal; NLS; cytostatic; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLS-containing isolated peptide sequence #15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR39214 standard;
                                                                                                                                                                                                e therapy, and for other in vivo regulatory functions, as probes diagnostic purposes and for research. The peptides are also ful for treating viral infection or cancer. The present sequence
                                                                                                                                                                                                                                                                                                                                                                      2003-167140/16.
                                                                                                                                                                                        peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                      9;
                                                                                                                                   Similarity
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                                                                           TPPKKKKKV 17
                                                                                          TPPKKKKRKV
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                                                                                                                                                                                                                                                                                         Page 4; 89pp; English.
                                                                                                                                                                   17
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                                                                                                                      Conservative
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                                                                                                                                                                                         invention.
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                                                                                                                               100.0%;
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                                                                                                                                Score 48;
Pred. No.
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                                                                                                                                0.4;
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CC A branched synthetic peptide conjugate is provided which can be CC designed to bind to a target cell surface receptor to penetrate into CC target cells and to deliver a diagnostic probe or cytotoxic CC functionality to a desired site of action.

CC The conjugate may be described as a series of peptide and chemical CC domains which may be separated by junctions. Each domain performs a CC particular cell targetting or a cellular function. Unctional segments CC are spacer regions that may in some cases allow the incorporation of CC chemically active moleties or markers. These domains and junctions are assembled on a branched polymer (BP) scaffold. The branching of the peptide is preferably provided by a polylysine construct having free CC alpha and epsilon amino groups to which linear series of domains and CC junctions can be attached. A preferred number of branches for the BP CC unit is 8, such structures being referred to as octopeptides.

CC The conjugate is a relatively small molecule of flexible design desired contains a branched structure for systematically incorporating a desired contains and structure for systematically incorporating a desired contains and structure for systematically incorporating a desired contains and cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New branched synthetic peptide conjugate - can be designed to bind to a tablet cell surface receptor or to deliver a diagnostic probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 12; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or cytotoxic functionality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-040185/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gariepy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9533766-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
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/note= "nuclear localisation signal of
large T antigen"
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/note= "used in analytical evaluation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "The N-terminal has an acridine molecule condensed onto it to act as a DNA intercalator having fluorescence properties to allow visualisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               branched polylysine of formula (Lys)4(Lys)2Lys providing eight amino terminal sites (including alpha-and omega-amino groups), there being a TPPKKKRKVEDP-GG-peptide chain attached to each amino group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= junctional_segment
15..17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "the longest progressive chain from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= branched_polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= bAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              branched synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
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Best Local S
Matches
                                                                                                                                                                                                                           14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endosomal/lysosomal
                                               Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
                                                                                                                                                                                                                                                                                                05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                   21-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                     US6150168-A
                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                       bacterial antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid transporter system peptide ligand SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB45821 standard; Protein;
              Claim 9; Column 105-106; 105pp; English
                                                                                                                      WPI; 2001-049093/06
                                                                                                                                                       Gottchalk S,
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                                                                                                                                                                                           BAYLOR
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92US-0855389.
93WO-US02725.
                                                                                                                                                         Sparrow
                                                                                                                                                                                          COLLEGE MEDICINE
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                                                                                                                                                         Cristiano RJ,
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Pred.
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No.
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                                                                                                                                                         Smith LC,
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RESULT 12
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ID ABR39
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid. The nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor suppressors, viral antigens, parastitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic nuclear ligand.
        The present invention relates to isolated peptides comprising an amino acid sequence of a nuclear localization signal (NLS), thought to be cytostatic and virucidal in their action. The peptides are useful for screening anti-viral agents, as regulatory elements in gene therapy, and for other in vivo regulatory functions, as probes for diagnostic purposes and for research. The peptides are useful for treating viral infection or cancer. The present sequence is a peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                  New isolated peptides, useful for screening anti-viral agents, as regulatory elements in gene therapy and other in vivo regulatory functions, as probes for diagnostic purposes and research, or for treating viral infection or cancer
                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-2001; 2001US-289084P.
24-OCT-2001; 2001US-344706P.
                                                                                                                                                                                                                                                                                                                       Bullock
                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simian virus 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-viral agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear localization signal; NLS; cytostatic; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLS-containing isolated peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR39210 standard;
                                                                                                                                                                Claim 22; Page 2; 89pp; English.
                                                                                                                                                                                                treating
                                                                                                                                                                                                                                                                                       WPI; 2003-167140/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                          TUFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                           2002WO-US14372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ß,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48; DB 2
Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a nucleic acid transport system (NTS) for Cd delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or C antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moving or initiating movement through a nuclear membrane; and/ or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytoplasm of the cell. The NTS con the cell. The NTS can be used to treat disorders by targeting specific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells specific expression into specifically targeted tissue culture cells. The NTS avoids the problem of endosomal/lysosomal
                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
14-DEC-1993;
               US6177554-B1
                                       Synthetic
                                                             Nucleic acid transport; cytosis; ligand; lysis agent;
                                                                                                       Nuclear ligand Pep3 used in nucleic acid transporter system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĕ
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                                                                  23-OCT-2001
                                                                                                                                                                                      AAU04262 standard; Peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-038262/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-1999
                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                1 TPPKKKRKV 9
                                                                                                                                                                                                                                                                                                       Similarity 100 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAYLOR
                                                                                                                                                                                                                                                      TPPKKKRKV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                delivery; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-0167641.
92US-0855389.
93WO-US02725.
93US-0167641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0460890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                     Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                   DB 21;
0.36;
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                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                 Length 15;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith
                                                                            spacer molecule;
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                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 10
AAB45815
ID AAB45
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules, lysis agents and spacer molecules are used in nucleic acid transporter systems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells.
                                                                 14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene tumor antigen; tumor suppressor; viral antigen; parasitic antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                     Gottchalk S,
                                                                                                                05-JUN-1995;
                                                                                                                                      21-NOV-2000.
                                                                                                                                                             US6150168-A.
                                                                                                                                                                                                        bacterial antigen.
                                                                                                                                                                                                                                                                                       21-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 18; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                Nucleic acid
                                                                                                                                                                                                                                                                                                             AAB45815;
                                                                                                                                                                                                                                                                                                                                   AAB45815 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-365933/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1995;
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                                            (BAYU ) BAYLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                 1 TPPKKKRKV
                                                                                                                                                                                                                                                                                                                                                                                                                                       9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                           TPPKKKRKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                              transporter system peptide ligand SEQ
                                                                                                                                                                                                                                                                                       (first entry)
                     Sparrow
                                                                 93US-0167641.
92US-0855389.
93WO-US02725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0167641.
92US-0855389.
93WO-US02725.
                                            COLLEGE MEDICINE
                                                                                                                95US-0460971
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                                                                                                                                                                                                                                                                                                                                                                                            12
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                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                    ŗ
                     Cristiano
                                                                                                                                                                                                                                                                                                                                    15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.36;
                     Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                     SLC;
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                                                                                                                                                                                                                             oncogene;
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WPI; 2001-049093/06

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RESULT 6
AAY98468
                                                       RESULT 7
AAY59007
ID AAY5
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SAXAX
                                                                                                                                                                                                                                                                                                               The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36633-A36652 and peptide sequences AAY99456-Y98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transport animals (as models for human carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular
                                                                                                                                                                                              Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                         degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Figure 18; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            System for transporting nucleic acid into cells, useful e.g. in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-281993/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-1992;
19-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pep 3 used in nucleic acid transporter system production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY98468 standard; Peptide; 15
                            AAY59007;
07-MAR-2000
                                                       AAY59007 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BAYU ) BAYLOR
                                                                                                                                                                                                                                                                                                        nterior,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                herapy and for

y and for generating transgenic animals,

to nucleic acid, surface ligand and lyt

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                                                                                                                                                                                              9;
                                                                                                                                                                                                              Similarity
                                                                                                                                                                   TPPKKKKKKV
                                                                                                                                     TPPKKKRKV 12
                                                                                                                                                                                                                                                                                                        from
                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sparrow J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-0855389
93WO-US02725
                                                                                                                                                                                                                                                                                                     endosomes, without requiring endosomal or lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-0167641
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                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cristiano RJ,
                                                                                                                                                                                              0;
                                                                                                                                                                                              Score 48; DB 21; Length 15; Pred. No. 0.36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ligand and lytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprises binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith LC;
                                                                                                                                                                                              0
                                                                                                                                                                                                Gaps
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RESULT 8
AAY59013
ID AAY5
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                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a nucleic acid transport system (NTS) for CC delivering nucleic acid into a cell. The NTS contains but is not limited CC to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or CC antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is CC capable of moving or initiating movement through a nuclear membrane; and/ CC or (e) a lysis moiety that enables the transport of the entire complex; CC from the cell surface directly into the cytoplasm of the cell. The NTS CC delivers nucleic acid into the cellular interior as well as the nucleus of specific nucleic acid accordingly. The NTS can also be used to create CC unimal model. The NTS can be used to treat disorders by targetting cC which allows the role of various nucleic acids to be studied by targeting specific expression into specifically targeted tissue culture cells. The CC derivation of the NTS avoids the problem of endosomal/lysosomal
                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 9
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nuclear
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19-MAR-1993;
14-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nuclear membrane; lysis moiety; transgenic anima nucleic acid delivery; cancer; c-myc; promoter.
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 17B; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-038262/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide fragment present in a ligand for c-myc promoter
Nucleic acid transport system; NTS; cell surface receptor; cytosi nuclear membrane; lysis moiety; transgenic animal; human disease;
                                                Sequence of a peptide ligand Pep3.
                                                                                                               AAY59013;
                                                                                                                                             AAY59013 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                      degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLC,
                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                          Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid transport system; NTS; cell surface receptor; cytosis; membrane; lysis moiety; transgenic animal; human disease;
                                                                                                                                                                                                                                                     TPPKKKKKKV
                                                                                                                                                                                                                            TPPKKKKKV 12
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                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                        100.0%; Score 48; DB 2: ilarity 100.0%; Pred. No. 0.36; Conservative 0; Mismatches
                                                                              (first entry)
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93WO-US02725.
93US-0167641.
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                                                                                                                                               8
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                                                                                                                                                                                                                                                                                                                         21;
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                                                                                                                                                                                                                                                                                                                         Length 15;
                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith
                  cytosis;
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                                                                                                                                                                                                                                                                                           Gaps
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RESULT 4
AAO18298
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                                     The present invention relates to a method of transfecting cells using at least one protein capable of forming a nucleoprotein filament. The protein is first modified with at least one functional component that affects at least one stage of transfection, then the DNA to be transferred is loaded with the modified protein to form a thread-shaped complex and this is administered to the cells. Transfection agents such as this are useful in human or animal gene therapy, to identify activators and inhibitors of the expression products from the DNA, and to identify physiologically active nucleic acids. The present sequence is a peptide described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schmidt H, Altrogge L, Lenz
Helfrich J, Hein K, Gremse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha.and epsilon amino groups to which linear series of domains and junctions can be attached. A preferred number of branches for the BP unit is 8, such structures being referred to as octopeptides. The conjugate is a relatively small molecule of flexible design having a branched structure for systematically incorporating a desire number of cytotoxic functions, peptide-based localisation signals or
                                                                                                                                                                                                                                                                                                                                                             Transfecting cells using modified nucleoprotein filament-forming protein, useful e.g. in gene therapy, using complex of the protein DNA, applicable to all cells -
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present sequence represents residues 124-135 of the SV40 large present sequence represents residues 124-135 of the SV40 large igen, corresponding to the nuclear localisation signal (NLS). It preferably used as one of the domains in the above conjugate.
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9; Conserv
                                                                                                                                                                                                                                                                                                                  5; Page 32; 83pp; German.
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emse M, Males T, Christine
B, Turbanski T, Klaes A;
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                                                                                                                                                                                                                                                     in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transgenic animals (as models for human carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from endosomes, without requiring endosomal or lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide bequences AA33633-A5652 and peptide sequences AA36633-A5652 are used in the construction of the permission of the sequences and the construction of the permission of the construction of the sequences and the construction of the construction of the construction of the construction of the sequences and the construction of the constructio
                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residue and nucleic aci
polypeptide by residue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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The inventors claim an oligo-peptide-carrier conjugate in which the three moieties are covalently linked to one another. The peptide provides a cleavable linker which is cleaved by enzymes which do no
                                                                                                                                               New covalently linked conjugates of oligo:nucleotide, peptide and carrier - utilising surfactant, poly:amine or targetting ligand as lyso somotropic drug carrier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense oligonucleotide; ODN; ODN-peptide conjugate.
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                                                                                                                                                                                                                                                                                                       Meyer RB,
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Matches 9
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The conjugate may be described as a series of peptide and chemical domains which may be separated by junctions. Each domain performs a particular cell targetting or a cellular function. Junctional segments are spacer regions that may in some cases allow the incorporation of chemically active moleties or markers. These domains and junctions are assembled on a branched polymer (BP) scaffold. The branching of the peptide is preferably provided by a polylysine construct having free
                                                                                                                       A branched synthetic peptide conjugate is provided which can be designed to bind to a target cell surface receptor to penetrate target cells and to deliver a diagnostic probe or cytotoxic functionality to a desired site of action.
                                                                                                                                                                                                                                             New branched synthetic peptide conjugate - can be designed to bind to a tablet cell surface receptor or to deliver a diagnostic probe or cytotoxic functionality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               branched; conjugate; polylysine; scaffold; nuclear localisation signal; NLS; cytoplasmic translocation signal; CTS; domain; junction; octopeptide.
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                                                                                                                                                                                                                                                                                                                     WPI; 1996-040185/04.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Nuclear ligand Pep	Sequence of a pept	Peptide fragment p	Pep 3 used in nucl	Peptide CXLIIi use	Cell transfection	Nuclear localisati	Sequence of model	Simian virus 40 la	Description	

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ALIGNMENTS

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) MARASCO) SCHERMAI	(QUAN/) QUAN Z. (LAUR/) LAURENT O.	_	(HUST/) HUSTON J S.		23-JUN-2000; 2000US-213653F.		25-JUN-2001; 2001WO-US20182.		03-JAN-2002.		WO200200914-A2.		Rhesus macaque polyoma virus.		nuclear localisation signal.	gene therapy; targetted gene delivery; Simian virus 40; SV40; NLS;	nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;	Gene-delivery compound; single-chain binding polypeptide; SCBP;		Simian virus 40 large T-antigen nuclear localisation signal peptide.		18-JUN-2002 (first entry)		AAE20403;		AAE20403 standard; peptide; 9 AA.	LT 1 0403

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SEKDEL 6 SEKDEL

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RESULT 13
AAY49942
scleroderma and systemmine diseases such as treat T-cell mediated autoimmune diseases such architis, myasthenia encephalomyelitis, multiple sclerosis, rheumatoid arthritis, myasthenia gravis, thyroiditis, experimental uveoretinitis and celiac disease of the intestine. Production of edible transgenic plants which synthesise disease-specific autoantigens as CTB fusion proteins provides a convenient, effective, affordable and palatable method for prevention of autoimmune diseases. CTB is included to increase the tolerigenic nature of orally administered antigens. High concentrations of autoantigen can be delivered in a site-specific manner, avoiding the need for repeated administration of large amounts of autoantigen. The need for repeated administration of large amounts of autoantigen. The
                                                                                                                                                                                                                                                                                        The present invention describes a chimeric gene construct (I) comprising a plant promoter operatively associated with DNA coding for: (i) a cholera toxin B subunit (CTB); and (ii) an autoantigen. The chimeric construct is used for expressing an autoantigen in plants, e.g. potato or tomato. The resulting cells and transgenic plants which express the autoantigen are useful as edible vaccines for inducing oral tolerance. Depending on the identity of the autoantigen, the vaccines are useful for suppressing allograft rejection or for treating autoimmune diseases including insulin-dependent diabetes mellitus (IDDM), Addison's disease, scleroderma and systemic lupus erythematosus. In particular the vaccines can treat T-cell mediated autoimmune diseases such as autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chimeric gene construct for expressing autoantigens in plants, useful for producing edible vaccines to treat autoimmune diseases including insulin-dependent diabetes mellitus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY49942 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microsomal retention signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Langridge WHR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple sclerosis; rheumatoid arthritis; myasthenia gravis; thyroiditis; experimental uveoretinitis; cellac disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chimeric gene; transgenic plant; expression; cholera toxin B subunit CTB; allograft rejection; insulin-dependent diabetes mellitus; IDDM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microsomal retention signal; autoimmune disease; vaccine; autoantigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYLO-) UNIV LOMA LINDA.
(LANG/) LANGRIDGE W H R.
(ARAK/) ARAKAWA T.
                                         present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Addison's disease; scleroderma; systemic lupus erythematosus;
T-cell mediated autoimmune disease; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87pp; English.
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Sequence

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Query Match Best Local S Matches 6

6; Similarity

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Score 29; Pred. No.

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Length

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Best Local Similarity
Matches 6; Conserv
                                        expresses the measies virus antigen. The transgenic plant is used to induce an immune response to an antigen in a subject. Diseases such as canine distemper, rabies, canine hepatitis, parvovirus, feline leukemia, foot and mouth, and fowl cholera may be controlled. More than one antigen can be produced in the DNA vaccine. Availability of the vaccine in an edible form as a constituent of a fruit or vegetable crop will enhance vaccination coverage by providing an inexpensive and relatively heat—stable package for distribution. The present sequence represents a C-terminal endoplasmic reticulum (ER)-retention sequence. This sequence is fused C-terminally to a measles virus hemagglutinin (H) antigen, where the material
                                                                                                                                                                                                                                                                                                                  Transgenic plant for inducing an immune response to an antigen, for treating e.g. measles, canine distemper and feline leukemia, comprises a DNA molecule with a sequence encoding the antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenio; measles virus antigen; immune response; canine distemper rabies; canine hepatitis; parvovirus; feline leukemia; fowl cholera; endoplasmic reticulum; hemagglutinin; H antigen; immunostimulant; virucide; anti-HIV; antiprotozoal; cytostatic; antibacterial; vaccin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB85340 standard; peptide; 6 AA.
                                                                                                                                                                                                                                The invention provides a transgenic plant transformed with a DNA molecule comprising a sequence encoding a measles virus antigen so that the plant
                                                                                                                                                                                                                                                                                    Claim 5; Page 26; 38pp;
                                                                                                                                                                                                                                                                                                                                                                                                                       Wesselingh S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ALFR-) ALFRED HOSPITAL.
(CSIR ) COMMONWEALTH SCI & I
(UYME ) UNIV MELBOURNE.
(AUSU ) UNIV AUSTRALIAN NAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JAN-2001; 2001WO-AU00059.
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COMMONWEALTH SCI & IND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reticulum (ER)-retention C-terminal sequence
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AA;
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                                                                                                                                                                                                                                                                                   English.
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Pred. No. 9.3e+05;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Ramshaw IA;
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RESULT 15
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ID AAE28
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AAU97200
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Best Local &
                                                                                                                                                                                                                                                                                                         The invention relates to human alpha-galactosidase truncated at the carboxy terminus and the production of enzymatically active recombinant human and animal lysosomal enzymes. The invention is useful for producing lysosomal enzymes for treating lysosomal storage diseases, producing altered or mutated proteins, enzymatically active or otherwise, to serve as precursors or substrates for further in vivo or in vitro processing to a specialised industrial form for research or therapeutic uses, to produce more effective therapeutic enzyme, for producing antibodies against lysosomal enzymes for medical diagnostic use, and in any commercial process that involves substrate hydrolysis. The present sequence is rice ER retention signal peptide used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice ER retention signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human alpha-galactosidase polypeptide useful for treating lysosomal storage diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-galactosidase; lysosomal enzyme; lysosomal storage disease; therapeutic; rice; GCB.
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           Endoplasmic
                                      27-AUG-2002
                                                                                          AAU97200 standard; peptide; 6 AA
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page 69; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-681656/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-2000; 2000US-0626127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GARG/) GARGER S J. (TURP/) TURPEN T H.
                                                                                                                                                                                                           Local Similarity 100.0%;
les 6; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SJ,
                                                                                                                                                                                        1 SEKDEL 6
                                                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KUMAGAI M H.
                                                                                                                                                                                                                                                                       6 AA;
            reticulum retention signal.
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                                      (first entry)
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Pred. No.
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. 9.3e+05;
ches 0;
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Matches 6
                                                                                                                                                        Gene-delivery compound; single-chain binding polypeptide; SCBP; nucleic acid-binding moiety; NABM; lipid-associating moiety; LA gene therapy; targetted gene delivery; endoplasmic reticulum; E
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human IgM phage display library using EGFR as antigen. Two isolates with different amino acid sequences were identified. The anti-EGFR-screy are useful for treating cancer, and for the diagnostic location and assessment of tumour growth, where the anti-EGFR-scFV is radiolabelled. The present sequence representing an endoplasmic reticulum retention signal can be used to target scFvs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human anti-epidermal growth factor receptor single-chain antibody useful for diagnostic location and assessment of tumour growth, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-epidermal growth factor receptor single-chain antibody; anti-EGFR-scFv; IgM; cancer; tumour growth;
                                                           25-JUN-2001; 2001WO-US20182
                                                                                   03-JAN-2002.
                                                                                                                                                                                                         SEKDEL,
                                                                                                                                                                                                                                 18-JUN-2002
                                                                                                                                                                                                                                                         AAE20414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to human anti-epidermal growth factor receptor single-chain antibodies (anti-EGFR-scFvs) isolated from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raisch
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(WILS/) WILS P.
                                    23-JUN-2000; 2000US-213653P
                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                               AAE20414 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the lumen of the
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                                                                                                           WO200200914-A2
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                                                                                                                                                                                                                                                                                                                                                          1 SEKDEL 6
                                                                                                                                                                                                                                                                                                                                                                                         Similarity 6; Conser
                                                                                                                                                                                                         ER retention signal peptide
                                                                                                                                                                                                                                                                                                                                         SEKDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AA;
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                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                               peptide; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                              endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Pred. No.
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Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to gene-delivery compound comprising a single-chain binding polypeptide (SCBP) having at least one effector segment having a cysteinyl residue, and a nucleic acid-binding motety (NABM) or a lipid-associating motety (IAM) coupled to SCBP by the residue. Gene-delivery compound is useful for targetted gene delivery for treating diseases by gene therapy. The present sequence is endoplasmic reticulum (ER) retention signal peptide used to prepare SCBP fusion construct.
                                                                                                                                                                                                                                                                                                            Glucocerebrosidase;
                                                                                                                                                                                                                                                                                                                                   ER-retention signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                   AAE19268;
                                                                                                                                                                                                                                                                                                                                                                                                       AAE19268 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene-delivery compound for targeted gene delivery, comprises single-chain binding polypeptide having effector segment with residue and nucleic acid-binding/lipid-associating moiety compolypeptide by residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (QUAN/)
(LAUR/)
(MARA/)
                                                                                                                                                                                                                                          WO200208404-A2
                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                  enzyme
                                                                                                                                                                                                                                                                                                                                                           21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huston
                                          for treating lysosomal storage diseases, Niemann-Pick disease, Fabry disease -
                                                                New glucocerebrosidase and alpha-galactosidase having post-translational modification, useful in enzyme rep
                                                                                                                                                                                            26-JUL-2001; 2001WO-US24111.
                     Example 11;
                                                                                                                                                                       26-JUL-2000; 2000US-0626127
                                                                                                                                                (LARG-)
                                                                                                   2002-195873/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-268789/31
                                                                                                                                                                                                                                                                                     cerebrosidase; alpha-galactosidase; Tay-Sachs disease;
e replacement therapy; Niemann-Pick disease; Gaucher d
disease; lysosomal storage disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QUAN Z.
LAURENT O.
MARASCO W A.
SCHERMAN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SEKDEL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conserv
                                                                                                                                                LARGE SCALE BIOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEKDEL
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                   Page 49; 102pp; English
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                                                                                                                         Turpen TH,
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Pred. No.
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                                                    in enzyme repl
, e.g. Gaucher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marasco WA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           segment with cysteinyl ng moiety coupled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                  Gaucher disease;
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                                                                                                                                                                                                                                                                                                            plant;
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invention relates to production of lysosomal enzymes in plants

Association of secretory component

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Matches 6
        (b) optionally a J chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin has plant-specific glycosylation and virucide activity. The immunoadhesin is useful for reducing infection by human rhinovirus (HRV) and hence the initiation or spread of the common cold by HRV. The immunoadhesin binds to HRV and reduces its infectivity, competing with cell surface ICAM-1 for binding sites, interfering with virus entry or uncoating and directing premature release of viral RNA and formation of empty capsids. Expression of the immunoadhesin in plants would be tetrameric, rather than dimeric. Immunoadhesin having multiple binding sites have a higher effective affinity for the virus, thereby increasing the effectiveness of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucocerebrosidase and alpha-galactosidase having a post-translational modification. The enzymes are useful in enzyme replacement therapy for treating lyosomal storage diseases (e.g. Gaucher disease, Niemann-Pick disease, Fabry disease and Tay-Sachs disease), in researches for developing new approaches to medical treatment of lyosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is ER-retention signal peptide used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                              Immunoadhesin for treating human rhinovirus infection comprises chimeric intercellular adhesion molecule-1, and optionally a J and secretory component in association
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-041481/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immunoadhesin; intercellular adhesion ihuman rhinovirus; immunoglobulin heavy chain; transgenic plant; endoplasmic reticulum; ER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant endoplasmic reticulum retention signal peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM47850;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by transient expression. The invention particularly relates to
                                                                                                                                                                                                                  (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising
                                                                                                                                                                                                                                                      The invention relates to an immunoadhesin comprising:
                                                                                                                                                                                                                                                                                      Examples; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                              Larrick JW
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                                                                                                                                                                                                    immunoglobulin heavy chain; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PLAN-) PLANET BIOTECHNOLOGY INC
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                          and optionally a J chain
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; J chain;
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HRV; common
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RESULT 20
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Best Local Similarity
Matches 6; Conserv
                                                                                   The present invention relates to a stable plastid transformation and expression vector for stably transforming a plastid genome. The vector can be used to stably transform a plant for the expression of heterologous genes e.g. insulin, cholera toxin beta, interferon gene, insulin-like growth factor gene, a human serum albumin (HSA) gene, or a biopolymer fusion gene. The vector can be used to produce edible tobacco, or alfalfa plants. By producing the heterologous genes in an edible plant, the proteins can be orally delivered to patients that require them, e.g. insulin to diabetics, without the need for injections. The present sequence is an endoplasmic reticulum retention signal. This peptide was used to illustrate the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chain increases the stability of the immunoadhesin in the mucosal environment. Production is significantly less expensive in plants than animal cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present sequence is that of a plant endoplasmic reticulum (ER) retention signal
                                                                                                                                                                                                                                                                                                                                                                                                                               (AUBU )
(UYFL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2000; 2000US-185987P
23-JAN-2001; 2001US-263424P
23-JAN-2001; 2001US-263473P
23-JAN-2001; 2001US-263668P
23-FEB-2001; 2001US-0185987
                                                                                                                                                                                                                                                                                                                    Stable plastid transformation and expression vector competent for stably transforming a plastid genome for expression of heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-2001
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                                                            Sequence
                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-055149/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endoplasmic
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h 100.0%; Similarity 100.0%; 6; Conservative 0;
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                                                                                                                                                                                                                                                                           Page 13;
                                                                                                                                                                                                                                                                                                          insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reticulum retention signal.
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Pred. No.
Score 29; DB 23;
Pred. No. 9.3e+05;
; Mismatches 0;
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9.3e+05;
                              Length 6;
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                                                                         S
                                                                                                       glycosylation and virucide activity. The immunoadhesin is useful for creducing infection by human rhinovirus (HRV) and hence the initiation or spread of the common cold by HRV. The immunoadhesin binds to HRV and creduces its infectivity, competing with cell surface ICAM-1 for binding reduces its infectivity, competing with cell surface ICAM-1 for binding sites, interfering with virus entry or uncoating and directing premature release of viral RNA and formation of empty capsids. Expression of the immunoadhesin in plants would be tetrameric, rather than dimeric. Immunoadhesin having multiple binding sites have a higher effective affinity for the virus, thereby increasing the effectivence immunoadhesin. Association of secretory component and immunoglobulin J chain increases the stability of the immunoadhesin in the mucosal cenvironment. Production is significantly less expensive in plants than in cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present sequence is that of a plant endoplasmic reticulum (ER) retention signal.
 Query Match
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Matches 6
                                                                                                                                                                                                                                                                                                                                                                                   (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprisin rhinovirus receptor protein linked to at least a portion of an immunoglobulin heavy chain; and (b) optionally a J chain and secretory component associated with chimeric ICAM-1 molecule. The immunoadhesin has plant-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoadhesin for treating human rhinovirus infection comprises chimeric intercellular adhesion molecule-1, and optionally a {\tt J} chain and secretory component in association
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM47851 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immunoadhesin; intercellular adhesion molecule; ICAM-1; human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant endoplasmic reticulum retention signal peptide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM47851;
                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an immunoadhesin comprising: (a) a chimeric intercellular adhesion molecule (ICAM)-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Examples; Fig 9; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-041481/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PLAN-)
 Similarity 6; Conserv
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   100.0%; Score 29; D
100.0%; Pred. No. 9.
tive 0; Mismatches
DB 23,
. 9.3e+05;
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                                     Length
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RESULT 22
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                                                                                                                                                                                                                                                            heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astromytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence is a detectably labeled peptide which binds the erd 2 receptor may be determined by measuring the ability of the inhibitor to compete with this labeled peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia; melanoma; carcinoma; glioblastoma; astromytoma; oncogene; infectious disease; allergy; autoimmune disease; erd 2 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY44968 standard;
            AAR94942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 26; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rothman JE, Mayhew M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200006729-A1
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                                      AAR94942 standard; Protein; 10
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                                                                                                                                                                        Similarity
6; Conserv
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                                                                                                                                               SEKDEL 6
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                                                                                                                                                                         0,
                                                                                                                                                                                      Score 29;
Pred. No.
                                                                                                                                                                           Mismatches
                                                                                                                                                                                         9.3e+05;
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RESULT 24
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   provides the first known functional method for immunising animals using transgenic plants, where the plants express bacterial antigens that act as both immunogens and adjuvants. The method provides an inexpensive production and delivery system for such antigens to animals. This is the LT-B Escherichia coli toxin subunit C-terminal peptide modified to also comprise a SEKDEL microsomal retention signal. The sequence coding for the whole LT-B gene was used in the construction of such a transgenic plant. The immunogenic agent preferably comprises the LT-B or CT-B (cholera toxin B subunit) or
            Measles virus.
Synthetic.
                                                     Transgenic; measles virus antigen; immune response; canine distemper rabies; canine hepatitis; parvovirus; feline leukemia; fowl cholera; endoplasmic reticulum; hemagglutinin; H antigen; immunostimulant; virucide; anti-HIV; antiprotozoal; cytostatic; antibacterial; vaccin
                                                                                                                                                           17-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A transgenic plant comprising or expressing a DNA sequence encoding an immunogenic agent can be be used as an oral vaccine for animals. The vaccine is administered by the oral consumption of the plant and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic plants contg. E. coli heat labile enterotoxin subunits used as oral vaccines for animals which consume the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT18801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat labile enterotoxin B subunit (LT-B) modified C-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-1996
                                                                                                                              C-terminal sequence ofa modified measles virus H protein
                                                                                                                                                                                        AAB85342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 39; 130pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toxin; subunit; vaccine; transgenic plant;
                                                                                                                                                                                                                  AAB85342 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                         optionally LT-A or CT-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TULA ) TULANE EDUCATIONAL FUND.
(TEXA ) UNIV TEXAS A & M SYSTEM.
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Pred. No. 4.3
0; Mismatches
                                                                                                 immune response; canine distemper;
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                                                                                                                                                                                                                                                                                                                                                                 4.3;
                                                                                                                                                                                                                                                                                                                                                                             BB
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                                                        vaccine
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RESULT 25
AAE28223
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising a sequence encoding a measles virus antigen so that the plant expresses the measles virus antigen. The transgenic plant is used to induce an immune response to an antigen in a subject. Diseases such as canine distemper, rabies, canine hepatitis, parvovirus, feline leukemia, foot and mouth, and fowl cholera may be controlled. More than one antigen can be produced in the DNA vaccine. Availability of the vaccine in an edible form as a constituent of a fruit or vegetable crop will enhance vaccination coverage by providing an inexpensive and relatively heat-stable package for distribution. The present sequence represents a C-terminal sequence of a modified measles virus hemaggluthin (H) antigen, used in the construction of transgenic tobacco plants producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic plant for inducing an immune response to an antige treating e.g. measles, canine distemper and feline leukemia, a DNA molecule with a sequence encoding the antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                             Alpha-galactosidase; lysosomal enzyme; lysosomal storage disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE28223 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides a transgenic plant transformed with a DNA molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Examples; Page 12; 38pp; English
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(GARG/)
(TURP/)
                                                                             26-JUL-2000;
                                                                                                                                                                                      04-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                  Tobacco mosaic virus rGAL-12R peptide
                                                                                                                                  13-NOV-2001; 2001US-0993059
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COMMONWEALTH SCI & IND
UNIV MELBOURNE.
UNIV AUSTRALIAN NAT.
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GARGER S J.
TURPEN T H.
                                                                                                                                                                                                                                                                                             mosaic virus.
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                                                                                2000US-0626127
                                                                                                                                                                                                                                                                                                                                                     rGAL-12R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Pred. No. 4.3;
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RESULT 26
AAE19266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human alpha-galactosidase truncated at the carboxy terminus and the production of enzymatically active recombinant human and animal lysosomal enzymes. The invention is useful for producing lysosomal enzymes for treating lysosomal storage diseases, producing altered or mutated proteins, enzymatically active or otherwise, to serve as precursors or substrates for further in vivo or in vitro processing to a specialised industrial form for research or therapeutic uses, to produce more effective therapeutic enzyme, for producing antibodies against lysosomal enzymes for medical diagnostic use, and in any commercial process that involves substrate hydrolysis. The present sequence is Tobacco mosaic virus rGAL-12R peptide.
                                                                                                                                                                                                                                                                                                                                                   Glucocerebrosidase; alpha-galactosidase; Tay-Sachs disease; plant; enzyme replacement therapy; Niemann-Pick disease; Gaucher disease; Fabry disease; lysosomal storage disease; human.
                                                               New glucocerebrosidase and alpha-galactosidase having a post-translational modification, useful in enzyme replacement therapy for treating lysosomal storage diseases, e.g. Gaucher disease, Niemann-Pick disease, Fabry disease
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lysosomal storage diseases -
                                                                                                                                                                                                                                                                     31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                        Human alpha-galactosidase C-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE19266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE19266 standard;
                                      Example 13; Page 54; 102pp; English.
                                                                                                                                  WPI; 2002-195873/25
                                                                                                                                                                                                                 26-JUL-2000; 2000US-0626127
                                                                                                                                                                                                                                            26-JUL-2001; 2001WO-US24111.
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                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                        LARGE SCALE BIOLOGY CORP
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                                                                                                                                                             Kumagai MH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29;
Pred. No.
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4.3;
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The invention relates to production of lysosomal enzymes in by transient expression. The invention particularly relates

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RESULT 27
AAE28217
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                                                                                                                                                                       The invention relates to human alpha-galactosidase truncated at the carboxy terminus and the production of enzymatically active recombinant human and animal lysosomal enzymes. The invention is useful for producing lysosomal enzymes for treating lysosomal storage diseases, producing altered or mutated proteins, enzymatically active or otherwise, to serve as precursors or substrates for further in vivo or in vitro processing to a specialised industrial form for research or therapeutic uses, to produce more effective therapeutic enzyme, for producing antibodies against lysosomal enzymes for medical diagnostic use, and in any commercial process that involves substrate hydrolysis. The present sequence is Tobacco mosaic virus rGAL-25R vector peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garger SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUL-2002
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                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human alpha-galactosidase polypeptide useful for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-DEC-2002
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(TURP/) TURPEN T H.
(KUMA/) KUMAGAI M H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
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   Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ه</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 60; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEKDEL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   storage diseases
                                                                                                                        11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Turpen TH,
100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kumagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
Score 29; DB 2
Pred. No. 4.8;
0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĭ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                       DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
   0;
                                                       Length 11;
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      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
   0
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   Gaps
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   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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RESULT 29
AAY95252
ID AAY95
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AAE19261
ID AAE19
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                                                                                                                   Query Match
Best Local S
Matches 6
                                                                                                                                                                                          modification. The enzymes are useful in enzyme replacement therapy for treating lysosomal storage diseases (e.g. Gaucher disease, Niemann-Pick disease, Fabry disease and Tay-Sachs disease), in researches for developing new approaches to medical treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is human recombinant alphagalactosidase-A C-terminal modified peptide.
                                                                                                                                                                                                                                                                                     The invention relates to production of lysosomal enzymes in plants by transient expression. The invention particularly relates to glucocerebrosidase and alpha-galactosidase having a post-translational
 AAY95252
                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                     New glucocerebrosidase and alpha-galactosidase having a post-translational modification, useful in enzyme replacement therapy for treating lysosomal storage diseases, e.g. Gaucher disease, Niemann-Pick disease, Fabry disease
                                                                                                                                                                                                                                                                                                                                            Example 11; Fig 5; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-195873/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garger SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-2000; 2000US-0626127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-2001; 2001WO-US24111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200208404-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enzyme replacement therapy; Niema
Fabry disease; lysosomal storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glucocerebrosidase; alpha-galactosidase; Tay-Sachs disease; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human recombinant alpha-galactosidase A modified peptide, rGal-25R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE19261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE19261 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LARG-) LARGE SCALE BIOLOGY CORP.
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                                                                                        1 SEKDEL 6
                                                                                                                   Similarity 6; Conserv
standard;
                                                                 SEKDEL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEKDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEKDEL
                                                                                                                                                                     11 AA;
                                                                                                                 ilarity 100.0%;
Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Turpen TH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
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Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kumagai MH;
 12
                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Niemann-Pick
                                                                                                                   Score 29; DB
Pred. No. 4.8
0; Mismatches
 B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease;
                                                                                                                               4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease; Gaucher disease; human.
                                                                                                                                           23;
                                                                                                                   0;
                                                                                                                                             Length 11;
                                                                                                                    Indels
                                                                                                                   0;
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HXAX

AAY95252;

12-SEP-2000

(first entry)

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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                               to demonstrate a method for the transfer of peptides into cells using histidylated oligolysine. The invention relates to the ability of novel oligomeric conjugates, such as histidylated oligolysine (see also AAY95255 and AAY95256), to transfer small biological molecules into cells. The novel oligomeric conjugates contain an oligomer with a polymerization degree (PD) of 5-50, preferably 10-40, and more preferably 20, formed from monomeric components having free NH3+ in a number equal to or higher than 50% of the PD. The oligomeric conjugates induce a membrane destabilization at acidic pH allowing the transfer of biological molecules to the cytoplasm or cell nucleus in vitro, in vivo or exvivo. Suitable biological molecules are antisense, triplex-forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligomeric conjugate; peptide transfer; graft rejection; allergy; inflammation; infection; antitumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fluorescein-labelled peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                          and ribozyme molecules, RNA decoys, and antigenic peptides, e.g. for the treatment of cancer, inflammatory or immunological diseases such as graft rejection, allergy or autoimmunity, or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New positively charged oligomeric conjugate, oligonucleotides to cytosol and cell nuclei,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200032764-A1
                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Midoux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IDMI-) IDM IMMUNO-DESIGNED MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
Neurological disorder; Huntington's disease; Alzheimer's disease;
                          ER retention
                                                     30-APR-2001
                                                                                AAB69627
                                                                                                           AAB69627 standard; Protein; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-431102/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۵,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of positively charged amino groups
                                                                                                                                                                              7
                                                                                                                                                                                                                                Similarity 6; Conserv
                                                                                                                                                                                                     SEKDEL 6
                                                                                                                                                                            SEKDEL 12
                                                                                                                                                                                                                                                                                                                (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pichon C,
                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                             100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 27; 64pp; English.
                         signal peptide
                                                    (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98EP-0403015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-EP08980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "fluorescein-labeled cysteine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bello-Rufai M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  that of a fluorescein-labeled peptide used
                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                            Score 29; I
Pred. No. 5
                                                                                                           B
                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monsigny M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; autoimmune disease;
antiinflammatory;
                                                                                                                                                                                                                                           DB
5.2;
                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for delivering contains a controlled
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                                                                                                                                                                                                                                                           Length 12;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                   Gaps
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RESULT 31
AAE19259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parkinson's disease; prion disease; frontotemporal dementia; amyotrophic lateral sclerosis; spinal and bulbar muscular at dentatorubal-pallidollysian atrophy; spinocerebellar ataxia SCA2; SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for inhibiting the formation of aggregates of certain proteins, involving contacting the protein with a binding molecule known as an intrabody. Proteins to be bound include those associated with neurological disorders, and so the method can be used in the prevention of diseases such as Alzheimer's, Parkinson's and Huntington's diseases, prion disease, frontotemporal dementia, amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy, dentatorubal-pallidoluysian atrophy, spinocerebellar ataxia type 1 (SCA1), SCA2, SCA3, SCA4, SCA5, SCA6 and SCA7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting intracellular polypeptide accumulation, useful for treating neurological disorders, e.g. Alzheimer's disease, comprises contacting the polypeptide with a specific intrabody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUST/)
(MESS/)
(LECE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-2001
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                                                                                                                                                                                                                                                                  Glucocerebrosidase; alpha-galactosidase; enzyme replacement therapy; Niemann-Pick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-182700/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huston JS, Messer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUL-1999;
21-JUL-2000;
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                                                                                                                                                        Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                     21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE19259 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 108pp; English.
                                                  31-JAN-2002.
                                                                                                                                                                                                                                      Fabry disease; lysosomal storage
                                                                                                                                                                                                                                                                                                                                             Human recombinant alpha-galactosidase A modified peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE19259;
                                                                                                      WO200208404-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 SEKDEL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) HUSTON J S.
) MESSER A.
) LECERF J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SEKDEL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0620955
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29; DB
Pred. No. 6.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.7;
                                                                                                                                                                                                                                                                  Tay-Sachs disease; plant; disease; Gaucher disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ia type 1;
intrabody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atrophy;
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26-JUL-2001; 2001WO-US24111.

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RESULT 32
AAE19257
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to production of lysosomal enzymes in plants by transient expression. The invention particularly relates to glucoccerebrosidase and alpha-galactosidase having a post-translational modification. The enzymes are useful in enzyme replacement therapy for treating lysosomal storage diseases (e.g. Gaucher disease, Niemann-Pick disease, Fabry disease and Tay-Sachs disease), in researches for developing new approaches to medical treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is human recombinant alphagalactosidase-A C-terminal modified peptide.
                                                                                                                                                                                                                                                                                                 Glucocerebrosidase; alpha-galactosidase; Tay-Sachs disease; plant; enzyme replacement therapy; Niemann-Pick disease; Gaucher disease; Fabry disease; lysosomal storage disease; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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New glucocerebrosidase and alpha-galactosidase having a post-translational modification, useful in enzyme replactor treating lysosomal storage diseases, e.g. Gaucher di Niemann-Pick disease, Fabry disease
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE19257 standard; peptide; 28
                                                                                                                                                                                                          31-JAN-2002
                                                                                                                                                                                                                                    WO200208404-A2
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                                                                                                                                                   26-JUL-2000; 2000US-0626127.
                                                                                                                                                                              26-JUL-2001; 2001WO-US24111.
                                                                                                                       (LARG-) LARGE SCALE BIOLOGY CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                           sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 AA;
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                                                                                              Turpen
                                                                                                                                                                                                                                                                                                                                                                                      (first
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                                                                                                                                                                                                                                                                                                                                                         alpha-galactosidase A modified peptide,
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                                                                                                                                                                                                                                                                                                                                                                                      entry)
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                                                                                              Kumagai MH;
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Pred. No.
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11;
            in enzyme replacement therapy, e.g. Gaucher disease,
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RESULT 33
AAE19255
ID AAE19
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Best Local S
Matches 6
The invention relates to production of lysosomal enzymes in plants by transient expression. The invention particularly relates to glucocerebrosidase and alpha-galactosidase having a post-translational modification. The enzymes are useful in enzyme replacement therapy for treating lysosomal storage diseases (e.g. Gaucher disease, Niemann-Pick disease, Pabry disease and Tay-Sachs disease), in researches for developing new approaches to medical treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is human recombinant alphagalactosidase-A C-terminal modified peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to production of lysosomal enzymes in plants by transient expression. The invention particularly relates to glucocerebrosidase and alpha-galactosidase having a post-translational modification. The enzymes are useful in enzyme replacement therapy for treating lysosomal storage diseases (e.g. Gaucher disease, Niemann-Pick disease, Fabry disease and Tay-Sachs disease), in researches for developing new approaches to medical treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is human recombinant alpha-galactosidase-A C-terminal modified peptide.
                                                                                                                                                                                                             New glucocerebrosidase and alpha-galactosidase having a post-translational modification, useful in enzyme replacement therapy for treating lysosomal storage diseases, e.g. Gaucher disease, Niemann-Pick disease, Fabry disease
                                                                                                                                                                                                                                                                                                                             Garger SJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human recombinant
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                                                                                                                                                                                                                                                                                                                                                            (LARG-) LARGE SCALE BIOLOGY CORP
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                                                                                                                                                                              11; Fig 5; 102pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEKDEL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-galactosidase A modified peptide, rGal-4R.
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                                                                                                                                                                                                                                                                                                                             Kumagai MH;
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Pred. No. 13;
D; Mismatches
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RESULT 35
AAY44964
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Best Local
                                                                                                  Matches
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Best Local
                                                                                                                                                                        The invention relates to production of lysosomal enzymes in plants by transient expression. The invention particularly relates to glucoccerebrosidase and alpha-galactosidase having a post-translational modification. The enzymes are useful in enzyme replacement therapy for treating lysosomal storage diseases (e.g. Gaucher disease, Niemann-Pick disease, Fabry disease and Tay-Sachs disease), in researches for developing new approaches to medical treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is human recombinant alphagalactosidase-A r(Gal-AR) C-terminal peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glucocerebrosidase; alpha-galactosidase; Tay-Sachs disease; plant; enzyme replacement therapy; Niemann-Pick disease; Gaucher disease; Fabry disease; lysosomal storage disease; human.
                                                                                                                                                                                                                                                                                                                                        New glucocerebrosidase and alpha-galactosidase having a post-translational modification, useful in enzyme replacement therapy for treating lyeosomal storage diseases, e.g. Gaucher disease, Niemann-Pick disease, Fabry disease
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                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                   Example 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human recombinant alpha-galactosidase A (rGal-AR) peptide
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                                                                                                              Similarity.
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                                                                                                                                                  36 AA;
                                                                                                                                                                                                                                                                                                                  Fig 5; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               Turpen TH,
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Pred. No.
                                                                                                              Score 29;
Pred. No.
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                                                                                                    Mismatches
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15;
                                                                                                               17;
                                                                                                                         DB 23;
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                                                                                                                         Length 36;
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Matches Query Match Best Local 9

Similarity 6; Conserv

Conservative

0,

Mismatches 48; 멂 21; 0

100.0%;

Score 29; Pred. No.

Length 90, Indels

0,

Gaps

0

1 SEKDEL

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cc shock proteins more accessible to the immune system and improves immune capponse to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has cat its carboxy terminus a region which binds to a KDEL receptor. The ctarget antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and castromytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present cleavable signal peptide; the oligomerisation domain of human cleavable signal peptide; the oligomeric matrix protein which provides concreased stability via disulphide bonds.
                                                                                                                                                                                                                                                                                         The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat
                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oligomerisation domain; neoplasia; sarcoma; lymphoma; leu melanoma; carcinoma; glioblastoma; astromytoma; oncogene;
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                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 7; 87pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rothman JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDEL receptor inhibitor; heat shock protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDEL receptor inhibitor protein-7.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-FEB-2000
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90
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AA,
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57..80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Camel IgG linker domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoe MH
                                                                                                                                                                                                                                                                                                                                                                                      English.
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SEKDEL

90

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RESULT 36
ABP10603
                                                                                                                       CC proteins given in ABP00010 to ABP11500. OFFX proteins are useful for CC treating or preventing a pathology associated with an OFFX-associated CC disorder in humans, and in the manufacture of a medicament for treating a CC syndrome associated with OFFX-associated disorder. OFFX polynucleotide CC sequences can be used in gene therapy. OFFX sequences can be used in the CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver, CC psoriasis, benign tumours, keloid, degenerative disorders related to organ transplantation, cardiovascular diseases, disorders related to organ CC tupus erythematosus, hypertension, hypothyroidism, cholesterol ester CC storage disease, various immune deficiencies and disorders, infectious CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid carthritis, autoimmune inflammatory eye disease. OFFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, CC useful for treating burns, incisions, ulcers, for treating osteoporosis, conception or regeneration and treatment of lung or liver fibrosis, consistency cytokine damage.

CC NB The degeneration and treatment of lung or liver fibrosis, consistency of the consist of the consistency of the consist of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID 21188; 1037pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preventing and treating cardiovascular disea hyperproliferative disorders and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; open reading frame; ORFX; gene therapy; cancer; cirrnosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage degenerative disorder; osteoarthritis; nemign tumour; desporder; osteoarthritis; nemign degenerative disorder; osteoarthritis; nemign desporder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP10603 standard; Protein; 97
                                                                              specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200192523-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORFX protein sequence SEQ ID NO:21188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the specification)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes substantially purified human protoneferred to as open reading frame, ORFX, where X is 1-11491 (see in the specification). ABN15762 to ABN27252 encode the human ORFX
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                                              ftp.wipo.int/pub/published_pct_sequences
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                                                                           The sequence data for this fication, but was obtained
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                                                                           for this patent did not form part of the printed
obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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(see Table 1
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Sequence

97

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Best Local Similarity
The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sercoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astromyroma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present
                                                                                                                                                                                                                                                                                              Disclosure; Fig 3; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                          Inhibitors of the KDEL receptor which domain useful for promoting secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAZ50494.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY44960 standard; Protein; 105 AA
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26..30
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                                                                                                                                                                                                                                                                                                                                                            comprises an oligomerization of proteins which are normally
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RESULT 38
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  The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell sues theat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted
                                                                                                                                                                   Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normal retained within the cell -
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                                                                                                                       Disclosure;
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)B; AAZ50495.
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                                                                                                                     Fig 4; 87pp;
                                                                                                                                                                                                                                                                                                                                    Mayhew
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76..99
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RESULT 39
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                      WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                   KDEL receptor inhibitor; heat shock protein; immune re oligomerisation domain; neoplasia; sarcoma; lymphoma; melanoma; carcinoma; glioblastoma; astromytoma; oncoginfectious disease; allergy; autoimmune disease.
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Inhibitors of the KDEL receptor which comprises an oligomerization

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RESULT 40
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 5; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain useful for promoting secretion of proteins which are normally retained within the cell -
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                    (SLOK ) SLOAN KETTERING INST CANCER RES
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Copyright (c) 1993 - 2003 Compugen Ltd
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10, Appl
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11, Appl
12, Appl
12, Appl
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14, Appl
15, Appl
16, Appl
17, Appl
18, Appl
19, Appl
19, Appl
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	ALIGNMENTS	US-08-066-167-1	US-08-064-174-1	US-08-867-921-61	US-08-448-194-61	US-09-347-801-21	US-09-347-801-22	US-09-347-801-20	US-09-347-801-14	US-09-134-001C-3546	US-09-581-001B-8	US-09-328-352-7414	5196523-13	US-08-441-139-11	US-08-441-139-10	US-09-124-671-34	US-09-124-671-15	US-09-124-671-13	US-09-124-671-29	
		Sequence 1, Appli	Sequence 1, Appli	Sequence 61, Appl	Sequence 61, Appl	Sequence 21, Appl	Sequence 22, Appl	20,	Sequence 14, Appl	Sequence 3546, Ap	Sequence 8, Appli	Sequence 7414, Ap	. 519	•	•	Sequence 34, Appl	-	Sequence 13, Appl	Sequence 29, Appl	

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US-08-406-192-37; Sequence 37, Application US/08406192; Patent No. 5739287
                                                               US-08-406-192-37
                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC^DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,192
FILING DATE: 16-MAR-1995
CLASSIFICATION DATA:
APPLICATION NOMBER: US 08/224,831
FILING DATE: 08-APR-194
ATTORNEY/AGENT INFORMATION:
NAME: Renzoni, George E
REGISTRATION NUMBER: 37,919
REFERENCE/DOCKET NUMBER: RECL18947
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682 8100
TELEPAX: 438023
                  Query Match
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APPLICANT: Wilbur, D.
                                                                                                                                                                                                                 TELEX: 4938023
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.Ā.
ZIP: WA 98101-2333
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC COMPO
                                                                               STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wilbur, D. Scott
APPLICANT: Prathare, Pradip M
TITLE OF INVENTION: Biotinylated Cobalamins
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1420 F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3E: Christensen, O'Connor, Johnson and Kindness
1420 Fifth Avenue, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
100.0%; Score 29; DB 1; 100.0%; Pred. No. 2.5e+05;
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                                                       US-08-373-190-10
                                                                               RESULT 3
                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-545-151-37
Sequence 10, Application US/08373190 Patent No. 5851829 GENERAL INFORMATION:
                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Worgan Jr, A. Charles
APPLICANT: Wilbur, D. Scott
APPLICANT: Wilbur, D. Scott
APPLICANT: Prathare, Pradip M
TITLE OF INVENTION: Water Soluble Vitamin B12 Receptor
TITLE OF INVENTION: Modulating Agents and Methods Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 4938023
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Renzoni, George E
REGISTRATION NUMBER: 37,919
REFERENCE/DOCKET NUMBER: REC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682 8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/545,151
FILING DATE: 19-0CT-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/0440
FILING DATE: 07-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 01
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1420 F
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (200) 224 0779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 16-MAR-1995
APPLICATION NUMBER: US 08/406,191
FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/406,192 FILING DATE: 16-MAR-1995 APPLICATION NUMBER: US 08/406,194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: WA 98101-2333
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                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                        amino acids
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                                                                                                                                                                                                                 100.0%; Score 29; DB 2; ilarity 100.0%; Pred. No. 2.5e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Christensen O'Connor Johnson & KindnessPLLC
                                                                                                                                                                                                                                                                                                                                                      single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MARASCO, WAYNE APPLICANT: HASELTINE, WILLIAM TITLE OF INVENTION: METHOD OF NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06735
PILING DATE: 16-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                   NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN;
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                              APPLICANT: MARASCO, WAYNE APPLICANT: HASELTINE, WILLIAM TITLE OF INVENTION: METHOD OF TITLE OF INVENTION: PROTEINS
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STREET: LUC
STREET: BOSTON
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ZIP: 02109
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REGISTRATION NUMBER: 34.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 17-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
                               ZIP:
                                                       CITY: BOSTON
STATE: MASSACHUSETTS
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                                        COUNTRY:
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130 WATER STREET
                                                                                      130 WATER STREET
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Floppy disk
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                                                                                                                    DIKE, BRONSTEIN, ROBERTS &
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US-08-350-215-13
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Best Local Similarity luu.
"-- hes 6; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: EISSNSTEIN, RONALD I.
REGISTRATION NUMBER: 4195

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-5440
TELEPAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION: DONE SEG ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE A.
APPLICANT: RICHARDSON, JENNIFER
APPLICANT: RICHARDSON, JENNIFER
TITLE OF INVENTION: INTRACELLULAR TARGETING OF ENDOGENOUS
TITLE OF INVENTION: PROTEINS
                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: EISENSTEIN, RONALD I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 4195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEFX: 200291 STRE UR
                                                                TELEX: 200291 STRE UK
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                               SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 130 W
TOPOLOGY:
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/01 FILING DATE: 12-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SEKDEL 6
                                                                                                                                                                                                                                                                                                                                                                                                                02109
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amino acid
               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08350215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 WATER STREET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS CUSHMAN
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 29; DB 2; 100.0%; Pred. No. 2.5e+05;
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                                                                                                                                                                   41956-CP3
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Query Match
Best Local Similarity
"""" 6; Conserv:
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                                                                                                                                     US-09-124-671-39
                                                                                                                                                        RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09287145A Patent No. 6072036 GENERAL INFORMATION:
                                                                                      GENERAL INFORMATION:
                                                                                                  Sequence 39, Appli
Patent No. 6160088
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Best Local Similarity
APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MARASCO, WAYNE APPLICANT: HASELTINE, WILLIAM TITLE OF INVENTION: METHOD OF TITLE OF INVENTION: PROTEINS NUMBER OF SEQUENCES: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: EISENSTEIN, RONALD I.
REGISTRATION NUMBER: 30628
REGERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SEKDEL 6
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                                                                                                                       Application US/09124671A
                                                                                                                                                                                                                                                                                                                                                                                             6 amino acids
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                                                                                                                                                                                                                                                                                                                                                             linear
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US-09-191-852-3
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                                                                                                                             US-09-191-852-3
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CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application Patent No. 6194560
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                                                               Matches
                                                                              Best Local Similarity
                                                                                           Query Match
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                                                                                                                                                                                                      TELEFAX: 713-651-5246
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US
FILING DATE: 24-OCT-1995
APPLICATION NUMBER: 08/817
FILING DATE: 04-AUG-1997
ATTORNEY AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Filbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: P01590US1
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
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CITY: Houston
TY: TX
                                                                                                                                        MOLECULE TYPE: peptide
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                              SEKDEL 6
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GY: linear
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                                                                                                                                                                                         6 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charles J. Arntzen, Hugh S. Mason, and Tariq A. Haq
VENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                               Conservative
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                                                            Score 29; DB 3; I
Pred. No. 2.5e+05;
; Mismatches 0;
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Pred. No. 2.5e+05;
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                                                                                           Length 6;
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RESULT 10
US-09-556-111-13
; Sequence 13, Application US/09556
; Patent No. 6329173
; GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE
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US-08-840-466A-27
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Best Local Similarity
Matches 6; Conserva
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
SOFTWARE: PATENTIN PATENTIN DATA:
APPLICATION NUMBER: US/08/840,466A
FILING DATE: 18 Apr-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Stewart, C. Neal
McKee, Marian L.
O'Brien, Alison D.
Wachtel, Marian R.
TITLE OF INVENTION: Method Of Stimulating An Immune Response
By Administration Of Host Organisms That Express Int
Alone Or As A Fusion Protein With One Or More Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Boone, Laural S.
REGISTRATION NUMBER: 43,505
REFERENCE/DOCKET NUMBER: 041
TELECOMMUNICATION INFORMATION:
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NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                     NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                  HASELTINE, WILLIAM TITLE OF INVENTION: METHOD OF
                                                                                                                                                                                                                                                                                                                           1 SEKDEL
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STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
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STREET: 130 WATER STREET CITY: BOSTON
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Pred. No. 2.5e+05;
; Mismatches 0;
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Best Local Similarity 100.
Warches 6; Conservative
                                                                   Query Match
Best Local S
Matches 6
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CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Mason, Hugh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                          -09-414-276-10
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Arntzen, Charles
TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
FILE REFERENCE: 4868/84453
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Peptide signal OTHER INFORMATION: which targets nascent protein to the endoplasmic OTHER INFORMATION: reticulum.
                                                                                                                                                                                                                                             LENGTH: 6
TYPE: PRT
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                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 13:
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                                                                 Similarity
6; Conserv
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FILING DATE: 21-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: EISENSTEIN, RONALD I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/438,190 FILING DATE: <Unknown>
                                SEKDEL 6
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TOPOLOGY: linear
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                                                                     Conservative
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                                                                                  100.0%; Score 29; DB 4;
100.0%; Pred. No. 2.5e+05;
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Pred. No. 2.5e+05;
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                                                                                                  Length 6;
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RESULT 13
US-09-696-188B-27
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US-08-817-906-3
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Matches
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                                                                                                                                                                                                                                                                                                                      Sequence 27,
                                                                                                                                                                                                                                                                             Patent No. 6406885
GENERAL INFORMATION:
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APPLICANT: Charle
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
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ZIP: 77010
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5151
TELEFAX: 713-651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US95/13376
FILING DATE: 24-OCT-1995
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fox, David L.
REGISTRATION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: UFFILING DATE: 08/04/97 CLASSIFICATION: 800
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les 6; Conserv
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                                                                                                     APPLICANT: Steman, McKee, Marian I.

McKee, Marian I.

O'Brien, Alison D.

Wachtel, Marian R.

Wachtel, Method Of Stimulating An Immune Response
By Administration Of Host Organisms That !

Alone Or As A Fusion Protein With One Or
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS: 27
CORRESPONDENCE Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Finnegan, L.L.P.
Dunner, L.L.P.
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                            APPLICANT: Stewart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 29; DB 4; llarity 100.0%; Pred. No. 2.5e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/381,464
CURRENT FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: PCT/EP 98/01731
PRIOR FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 1
SOFTWARE: WordPerfect version 6.1
SEQ ID NO 1
LENGTH: 6
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-696-188B-27
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Query Match
Best Local Similarity 1
"""heb 6; Conservat!
                                                                                     ; FEATURE:
; OTHER INFORMATION: Endoplasmic reticulum retention signal
US-09-381-464-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-381-464-1
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Conrad, Udo
TITLE OF INVENTION: Expression of herbicide-binding polypeptides in plants for gener:
TITLE OF INVENTION: herbicide
TITLE OF INVENTION: tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lerchl, Jens
APPLICANT: Mller, Achi
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                      ORGANISM: Unknown
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/696,188B
FILING DATE: 26-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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PILING DATE: 1997-04-18
ATTORNEY/AGENT INFORMATION:
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LENGTH: 6 amino acids
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REGISTRATION NUMBER: 43,505
REFERENCE/DOCKET NUMBER: 04995.0029-00000
TELECOMMUNICATION INFORMATION:
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Schmidt, Ralf-Michael
Schiffer, Helmut
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TELEFAX: (202) 408-4400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 29; DB 4; ilarity 100.0%; Pred. No. 2.5e+05; Conservative 0; Mismatches 0:
                  Conservative
                                  100.0%;
                    0
                                  Score 29; DB 4; 1
Pred. No. 2.5e+05;
                    Mismatches
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US-09-471-573A-4
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                    RESULT 17
PCT-US92-08090-5
; Sequence 5, Application PC/TUS9208090
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; FEATURE: ; OTHER INFORMATION: protein localization sequence US-09-423-097-2
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APPLICANT: Mason, Hugh
APPLICANT: Thanavala, Yasmin
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 6
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Patent No. 6551820
                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09423097 Patent No. 6569831
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/423,097
CURRENT FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Recombinant Lactoferrin, Methods of Production from Plants and
                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 1149-4
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OTHER INFORMATION: Microsomal retention signal
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                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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Pred. No. 2.5e+05;
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Pred. No.
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                                                                                               2.5e+05;
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Best Local Similarity
Matches 6; Conserv
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ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-572-6508
TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application PC/TUS9513376 GENERAL INFORMATION:
COUNTRY: USA
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
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HYPOTHETICAL: N
ANTI-SENSE: NO
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LENGTH: 6 amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08090
FILING DATE: 19920922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: The Texas A&M University System APPLICANT: 310 Wisenbaker APPLICANT: College Station, Texas 77843-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: College Station, Texas 77843-3369
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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ITLE OF INVENTION: Fusion in the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..6
OTHER INFORMATION: /note= "ER retention signal"
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                CITY: Houston
STATE: TX
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COUNTRY: U.S.
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                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                  E: Pravel, Hewitt, Kimball & Krieger 1177 West Loop South, 10th Floor
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100 Peachtree Street
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RESULT 19
US-08-753-159A-5
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Matches 6; Conserv
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Patent No. 5824500
                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,1
FILING DATE: Filed Herewith
PRIOR APPLICATION UNMBER:
APPLICATION NUMBER:
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INFORMATION FOR SEQ ID NO:
                                                                    TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
                                                   SEQUENCE CHARACTERISTICS
                                                                                                                        REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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LENGTH: 6 amino acids
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APPLICATION NUMBER: US 08/328,716
FILING DATE: 24-OCT-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jones, John W.
REGISTRATION NUMBER: 31,380
REFERENCE/DOCKET NUMBER: 36
                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Palo Alto
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STRANDEDNESS:
                                                                                                      TELEPHONE: 415-855-0555
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             : 8 amino acids amino acid
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ilarity 100.0%;
Conservative 0
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Pred. No. 2.5e+05;
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US-08-753-159A-5
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                                                         US-09-124-671-31
Sequence 31, Application US/09124671A
Patent NO. 6160088
GENERAL INFORMATION:
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US-09-133-735-5
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                                                                                                                        RESULT 21
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
              APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS
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TITLE OF INVENTION:
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MEDIUM TYPE: Diskette
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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NVENTION: NOVEL HUMAN KDEL RECEPTOR
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                                                                                                                                                                                                                                                100.0%; Score 29; DB 3; 100.0%; Pred. No. 2.5e+05;
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100.0%; Pred. No. 2.5e+05;
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PILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 90
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                               US-09-124-671-17
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CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31
                                                            CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 105
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APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
                                                                                                                                                                                                                                                       Sequence 17, Application US/09124671A Patent No. 6160088 GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                       APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: chimeric mouse TSP3-KDEL
                                ORGANISM: Artificial Sequence
                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                      85 SEKDEL
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100.0%; Pred. No.
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Pred. No. 2.5e+05,
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US-09-124-671-19
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                                                                                                              ; OTHER INFORMATION: chimeric Xenopus laevis TSP4-KDEL
US-09-124-671-21
                                                                                                                                                                 FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 109
TYPE: PRT
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: ROTHMAN, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
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Matches
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TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEO ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
FENOME: 100
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                                                  Query Match
Best Local Similarity
Matches 6; Conserv
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APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
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Best Local Similarity
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TYPE: PRT
ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Hoyhew, Mark
APPLICANT: Hee, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27
; Sequence 29, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Hothman, James
; APPLICANT: Hoe, Mee
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/09/124,671A
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US-09-124-671-29
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; OTHER INFORMATION: chimeric human TSP3-KDEL
US-09-124-671-27
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US-09-124-671-27
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Best Local S
Matches 6
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APPLICANT: ROCLMMAN, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
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SEQ ID NO 23
LENGTH: 109
TYPE: PRT
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Best Local Similarity 100.0%;
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TYPE: PRT
ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Rothman, James
APPLICANT: Hoe, Mee
TITILE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31468
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
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US-09-124-671-15
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; OTHER INFORMATION: chimeric rat COMP-KDEL
US-09-124-671-15
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NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29
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Patent No. 6160088
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OTHER INFORMATION: chimeric human TSP4-KDEL
-09-124-671-29
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TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
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                                           LENGTH: 115
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
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TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
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APPLICANT: Wittru
APPLICANT: Robins
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ORGANISM: Artificial Sequence
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            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: DIGISIO, Frank S.
REGISTRATION NUMBER: 31,346
                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, S
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                               APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
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REFERENCE/DOCKET NUMBER:
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ilarity 100.0%;
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Pred. No. 25;
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Pred. No.
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TELEPHONE: 516-742-4343

TELEPHONE: 510-742-4366

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Best Local Similarity
                                          Query Match
Best Local (
                                                                                                                                                 INJEK: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 654 amira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08441139 Patent No. 5773245
                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEPAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILLING DATE: 06-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
                                                                                                       MOLECULE TYPE:
                         Local Similarity
nes 6; Conserv
                                                                                                                                             LENGTH: 654 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 15-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 168 amino acids
TYPE: amino acid
                                                                                                                                STRANDEDNESS:
                                                                                                                     TOPOLOGY:
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1 SEKDEL 6
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                            Conservative
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Pred. No. 38;
                                       Score 29; DB 1; 1
Pred. No. 1.5e+02;
                            Mismatches
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                                                       Length 654;
                            Indels
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                          Gaps
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CALCIUM AND TEMPERATURE

NUMBER OF SEQUENCES: 28
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/35.
PILING DATE: 19-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 282,880
FILING DATE: 05-DEC-1988
FILING DATE: 05-DEC-1988
FILING DATE: 01-JAN-1985
SEQ ID NO:13:
1ENGTH: 187
GENERAL INFORMATION:
APPLICANT: No. 6472142cborn, Mathieu
APPLICANT: Danan-Van Oorschot, Astrid
TITLE OF INVENTION: METHODS AND MEANS FOR INI
TITLE OF INVENTION: BIP-LIKE PROTEINS
FILE REFERENCE: 2906-4940US
CURRENT APPLICATION NUMBER: US/09/581,001B
CURRENT FILING DATE: 2000-07-24
PRIOR APPLICATION UNMBER: PC7/NL98/00688
PRIOR FILING DATE: 1998-12-03
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5196523-13
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Best Local Similarity
""" hes 5; Conserv
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US-09-581-001B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7414, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7414
LENGTH: 197
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                                                                                                                                                                                 Sequence 8, Application US/09581001B Patent No. 6472142
                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LEE, AMY TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 187
                                                                                                                                                                                                                                                                                                178 SEKDOL 183
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83.3%;
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Pred. No. 1.
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Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                              FOR INDUCING APOPTOSIS BY INTERFERING WITH
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 197;
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Query Match
Best Local Similarity
Matches 5; Conserva
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-581-001B-8
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US-09-134-001C-3546
; NAME/KEY: UNSURE
; LOCATION: (391)
US-09-347-801-14
                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-347-801-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3546
                                                                                                                                                      APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
APPLICANT: Lee, Jian Ming
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILLING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTMARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING '
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3546
LENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Applica
Patent No. 6262345
GENERAL INFORMATION:
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                                                                                                                                       SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: EP 97203783.2 PRIOR FILING DATE: 1997-12-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                           FEATURE:
                                                                            TYPE: PRT
ORGANISM: Glycine max
                                                                                                                     ENGTH: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 NEKDEL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 AEKDEL 253
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Similarity 83.3%;
5; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                Application US/09347801
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Pred. No. 2.9e+02;
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Pred. No. 2.
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2.5e+02;
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RESULT 40
US-09-347-801-22
; Sequence 22, Ap
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                                                                                                               US-09-347-801-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6262345
GENERAL INFORMATION:
                                                                                                                            SEQ ID NO 22
LENGTH: 411
TYPE: PRT
ORGANISM: Medicago sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                         Matches
                                                                       Best
                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                Patent No. 62623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
                                                                                                                                                                                                                               FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
                                                                                                                                                                                                  EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                      APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Microsoft Office 97
                                                                                                                                                                                     SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 TEKDEL 159
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139 TEKDEL 144
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                                                         Conservative
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83.3%;
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Pred. No.
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Pred. No. 4e+0
1; Mismatches
                                                                       Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                         Mismatches 0;
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4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                      DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                    Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 399;
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Search completed: December 11, 2003, 09:59:51
Job time: 12.28 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
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Perfect score:
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Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10E_PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10E_PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10E_PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10E_PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US10E_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 2

45	44	43	42	41	40	39	38	37	36	ω G	34	ω G	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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10	12	12	9	10	14	12	12	14	14	12	12	12	12	12	12	12	12	12	15	5	5	15	15	12	10	10	12	15	15
-09-738-	US-10-238-075-489	2-224-5	09-925-301-139	US-09-738-626-4457	2-202-	-10-228-063-3	-10-228-063-	-10-047-542-4	-047-542-	8	-10-228-063-	8-063-	0-228-063-	28-	0-228-063-2	0-228-063-3	US-10-228-063-33	-10-2	US-10-103-327-6	0-103-327-	US-10-103-327-14	9	US-10-103-327-22	US-09-737-476B-57	88-721	US-09-888-721-38	US-09-737-476B-11	-10-103-327-	US-10-103-327-26
4810	e 489,	e 50,	1398,	e 445	e 32,	34,	e 24,	e 48,	e 8,	Œ	e 26,	e 40,	e 38,	ወ	e 28,	O	e 33,	e 14	Sequence 6, Appli	e 10	e 14	e 18	e 22	e 57	e 40	e 38	e 11,	Ф	6

ALIGNMENTS

RESULT 1 US-09-296-981-1

Sequence 1, Application US/09296981 Patent No. US20020055618A1

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GENERAL INFORMATION:

APPLICANT: Loma Linda University
APPLICANT: Langridge, William H.R.
APPLICANT: Langridge, William H.R.
APPLICANT: Arakawa, Takeshi
TITLE OF INVENTION: Methods and Substances for
FILE REFERENCE: 12476-1
CURRENT APPLICATION NUMBER: US/09/296,981
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/061,265
PRIOR FILING DATE: 1997-10-07
PRIOR APPLICATION NUMBER: 60/082,688
PRIOR FILING DATE: 1998-04-22
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 09/167,493
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 09/296,981
PRIOR APPLICATION NUMBER: 09/296,981
PRIOR APPLICATION NUMBER: 09/296,981
PRIOR APPLICATION NUMBER: 09/296,981
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                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
LENGTH: 6
                                                                                                      Query Match 100.0%; Score 29; DB 9; Best Local Similarity 100.0%; Pred. No. 6.1e+05; Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                      1 SEKDEL 6
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                                                                                                                                                            Length 6;
                                                                                                            Indels
                                                                                                            0,
                                                                                                            Gaps
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US-10-228-063-60
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; Sequence 27, Application US/10150058

; Publication No. US20030147902A1
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; OTHER INFORMATION: synthetic
US-10-228-063-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/228,063
CURRENT FILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 60
LENGTH C
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Matches 6; Conserv
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APPLICANT: Lanahan, Mike
TITLE OF INVENTION: Self-processing Plants and Plant Parts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                 TELEPHONE: (202) 408-4000
TELEPAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE : Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0/150,058
FILING DATE: 20-May-2002
FILING DATE: 20-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION UNMBER: US/08/840,466A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wachtel, Marian R.
TITLE OF INVENTION: Method Of Stimulating An Immune Response
By Administration Of Host Organisms That
Alone Or As A Fusion Protein With One Or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                               REGISTRATION NUMBER: 43,505
REFERENCE/DOCKET NUMBER: 04995.0029-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stewart, C. Neal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SEKDEL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1300 I Street, N.W., Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Finnegan, Henderson, Farabow, Dunner, L.L.P.
                                                                                                                                                                                           NAME: Boone, Laural S.
ENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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O'Brien, Alison D.
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Pred. No.
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; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-150-058-27
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OTHER INFORMATION:
US-10-334-729-1
                                                                                                                                                                                                                                                                                                                                                        US-10-181-633-1
                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Alfred Hospital
APPLICANT: Commonwealth Scientific and Industrial Research Organisation
APPLICANT: The University of Melbourne
APPLICANT: Australian National University
APPLICANT: Australian National University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                    SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10181633
Publication No. US20030191076A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mason, Hugh
APPLICANT: Mason, Charles
ITILE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed In
ITILE OF INVENTION: Transgenic Plants
FILE REFERENCE: 3121/1064
CURRENT APPLICATION NUMBER: US/10/334,729
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: 09/470,124
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 60/113,507
PRIOR PRIOR APPLICATION NUMBER: 60/113,507
PRIOR FILING DATE: 1998-12-22
PRIOR PRIOR APPLICATION NUMBER: 60/113,507
                                                                         PRIOR APPLICATION NUMBER: AU PQ 5208
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 7
                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/181,633
                                                                                                                                                                             TITLE OF INVENTION: Prime-boost vaccination FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
TYPE: PRT
                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEKDEL 6
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ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description of Artificial Sequence:microsomal retention signal.
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Pred. No. 6.1
0; Mismatches
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Pred. No. 6.1e+05;
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. 6.1e+05;
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ORGANISM: Artificial Sequence FEATURE:

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Best Local Similarity
Matches 6; Conserv
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Query Match
Best Local Similarity 100.
Ches 6; Conservative
                                                                                                                                        SEQ ID NO 4
LENGTH: 6
TYPE: PRT
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Best Local Similarity
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Publication No. US20020168367A1
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                                                                                                                                                                                                                                                      APPLICANT: WYCOFF, KEITH L.

APPLICANT: WYCOFF, KEITH L.

TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIP1
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR FILING DATE: 2001-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 1465-PCT-US-00
CURRENT APPLICATION NUMBER: US/09/807,742
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: PCT/US01/06288
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DANIELL, HENRY
TITLE OF INVENTION: PRODUCTION OF PHARMACEUTICAL PROTEINS IN TRANSGENIC
TITLE OF INVENTION: PLASTIDS
                                                                                                                                                                                                              PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LARRICK, JAMES W. APPLICANT: WYCOFF, KEITH L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/200,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Illustrative OTHER INFORMATION: endoplasmic reticulum retention signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                       ORGANISM: Homo sapiens
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                                            100.0%; Score 29; 100.0%; Pred. No.
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Pred. No. 6.1e+05;
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                                            6.1e+05;
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US-10-216-705-2
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                                                                                                                                                                           US-10-216-705-2
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics, S.A.
TITLE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants,
TITLE OF INVENTION: obtaining Such and Their Uses
FILE REFERENCE: 1149-3 DIV
CURRENT APPLICATION NUMBER: US/10/216,705
CURRENT APPLICATION NUMBER: US 09/331,347
PRIOR APPLICATION NUMBER: US 09/331,347
PRIOR PILING DATE: 1999-08-17
NUMBER OF SEC ID NOS: 22
COMMANDER OF SEC ID NOS: 22
                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 2
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                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/09/414,276
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 22
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APPLICANT: Palmer, Ker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Arntzen, Charles
TITLE OF INVENTION: Gemini Virus Vectors for
FILE REFERENCE: 4868/84453
                                                                                                                                                                                                                                                  LENGTH: 6
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/151,336
CURRENT FILING DATE: 2002-05-20
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OTHER INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                          OTHER INFORMATION: peptide localization sequence
                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                 ORGANISM: Unknown
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                                                                                                                       Local Similarity
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                                                                 SEKDEL 6
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No. US20030079248A1
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                                                                                                    Conservative
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                                                                                                                   Score 29;
Pred. No.
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Pred. No.
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                                                                                                    Mismatches
                                                                                                                       6.1e+05;
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                                                                                                                                      Length 6;
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Me

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Sequence 5. Application US/10047542

Publication No. US20020168367A1

GENERAL INFORMATION:
APPLICANT: HARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL INMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES

FILE REFERENCE: 030905.0004.CIP1
CURRENT APPLICATION NUMBER: US/10/047,542

CURRENT FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: PCT/US01/13932

PRIOR APPLICATION NUMBER: 60/200,298

PRIOR APPLICATION UNUMBER: 60/200,298

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 101

COPTRIBER OF SEC ID NOS: 101
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Publication No. US20030106095A1

GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: TUMAGAI, Monto H.
APPLICANT: APPLICANT: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION FILE REFERENCE: 008010087CPUS06

FILE REFERENCE: 008010087CPUS06

CURRENT APPLICATION NUMBER: US/10/103,327

CURRENT FILING DATE: 2002-03-20

PRIOR APPLICATION NUMBER: US/9/993,059

PRIOR TILING DATE: 2001-11-13

INUMBER OF SEQ ID NOS: 37

ROFERENCE SEG ID NOS: 37

ROFERENCE 
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US-10-103-327-37
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; ORGANISM: Rice
US-10-103-327-37
                                                                                                                                                                                                    RESULT 12
US-10-181-633-5
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SEQ ID NO 37
LENGTH: 6
                                                                                                                    Sequence 5, Application US/10181633
Publication No. US20030191076A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local S
                                                                                    GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 5
APPLICANT: Alfred Hospital APPLICANT: Commonwealth Scientific and Industrial Research Organisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
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100.0%; Pred. No.
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APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGAI, Monto H.
ITILE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
ITILE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPUS6
CURRENT APPLICATION NUMBER: US/10/103,327
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US/9/93,059
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 11
CRGANISM: Tobacco mosaic virus
TUPE: PRT
CRGANISM: Tobacco mosaic virus
Sequence 30, Application US/10103327

Publication No. US20030106095A1

GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGAI, Monto H.
APPLICANT: KUMAGAI, Monto H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION FILE REFERENCE: 008010087CPUS06

CURRENT APPLICATION UNUMBER: US/10/103,327

CURRENT APPLICATION UNUMBER: US/10/103,327
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Best Local Similarity
"hes 6; Conserv?
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US-10-103-327-32
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PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32, Application US/10103327 Publication No. US20030106095A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 6; Conser
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CURRENT APPLICATION NUMBER: US/10/181,633
CURRENT FILING DATE: 2002-12-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: C-terminal end of measles H p OTHER INFORMATION: fused with ER retention signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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100.0%; Pred. No. 10;
Live 0; Mismatches
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APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGAI, Monto H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPUS06
CURRENT APPLICATION NUMBER: US/10/103,327
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US/9/993,059
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/103,327
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 29
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US-10-103-327-28
; Sequence 28, Application US/101; Publication No. US20030106095A1
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; TYPE: PRT; ORGANISM: Tobacco mosaic virus US-10-103-327-26
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US-10-103-327-28'
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Best Local Similarity luu.
"--ches 6; Conservative
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Best Local Similarity 100.
"--- 6; Conservative
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LENGTH: 24
TYPE: PRT
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                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGAI, MONTO H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPUS
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2001-11-13
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Pred. No.
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Mismatches
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GENERAL INFORMATION:

APPLICANT: GRAGER, Stephen A.

APPLICANT: TURPEN, Thomas H.

APPLICANT: KUMAGAI, Monto H.

APPLICANT: KUMAGAI, Monto H.

TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN

TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION

FILE REFERENCE: 008010087CPU806

CURRENT APPLICATION NUMBER: US/10/103,327

CURRENT FILING DATE: 2002-03-20

PRIOR APPLICATION NUMBER: US/9/993,059

PRIOR FILING DATE: 2001-11-13

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 36

TYPE: PRT

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US-09-737-476B-11
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US-10-103-327-24
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APPLICANT: Vin-min TEH
APPLICANT: Wartine E. VERHOEYEN
APPLICANT: Joy E. WILKINSON
APPLICANT: Stephen A. JOBLING
TITLE OF INVENTION: Production of Antibodies
FILE REFERENCE: PNK/060113/0275850 - T7060C
CURRENT APPLICATION NUMBER: US/09/737,476B
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-103-327-24
                                                                                                                                                  SOFTWARE: MS WORD
SEQ ID NO 11
LENGTH: 153
TYPE: PRT
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APPLICANT: Leo G.J. I
APPLICANT: Cornelis
APPLICANT: Vin-miin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity luu.
Conservative
Query Match 100.0%; Score 29; DB 12; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 6; Conservative 0; Mismatches 0;
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Publication No.
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Best Local Similarity
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                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: EP 99310188.0 PRIOR FILING DATE: 1999-12-17 NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Tobacco mosaic virus
                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                            OTHER INFORMATION: VHH with linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>υ</u>
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No. US20030106095A1
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Pred. No. 35;
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                                     Length 153;
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RESULT 19 US-09-888-721-38 음 성

SEKDEL

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APPLICANT: Laurent, Olivier
APPLICANT: Marasco, Wayne A.
APPLICANT: Scherman, Daniel
ITITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
ITITLE OF INVENTION: DELIVERY
ITITLE OF INVENTION: DELIVERY
ITITLE OF INVENTION: DELIVERY
ITITLE OF INVENTION: DELIVERY
CURRENT APPLICATION NUMBER: US/09/888,721
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 060/213,653
PRIOR APPLICATION NUMBER: 060/213,653
PRIOR TILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38
LENGTH: 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
; OTHER INFORMATION: Description of Artificial Sequence:Human/murine; OTHER INFORMATION: chimeric single chain binding polypeptide; OTHER INFORMATION: (C6ML3-9sfv'-L2-KDEL)
US-09-888-721-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-888-721-40
                                                                                                                                                                                                                                                                                                                                                          Sequence 40, Application US/09888721
Patent No. US/09020132990A1
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Wils, Pierre
APPLICANT: Zhu, Quan
APPLICANT: Laurent, Olivier
APPLICANT: Marasco, Wayne A.
APPLICANT: Marasco, Wayne A.
APPLICANT: Scherman, Daniel
TITLE OF INVENTION: BIOENGOINEERED VEHICLES FOR TARGETED NUCLEIC ACID
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 23611-A USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. US20020132990A1 GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/888,721
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/213,653
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Huston, James S.
APPLICANT: Wils, Pierre
APPLICANT: Zhu, Quan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:Human/murine OTHER INFORMATION: chimeric single chain binding polypeptide OTHER INFORMATION: (C6ML-3-9sFv'-L1-KDEL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                    LENGTH: 287
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity hes 6; Conserv
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Pred. No.
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APPLICANT: CORNELIS P.E. van der LOGT
APPLICANT: Vin-Min TEH
APPLICANT: Win-Min TEH
APPLICANT: Martine E. VERHOEYEN
APPLICANT: Joy E. WILKINSON
APPLICANT: Stephen A. JOBLING
TITLE OF INVENTION: Production of Antibodies
FILE REFERENCE: PNK/060113/0275850 - T7060C
CURRENT APPLICATION NUMBER: US/09/737,476B
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION WINDER: EP 9310188.0
PRIOR FILLNG DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 67
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                                                                                                                                                                                         APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: TURAPAI, Monto H.
APPLICANT: KUMAGAI, Monto H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPUS06
CURRENT APPLICATION NUMBER: US/10/103,327
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US/9/993,059
PRIOR PILLING DATE: 2001-11-13
NUMBER OF SEQ 1D NOS: 37
NUMBER OF SEQ 1D NOS: 37
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US-09-737-476B-57
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                                                                              ; ORGANISM: Homo sapiens US-10-103-327-22
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SEQ ID NO 57
LENGTH: 383
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Best Local Similarity
Matches 6; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/10103327 Publication No. US20030106095A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Leo G.J. FRENKEN
                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                      Query Match
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Query Match 100.0%; Score 29; DB 15; Length 409; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                       LENGTH: 409
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
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100.0%; Pred. No. 4e-
tive 0; Mismatches
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Pred. No. 3e+02;
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404

SEKDEL 409

RESULT 23 US-10-103-327-18

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GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGAI, MONTO H.
APPLICANT: KUMAGAI, MONTO H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILLE REFERENCE: 008010087CPUS06
CURRENT APPLICATION NUMBER: US/10/103,327
CURRENT APPLICATION NUMBER: US/10/103,327
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US/9/993,059
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
RESULT 25
US-10-103-327-10
; Sequence 10, Application US/10103327
; Publication No. US20030106095A1
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Best Local Similarity
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; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-327-18
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Publication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGAI, MONTO H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPUS06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GARGER, Stephen A. APPLICANT: TURPEN, Thomas H. APPLICANT: KUMAGAI, Monto H.
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PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2002-03-20
                                                                                                                                                                                                                                                                                             LENGTH: 427
TYPE: PRT
ORGANISM: Homo sapiens
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mes 6; Conserv
                                                                                                                          422
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Pred. No. 4.5e+02;
; Mismatches 0;
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Sequence 6, Application US/10103327

Publication No. US20030106095A1

GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TUREN, Thomas H.
APPLICANT: TUREN, Thomas H.
APPLICANT: WAMGAI, Monto H.
ITITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
ITITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPUS06

CURRENT APPLICATION NUMBER: US/10/103,327
CURRENT APPLICATION NUMBER: US/09/993,059
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR TILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
NUMBER OF SEQ ID NOS: 37
                                                                                                                       RESULT 27
US-10-228-063-14
; Sequence 14, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Mike
; TITLE OF INFERTION: Self-processing Plants and Plant Parts
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US-10-103-327-6
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-327-10
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APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGAI, Monto H.
FILE REFERENCE: 109846.317
CURRENT APPLICATION NUMBER: US/10/228,063
CURRENT FILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local (
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TYPE: PRT
ORGANISM: Homo sapiens
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Local Similarity 100.0%;
les 6; Conservative C
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Pred. No. 4.6e+02;
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LENGTH: 460

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; OTHER INFORMATION: synthetic US-10-228-063-14
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US-10-228-063-33
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                                                                                                                          ; OTHER INFORMATION: synthetic US-10-228-063-35
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Best Local S
Matches 6
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Publication No. US20030135885A1
GENERAL INFORMATION:
APPLICANT: Lanahan, Mike
TITLE OF INVENTION: Self-processing Plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 109846.317
CURRENT APPLICATION NUMBER: US/10/228,063
CURRENT FILING DATE: 2002-12-12
NUMBER OF SEO ID NOS: 60
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
                                                                            Query Match
Best Local
                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: synthetic -10-228-063-33
                                                                                                                                                                                                                                                                   APPLICANT: Lanahan, Mike TITLE OF INVENTION: Self-processing Plants and Plant Parts FILE REFERENCE: 109846.317
CURRENT APPLICATION NUMBER: US/10/228,063
CURRENT FILING DATE: 2002-12-12
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                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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455 SEKDEL 460
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                                                                              Similarity
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                                                           Conservative
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100.0%; Pred. No.
                                                                            100.0%;
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Pred. No. 4.9e+02;
; Mismatches 0;
                                                           Score 29; DB 12;
Pred. No. 4.9e+02;
Mismatches 0;
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Sequence 28, Application US/10228063

Publication No. US20030135885A1

GENERAL INFORMATION:
APPLICANT: Lanahan, Mike
TITLE OF INVENTION: Self-processing Plants and Plant Parts
FILE REFERENCE: 109846.317

CURRENT APPLICATION UNMER: US/10/228,063

CURRENT FILING DATE: 2002-12-12

INVESE OF SEQ ID NOS: 60

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 469
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
APPLICANT: Lanahan, Mike; TITLE OF INVENTION: Self-processing Plants an; FILE REFERENCE: 109846.317; CURRENT APPLICATION NUMBER: US/10/228,063; CURRENT FILING DATE: 2002-12-12; NUMBER OF SEQ ID NOS: 60; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 38; LENGTH: 477
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Best Local Similarity
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US-10-228-063-28
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Sequence 38, Application US/10228063
Publication No. US20030135885A1
GENERAL INFORMATION:
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SEQ ID NO 29
LENGTH: 469
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Publication No. US20030135885A1
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Best Local Similarity 100.0%;
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CURRENT FILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 60
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TITLE OF INVENTION: Self-processing Plants
FILE REFERENCE: 109846.317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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nilarity 100.0%;
Conservative (
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100.0%; Pred. No. 5e+02;
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Pred. No. 5e+02;
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RESULT 34
US-10-228-063-26
US-10-228-063-26
; Sequence 26, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
RESULT 35
US-10-228-063-36
; Sequence 36, Application US/10228063
; Publication No. US20030135885A1
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Best Local Similarity lou.
""" tohes 6; Conservative
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Best Local Similarity luu.
Thes 6; Conservative
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Publication No. US20030135885A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              SEQ ID NO 26
LENGTH: 718
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                                                                                                                                                                    Matches
                                                                                                                                                                                               Query Match
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CURRENT APPLICATION NUMBER: US/10/228,063
CURRENT FILING DATE: 2002-12-12
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/228,063
CURRENT FILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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les 6; Conserv
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Pred. No. 5.1e+02;
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Pred. No. 5.1e+02;
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Sequence 8, Application US/10047542

PUBLICANT: LARRICK, JAMES W.
APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES

FILE REFERENCE: 030905,0004 CIP1
CURRENT APPLICATION NUMBER: US/10/047,542
CCHRENT FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: PCT/US01/13932

PRIOR APPLICATION NUMBER: PCT/US01/13932

PRIOR APPLICATION NUMBER: PCT/US01/13932

PRIOR APPLICATION NUMBER: DO/200,298

PRIOR PILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 101

CORTWADE: DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 101
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APPLICANT: Lanahan, Mike
TITITE OF INVENTION: Self-processing Plants and
FILE REFERENCE: 109846.317
CURRENT APPLICATION NUMBER: US/10/228,063
CURRENT FILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
               US-10-047-542-48
; Sequence 48, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
APPLICANT: LAVICOFF, KEITH L.
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION UNMBER: US/10/047,542
; CURRENT PILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR FILING DATE: 2001-04-28
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-8
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Best Local Similarity
Thes 6; Conserva
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ORGANISM: Artificial Sequence
FEATURE:
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APPLICATION NUMBER: 60/200,298
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illarity 100.0%;
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Pred. No. 8.7e+02;
); Mismatches 0;
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Pred. No. 7.8e+02;
); Mismatches 0;
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OTHER INFORMATION: Description of Artificial Sequence: Protein OTHER INFORMATION: encoded by plasmid pSSPICAMHUA2 US-10-047-542-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 48
LENGTH: 822
TYPE: PRT
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US-10-228-063-34
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                                                                            ; OTHER INFORMATION: synthetic US-10-228-063-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Lanahan, Mike
TITLE OF INVENTION: Self-processing Plants and Plant Parts
FILE REFERENCE: 109846.317
CURRENT APPLICATION NUMBER: US/10/228,063
CURRENT FILING DATE: 2002-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 825
                                                                                                                                                               APPLICANT: Lanahan, Mike
TITLE OF INVENTION: Self-processing Plants and Plant Parts
FILE REFERENCE: 109846.317
CURRENT APPLICATION NUMBER: US/10/228,063
CURRENT FILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 825
                                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/10228063 Publication No. US20030135885A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/10228063 Publication No. US20030135885A1
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Best Local :
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ORGANISM: Artificial Sequence
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                                                                                                             ORGANISM: Artificial Sequence FEATURE:
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Pred No.
     Score 29; DB 12; Length 825; Pred. No. 9e+02; ); Mismatches 0; Indels
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8.9e+02;
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RESULT 40
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Search completed: December 11, 2003, 10:13:39 Job time : 22.6 secs
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Publication No. US20020136733A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICATION NUMBER: US/10/042,202
FILING DATE: 11-Jan-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,175
FILING DATE: 28-JAN-1997
APPLICATION NUMBER: WO PCT/GB95/26982
FILING DATE: 30-MAR-1995
FILING DATE: 31-MAR-1995
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: GB 9406492.0
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M Cheek, Jr.
REGISTRATION NUMBER: 33,367
REGERENCE/DOCKET NUMBER: 2002_0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20006-1021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPad for Windows 95
CURRENT APPLICATION DATA:
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ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.
STREET: 2033 K Street, N.W., Suite 800,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Adrian Vivian Sinton HILL, Michael AIDOO,
Catherine Elizabeth Margaret ALLSOPP, Ajit LALVANI, Magdalena
PLEBANSKI, Hilton Carter WHITTLE,
                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MALARIA PEPTIDES NUMBER OF SEQUENCES: 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 8 amino acids
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                                                                                                                                                                      Conservative
                                                                                                                                                                                            93.1%;
83.3%;
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Post-processing: Minimum Match 0% Maximum Match 10
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ALIGNMENTS

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submitted to the sequence of C. elegans cosmid K09C6
A;Cross-references: EMBL:AF022975; PIDN:AAB70669.1; GSPDB:GN00023; CESP:K09C6.2 A;Experimental source: strain Bristol N2; clone K09C6 C;Gene:ics:
A;Gene: CESP:K09C6.2
A;Map position: 5
A;Introns: 22/3; 129/2; 282/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein K09C6.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct.1999 #sequence_revision 29-Oct.1999 #text_change 29-Oct.1999 C;Accession: T32182
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-279 <HEI>
A;Cross-references: GB:AE004265; GB:AE003852; NID:g9656424; PIDN:AAF95048.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fatty acid metabolism regulator protein VC1900 [imported] - Vibrio cholerae (strain N169 c;Species: Vibrio cholerae
c;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 19-Jul-2002
C;Accession: B8214
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
Chardson, D.; Brmolaeva, M.D.; Vamathevan, J.; Bass, C.M.
Nature 406, 477-483, 2000
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A;Accession: B82144
                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-344 <GOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 1
C;Superfamily: pyruvate dehydrogenase complex repressor
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100.0%; Pred. No.
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C;Species: Clostridium acetopury.r.u...
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_chang
C;Date: 18-Sep-2001 #sequence_revision 14-Sep-2001 #text_chang
C;Accession: B96953
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.;
Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
J. Bacteriol. 183, 4823-4838, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-441 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK78413.1;
A;Experimental source: Clostridium acetobutylicum
C;Genetics:
esterase precursor - Caenorhabditis briggsae
C;Species: Caenorhabditis briggsae
C;Date: 17-Apr-1993 #sequence_revision 17-Apr
                                                     RESULT 5
S27782
                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-512 <WIL>
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submitted to the EMBL
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A;Experimental source: clone D2023
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Best Local S
Matches 6
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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Accession: B96953
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revision 17-Apr-1993 #text_change 18-Jun-1999
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Pred. No.
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Pred. No.
                                                                                                                                                                                      Score 29; DB 2;
Pred. No. 1.1e+02;
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ATCC824
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hypothetical protein all3010 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AC2182
C;Accession: AC2182
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2182
                                                                                               C:pate: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000 C;Accession: D71435  
C;Accession: D71435  
R;Bevan, M; Bancroft, I.; Bent, B.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 1998  
Nature 391, 485-488, 1998  
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech A;Authors: Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Anton Challer And 
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A;Description: The gut esterase gene (ges-1) from the nematodes Caenorhabditis A;Reference number: 827782
A;Accession: $27782
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                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
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A; Residues: 1-562 < KEN>
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A;Experimental source: strain PCC 7120
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A; Residues: 1-613 < KUR>
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A; Title: Analysis of 1.9 Mb
A; Reference number: A71400;
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   of contiguous sequence from chromosome MUID:98121113; PMID:9461215
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Pred. No. 1.4
0; Mismatches
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Pred. No. 1.3e+02;
; Mismatches 0;
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dnaK-type molecular chaperone GRP78 precursor - Chinese hamster
N;Alternate names: glucose-regulated 78K protein; Ig heavy chain-binding protein
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Aug-1999
C;Accession: A27414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Contains: steroidogenesis-activator polypeptide C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change C;Accession: A23948; A60134; A26257 R;Munro, S.; Pelham, H.R.B.
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R;Chang, S.C.; Wooden, S.K.; Nakaki, T.; Kim, Y.K.; Lin, A.Y.; Kung, L.; Attenello, J.W. Proc. Natl. Acad. Sci. U.S.A. 84, 680-684, 1987
A;Title: Rat gene encoding the 78-KDa glucose-regulated protein GRP78: its regulatory se A;Reference number: A26257; MUID:87118232; PMID:3468506
A;Accession: A26257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M14050; NID:g203150; R;Pedersen, R.C.; Brownie, A.C. Science 236, 188-190, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 46, 291-300, 1986
A;Title: An Hsp70-like protein in the BR: identity with A;Reference number: A23948; MUID:86245075; PMID:3087629
A;Accession: A23948
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N;Alternate names: BiP; glucose-regulated 78K protein;
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A;Residues: 1-28;'M',30-40 <CHA>
A;Cross-references: GB:M14866; NID:g204478; PIDN:AAA41277.1; PID:g554440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Steroidogenesis-activator polypeptide isolated A; Reference number: A60134; MUID:87177981; PMID:3563495
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;21-654/Product: Ig heavy chain binding protein #status predicted
;651-654/Region: endoplasmic reticulum retention signal
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S.K.; Kriz,
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R.; Kelleher, K.;
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Pred. No.
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R.J.; Lee,
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dnaK-type molecular chaperone grp78 precursor - mouse N;Alternate names: BiP; glucose-regulated 78K protein; Ig heavy chain-bindir C;Species: Mus musculus (house mouse) C;Date: 15-Jan-1993 #sequence revision 15-Jan-1993 #text_change 20-Aug-1999 C;Accession: A37048; M37048; M0ID:90130686; PMID:2559088 A;Accession: A37048 M0ID:90130686; PMID:2559088
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 488-590,'G',592-595,'E',597-655 <PAR>
A;Residues: 488-590,'G',592-595,'E',597-655 <PAR>
A;Cross-references: GB:M30779; NID:g193644; PIDN:AAA37742.1;
A;Cross-references: GB:M3079; NID:g193644; PIDN:AAA37742.1;
A;Cros
                                                                                                                                                                                                                                A;Cross-references: EMBL:U16277; NID:g829364; PIDN:AAA76 R;Haas, I.G.; Meo, T. Proc. Natl. Acad. Sci. U.S.A. 85, 2250-2254, 1988 A;Title: cDNA cloning of the immunoglobulin heavy chain A;Reference number: A31934; MUID:88176922; PMID:2895472 A;Accession: A31934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Tillman, J.B.; Mote, P.L.; Walford, R.L.; Spindler, S.R. Gene 158, 225-229, 1995
A;Title: Structure and regulation of the mouse GRP78 (BiP)
A;Reference number: 149137; MUID:95331621; PMID:7607546
A;Accession: 149137
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A;Title: Differential Screening of a cDNA library with cDNA probes amplified A;Reference number: JQ0094; MUID:90060818; PMID:2583523
A;Accession: JQ0094
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R;Parfett, C.L.J.; Hofbauer, R.; Brudzynski, K.; Edwards, D.R.; Denhardt,
Gene 82, 291-303, 1989
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A; Residues: 1-655 < KZ1>
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C;Superfamily: heat shock protes
C;Keywords: ATP; heterotetramer;
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A; Residues: 1-654 <TIN>
A;Gene: grp78
C;Function:
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A; Residues: 514-589, '
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A; Reference number: A27414; MUID:87305586; PMID:3623104
                                                                              C;Genetics:
                                                                                                                A;Residues: 514-589,'D',591-595,'E',597-655
A;Cross-references: GB:M19351; NID:g192231;
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A;Residues: 1-28 <RES>
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Pred. No. 1.5e+02;
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PIDN:AAA37315.1;
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A;Description: involved in

protein folding and assembling/disassembling of protein compl

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C;Species: Ustilago way...
C;Date: 06-Jan-1995 #sequence_revision U6-Uan-1992
C;Accession: S27473
R;Volsard, C.P.; Wang, J.; Xu, P.; Leong, S.A.
submitted to the EMBL Data Library, January 1992
submitted to the EMBL Data Characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: heat shock protein 70
C;Keywords: ATP; endoplasmic reticulum; glycoprotein; heterotetramer; molecular chaperon F;1-19/Domain: signal sequence #status predicted <SIG>F;20-655/Product: dnaK-type molecular chaperone grp78 #status experimental <MAT>F;652-655/Region: endoplasmic reticulum retention signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: S56186
A;Accession: S56268
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-787 <MUR>
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                                                                                                                               A; Molecule type; DNA
A; Residues: 1-950 <VOI>A; Residues: 1-950 <VOI>A; Cross-references: EMBL: M80547; NID: 9295416; PID: 917059
A; Cross-references: EMBL: M80547; NID: 9295416; PID: 917059
C; Superfamily: GATA-type zinc finger homology <GZF1>
F; 335-388/Domain: GATA-type zinc finger homology <GZF1>
F; 479-532/Domain: GATA-type zinc finger homology <GZF2>
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                                                                                                                                                                                                                                                                                                                                                                                            URBS1
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Best Local S
Matches 6
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;Species: Ustilago maydis (corn smut)
;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
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ata Library, May 1995
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RESULT 13

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A;Genome: nuclear
A;Genome: nuclear
A;Genome: nuclear
A;Roto: starch phosphorylase
C;Function:
C;Function: catalyzes the formation of glucose 1-phosphate from polyglucose
C;Superfamily: phosphorylase
C;Superfamily: phosphorylase
C;Keywords: chloroplast; glycosyltransferase; hexosyltransferase; phosphoprotein;
F;1-43/Domain: transit peptide (chloroplast) #status predicted <TNP>
F;44-955/Product: starch phosphorylase #status predicted <MAT>
F;44-955/Product: starch phosphorylase #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-1992 <WIL>
A;Cross-references: EMBL:Z78199; PIDN:CAB01576.1; GSPDB:GN00023;
A;Experimental source: clone K12F2
R;Dibb, N.J.; Maruyama, I.N.; Krause, M.; Karn, J.
J. Mol. Biol. 205, 603-613, 1989
A;Title: Sequence analysis of the complete Caenorhabditis elegans
A;Reference number: S02771; MUID:89178677; PMID:2926820
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submitted to the EMBL Data Library, July 1991
A;Description: Primary structure of sweet potato starch phosphorylase deduced from its
                                                                      A;Introns: 46/1; 192/1; 292/1; 468/2; 1921/3
C;Superfamily: myosin heavy chain; myosin motor domain k
C;Keywords: actin binding; ATP; coiled coil; hydrolase;
C;Keywords: myosin motor domain homology <MMOT>
F;89-802/Domain: myosin motor domain homology <MMOT>
F;202-209/Region: nucleotide-binding motif A (P-loop)
F;690-712/Region: actin binding #status predicted
F;793-807/Region: actin binding #status predicted
F;793-807/Region: actin binding #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z17224
A; Accession: T10947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequ
A;Molecule type: DNA
A;Residues: 1-116,140-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T23622
A;Status: translated from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession:
R;Harris, B.
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F;875-1992/Domain: coiled
F;875-1189/Region: S2
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                                                                                                                                                                                                                                                                                                                                                                                    A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: myo-3; CESP:K12F2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references:
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ce: cv. Tainong 57; tuberous root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL:X08067; NID:g6798;
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Pred. No. 2.2e+02;
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Science 294, 849-852, 2001

A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.; A; M.; C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AE1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein lin0637 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua C;Species: Listeria innocua C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AE1512
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A;Molecule type; DNA
A;Residues: 1-91 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC98706.1; PID:g16410017; GSPDB:GN00177
A;Cross-referental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.; M.; A;Authors: Kreft, T.; Schlueter, T.; Simmees, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AD1153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nypothetical protein lmo0628 [imported] - Listeria monocytogenes (strain EGD-e) C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AD1153
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                                                                                                                                                                       A;Cross-references: GB:AL592022; PIDN:CAC95869.1; PID:g16413077; GSPDB:GN00178
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-91 <GLA>
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                                                                                                                                   A;Gene: lin0637
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; Jones, L.M.; Karst, l
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Entian, K.D.; Fsihi, H.
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RESULT 18
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A;Residue: 1-289 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74283.1; PID:g17131677; GSPDB:GN00179
A;Cross-imental source: strain PCC 7120
probable two-component sensor PA4886 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; MUID:21608550; A; Accession: AB3022
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; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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G;Accession: AI2128

G;Accession: AI2128

R;KaneKo, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AI2128
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain EC;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2001
                                                                               H98262
                                                                                                    RESULT 19
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A;Experimental source: strain C50
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A; Residues: 1-451 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AB3022
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A;Molecule type: DNA
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Best Local S
Matches 5
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Best Local
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83.3%;
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8 (Dupont)
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Pred. No. 2.8e
1; Mismatches
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Pred. No. 1.8e+02;
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2.8e+02;
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AI1436
C;Accession: AI1436
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitourna ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AI1436
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R;Goodner, B.; Hinkle, G.; Gattung, S.;
A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein glmS [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: F86750 C;Accession: F86750 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl.
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A;Molecule type: DNA
A;Residues: 1-451 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: F86750
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A; Experimental source: strain
                                                                          A;Status: preliminary A;Molecule type: DNA
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                                                     A;Residues: 1-800 <GLA>
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;Gene: AGR_L_2107
  ;Cross-references: GB:AL592022; PIDN:CAC95265.1; PID:g16412453; GSPDB:GN00178;Experimental source: strain Clip11262
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Pred. No.
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Pred. No. 3.9e+02;
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Doughty, D.; Scott, C.; Lappas, C.; Markelz,
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Voss, H.; Wehland
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R;Guerin-Marchand, C.; Druilhe, P.; Galey, B.; Londono, Nature 329, 164-167, 1987
A;Title: A liver-stage-specific antigen of Plasmodium f. A;Reference number: S29393; MUID:87315391; PMID:3306406
A;Accession: S29393
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A;Residues: 1-1909 <ZHU>
A;Residues: 1-1909 <ZHU>
A;Cross-references: EMBL:X56203; NID:g9915; PID:g9916
A;Zhu, J.; Hollingdale, M.R.
Mol. Blochem. Parasitol. 48, 223-226, 1991
A;Title: Structure of Plasmodium falciparum liver stage
A;Reference number: A45592; MUID:92107224; PMID:1840628
A;Accession: A45592
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A;Residues: 323-381, 'HKAI' <GUE2>
A;Residues: 323-381, 'HKAI' <GUE2>
A;Residues: 323-381, 'HKAI' <GUE2>
A;Cross-references: EMBL:M.8266
A;Note: difference at carboxyl end due to frameshift error
C;Comment: This protein is found as flocculent material in the parasitoph
C;Comment: trichohyalin; calmodulin repeat homology
C;Keywords: EF hand
C;Keywords: EF hand
C;Keywords: EF hand
C;Keywords: EF hand
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C;Accession: $24597; A45592; $29393; $34842; B45592; C45
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A;Residues: 1-195;638-688;1165-1215;1590-1909 <ZH2>
A;Residues: 1-195;638-688;1165-1215;1590-1909 <ZH2>
A;Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75014, NC A;Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75014, NC A;Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75014, NC A;Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75014, NC A;Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75014, NC A;Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75014, NC A;Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75014, NC A;Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75014, NC A;Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75012, NCBIN:75014, NC A;Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75014, NC A;Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75012, NCBIN:75012, NCBIN:75012, NCBIN:75014, NC A;Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75012
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A; Residues: 323-387 <GUE1>
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myosin heavy chain - yeast (Saccharomyces N;Alternate names: protein YHR033w; type I C;Species: Saccharomyces cerevisiae C;Date: 07-Oct-1994 #sequence revision 11-C;Accession: S46773; S05806; S12323

e_revision 11-Aug-1995 #text_change S12323

23-Mar-2001

cerevisiae) II myosin

\$46773

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A;Residues: 1-45,'T',47-58,'S',60-329,331-342,'S',344-528,'ARGHDR',536-540,'V',A,Cross-references: EMBL:X06187; NID:g4015; PIDN:CAA29550.1; PID:g4016 R;Sweeney, F.P.; Watte, F.Z.; Pocklington, M.J.; Orr, E. Nucleic Acids Res. 18, 7147, 1990 A;Title: The MY01 gene from Saccharomyces cerevisiae: its complete nucleotide s.A;Reference number: S12323; MUID:91088308; PMID:2263482 A;Accession: S13323
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EMBO J. 6, 3499-3505, 1987
A;Title: The yeast MYO1 gene encoding a myosin-like protein reconstruction of the protein r
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                                          A;Experimental source: clone C38C6 R;Percy, C.
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;Residues: 1-2441,'R','KRKH',3369,'GN',3372-3373,'G',3375,'RLRHRRRNAQNGPLSRKTRTTTKLFGSP;Cross-references: EMBL:Z33375; PIDN:CAB07567.1; GSPDB:GN00020; CESP:ZC101.2a;Experimental source: clone C38C6
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;180-187/Region: nucleotide-binding motif A (P-loop)
;459-528/Domain: actin binding #status predicted <AC
;186/Binding site: ATP (Lys) #status predicted
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;Cross-references: EMBL: 293375; PIDN: CAB07569.1; Experimental source: clone C38C6
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Keywords: actin binding; ATP; co
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                                                                                                                 Residues: 1-1694,'H',1883-2441,'R','KRKH',3369,'GN',3372-3373,'G',3375,'RLRHRRRNAQNGPL
Cross-references: EMBL:Z93375; PIDN:CAB07568.1; GSPDB:GN00020; CESP:ZC101.2c
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to the EMBL Data Library, March
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP: ZCI
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-546,'P',548-2198,'D',2290,'NAR',2294,'L',2296,'WHATE',2302-2303,'V',2305,'
1,'ANIV',2516-2517,'LQQG',2522,'IDG',2526,'S',2528,'SRGFHV',2535,'F' <RO2>
A;Croos-references: GB:L13458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: Clone ZCI01
R;Rogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G. Genes Dev. 7, 1471-1484, 1993
A;Title: Products of the unc-52 gene in Caenorhabditis elegans A;Reference number: A47648; MUID:93339574; PMID:8393416
A;Accession: A47648
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A;Cross-references: EMBL:Z93395; PIDN:CAB07707.1; GSPDB:GN00020; CESP:ZC101.2c
A;Experimental source: clone ZC101
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A;Residues: 1-3375 <WT2>
A;Cross-references: EMBL:Z93395; PIDN:CAB07708.1; GSPDB:GN00020; CESP:ZC101.2e
A:Fxnerimental source: clone ZC101
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A;Accession: T27490
A;Status: preliminary; translated
                                                                                                                                                                                                                                                             F;149-183/Domain: LDL receptor ligand-binding repeat homology F;190-224/Domain: LDL receptor ligand-binding repeat homology F;233-268/Domain: LDL receptor ligand-binding repeat homology F;233-268/Domain: laminin-type EGF-like homology <LEG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-546,'P',548-1128,1290,'DFARNSPS',1299,'NSS',1303-1304,'R','RHR',1544-1545.
A;Cross-references: GB:L13458
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A;Molecule type: DNA
A;Residues: 1-546,'P',548-2441,'R','KRKH',3369,'GN',3372-3373,'G'
A;Cross-references: GB:L13458
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A;Residues: 1-1128,1290,'DFARNSPS',1299,'NSS',1303-1304,'R','RHR'
A;Cross-references: EMBL:Z93395; PIDN:CAB07704.1; GSPDB:GN00020;
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                                                                                                                                                                                                                              F;955-1002/Domain: laminin-type EGF-like homology <LEG1>F;1011-1058/Domain: laminin-type EGF-like homology <LEG2>
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                                                                                                                                                 Similarity
                                                       SEKDEL 6
SEKDEI
                                                                                                                  Conservative
                                                                                                                                              93.1%;
83.3%;
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Pred. No.
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homology <LDL2>
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CESP:ZC101.2b
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hypothetical protein STY4564 [imported] - Salmonella enterica C;Species; Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_chang

#text_change 18-Nov-2002

subsp.

enterica

serovar

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RESULT AC1030

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C;Accession: A69177

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, P.; Oiu, S.; Shurch, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Marhanobacterium thermoautotrophicum Delta H: fu
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Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;

A;Title: Complete genome sequence of a multiple drug resistant

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AC1030
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R; Parkhill, J.; Dougan,
A; Molecule type: mRNA
A; Residues: 1-144 < CHU>
A; Residues: 1-144 < CHU>
C; Superfamily: tetranectin; C-type
C; Keywords: disulfide bond; platele
                                                                                                              R;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggretin, A;Reference number: PC7027; MUID:99443731; PMID:10512747
A;Accession: PC7027
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A;Restidues: 1-90 <PAR>
A;Croser-references: GB:AL513382; PIDN:CAD09340.1; PID:g16505340; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                             aggretin alpha chain - Malayan pit viper (fragment) C;Species: Calloselasma rhodostoma (Malayan pit vip C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 C;Accession: PC7027
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A; Residues: 1-126 < M
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A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: A69177
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Best Local S
Matches 5
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Experimental source: Strain Delta H
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nes 5; Conserv
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                                                                                                                                                                                L.C.; Huang, T.F.
Res. Commun. 263, 723-727, 1999
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  ectin; C-type lectin homology
bond; platelet aggregation;
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Cronin, A.;
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83.3%;
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83.3%;
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Pred. No.
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Pred. No. 1
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Davis, P.; Davies, R.M.; Dowd,
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ced. No. 85;
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                                                                                                                                                           collagen-like
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I.; Farrar,
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 172-198 <SH2>
A; Residues: 172-198 <SH2>
A; Cross-references: EMBL; X55111; NID:g16141; PIDN:CAA38909.1; PID:g16142
R; Parnell, L.D.; Gnoj, L.; de la Bastide, M.; Hameed, A.; Habermann, K.;
submitted to the EMBL Data Library, May 1998
submitted to the EMBL Data Library, May 1998
reference of BAC T419 from Arabidopsis thaliana, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  auxin-binding protein T419.14 precursor - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 16-Jul-1999 C;Accession: S31584; JQ1598; A43037; S14524; T01395 R;Shimomura, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Shimomura, S.
submitted to the EMBL Data
A;Reference number: S14524
A;Accession: S14524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:S40550;
A;Accession: A43037
A;Molecule type: protein
A;Residues: 34-68 <PA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Cell 4, 193-201, 1992
A;Title: Molecular analysis of an auxin binding protein
A;Reference number: JQ1598; MUID:92338848; PMID:1321684
A;Accession: JQ1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Experimental source: strain Columbia R,Palme, K.; Hesse, T.; Campos, N.; Gar Plant Cell 4, 193-201, 1992
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                                                                                                                                                                                              F;1-33/Domain: signal sequence #status predicted <SIG>F;34-198/Product: auxin-binding protein #status experimental F;195-198/Region: endoplasmic reticulum retention signal
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A; Residues: 1-198 < PAL>
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                                                                                                                                                                                                                                                              C;Superfamily: auxin-binding protein
C;Keywords: endoplasmic reticulum; glycoprotein
                                                                                                                                                                                                                                                                                                                            A; Map position: 4
A; Introns: 40/1;
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF069442; NID:g3242970; PIDN:AAC79108.1; PID:g3924607
A;Experimental source: cultivar Columbia
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                            A; Note: T4I9.14
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Best Local Similarity
Matches 5; Conserv
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Best Local (
                                                                                    Matches
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193 SQKDEL 198
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                                                                                  Similarity 5; Conserv
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                                           SEKDEL
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                                                                                    Score 26; DB
Pred. No. 2e+0
1; Mismatches
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2e+02;
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RESULT 31
T39945
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C;Superfamily: auxin-binding protein
C;Keywords: endoplasmic reticulum
C;Keywords: endoplasmic reticulum
F;1-33/Domain: signal sequence #status predicted <SIG>
F;1-33/Domain: signal sequence #status predicted <MAT>
                                                                                                        ribosomal protein - fission yeast (Schizosaccharomyces pombe) (fragment) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1 C;Accession: T39945
                                                                         R; Wood, V.; Rajandream, M.A.; submitted to the EMBL Data Li
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A; Cross-references: GB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology, A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Rote: see websites genome.wustl.edu/ggc/C_elegans/ and www_sanger.ac.uk/Projects/C_elapy,Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Genome sequence of the nematode C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; anonymous, The C. elegans Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein F26H11.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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A; Accession: T07791
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A;Title: Isolatin and Characterization of an auxin-binding
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C;Species: Raphanus sativus (radish)
C;Date: 14-May-1999 #sequence_revision 1
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                                 A; Accession: T39945
                                                       A; Reference number:
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Accession: A88363
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Plantarum 101, 606-611, 1997
                 preliminary;
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type: DNA
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5; Conserv
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83.3%;
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No.
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2e+02;
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A;Molecute (;r)
A;Residues: 1-221 (KUR)
A;Cross-references: GB:AE001437; PI
A;Cross-reference: Clostridium
                                                                    A;Residue: 1-228 <KAN>
A;Cross-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA18788.1;
A;Cross-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA18788.1;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June
                                                                                                                                                                                                                                                                                      C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 12-May-2003 C;Accession: S76876.
C;Accession: S76876.
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                      nypothetical protein - Synechocystis sp. C;Species: Synechocystis sp. A;Variety: PCC 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: H97242
                                                                                                                                                                                                      A; Reference number: S74322;
A; Accession: S76876
                                                                                                                                                                                                                                                            DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 31-Dec-2001 C;Accession: H97242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable phosphoprotein phosphatase (EC 3.1.3.16) CAC2787 - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
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                                                                                                                                                                A; Molecule type: DNA
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C;Accession: AB3441
C;Accession: AB3441
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.
R; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein F43G6.5 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_san A;Note: published errata appeared in Science 283, 35, 1999; Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; anonymous, The C. elegans Science 282, 2012-2018, 1998
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C; Mate: 1. C; Kaul, R.; Monke, D.; R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Perage, G.; Gillet, W.; Grant, C.; Guenthner, D.; P.; Karp, P.; Romero, P.; Zhang, S.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
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A;Kotatus; preliminary
A;Kolecule type: DNA
A;Kesidues: 1-272 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41773.1;
A;Cross-references: GB:AE008688; DIDN:AAL41773.1;
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C;Superfamily: enoyl-[acyl-carrier-protein]
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE008917; PIDN:AAL52693.1; A;Experimental source: strain 16M
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A; Residues: 1-272 < KUR>
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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A; Molecule type: DNA
A; Residues: 1-272 <KI
A; Cross-references: (
                                                                                                                       R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
                                                                                                                                                                             hypothetical protein AGR_C_1374 [imported] - Agroba C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 C;Accession: E97451
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C; Superfamily:
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                                                                                       A;Title: Genome Sequence of the Plant Pathogen and Biotechnology A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: AG2669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: The Genome of the Natural Genetic Engineer Agrobacterium A;Reference number: AB2577; MUID:21608550; PMID:11743193
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                                                      A;Status: preliminary
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 GB:AE007869; PIDN:AAK86566.1; PID:g15155730; GSPDB:GN00169
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T.; Levy, R.; Li,
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

Nature 390, 249-256, 1997

N; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Cardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Masueel R.; Guer, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wilpat, A.; Yamamoto, K.; Yasamoto, K.; Yasamoto, K.; Yasamo, K.; Yasamoto, K.; Yata, K.; Yoshida, K.; A; Hollis: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Maccession: H70080

A; Malcelle type. number: A65880; MUID:98044033; PMID:9384377

A; Michalle type. number: A65880; MUID:98044033; PMID:9384377

A; Malcelle type. number: A6580; MUID:98044033; PMID:9384377
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A;Gene: AGR C 1374
A;Map position: circular chromosome
C;Superfamily: enoyl-[acyl-carrier-protein] reductase (NADH); short-chain alcohol dehydr
                                                                                                                                               R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                                                                                                                   hypothetical protein BH1308 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Species: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                              A;Molecule type: DNA
A;Residues: 1-321 <STO>
                                                                                                                                                                                                                                                                                                            C; Accession: D83813
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;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB05027.1; GSPDB:GN0;Experimental source: strain C-125
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                                                                                                                         Status: preliminary
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Pred. No. 2.8e+02;
1; Mismatches 0
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ABP1_ARATH
FA11_EUGL
KSGE_ARATH
ENPL_MESAU
KSGE_ARATH
ARLY_SULSO
TGN2_HUMAN
SEO1_YEAST
SNX2_MOUSE
KLP3_CAEEL
SPO6_YEAST
GR78_CHICK
GR78_HUMAN
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Query Match
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Score 29; Pred. No.

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Length Indels

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Best Local (
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PROSITE; PS00014; ER TARGET; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
PROSITE; PS01036; HSP70_3; 1.
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01-AUG-1988 (Rel. 08, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP).
                                                                                                   SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and ic entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87305586; PubMed=3623104;
Ting J., Wooden S.K., Kriz R., Kellehe
"The nucleotide sequence encoding the
glucose-regulated protein (GRP78) and
hamster and rat.";
Gene 55:147-152(1987).
                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                PRINTS; PR00301;
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HSSP; P19120; 3HSC
                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: probably plays a role in facilitating the assemble in the protein complexes inside the ER.
-i- SUBCELUTLAR LOCATION: Endoplasmic reticulum lumen.
-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10036;
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Mammalia; Eutheria;
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Rodentia;
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                                                                                                   PREVENT SECRETION FROM ER 25CF665F59113A49 CRC64;
                                                            Score 29;
Pred. No. 8
                                                                                                                             78 kDa GLUCOSE-REGULATED PROTEIN
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ing the hamster 78-kDa
78) and its conservation
                                                 Mismatches
                                                                                                                                                       Signal.
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Query Match
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PRINTS; PR00301; HEATSHOCK70.

PRODOM; PD000089; HSP70; 1.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS00136; HSP70_3; 1.

PROSITE; PS001014; ER TARGET; 1.

ATP-binding; Endoplasmic reticu
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01-APR-1988 (Rel. 07, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP) (Steroidogenesis-activator polypeptide).
HSPAS OR GRP78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M14866; AAA41277.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - FUNCTION: Probably plays a role in facilitating the assembly multimeric protein complexes inside the ER.
- SUBCELUTUAR LOCATION: Endoplasmic reticulum lumen.
- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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MEDLINE=87118232; PubMed=3468506;
Chang S.C., Wooden S.K., Nakaki T.,
Attenello J.W., Lee A.S.;
"Rat gene encoding the 78-kDa glucos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86245075; PubMed=3087629;
Munro S., Pelham H.R.B.;
"An Hsp70-like protein in the ER: identity with the 78 kd glucose-
"egulated protein and immunoglobulin heavy chain binding protein.";
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (Su or send an email to license@isb-sib.ch).
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MEDLINE=87177981; PubMed=3563495;
Pedersen R.C., Brownie A.C.;
                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A23948; HHRTGB.
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  100.0%; Score 29;
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BY SIMILARITY.

78 kDa GLUCOSE-REGULATED PI
PREVENT SECRETION FROM ER.

T -> M (IN REF. 2).

S -> D (IN REF. 2).

K -> KK (IN PER. 2).
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Sciurognathi; Muridae; Murinae; Rattus.
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-!- SIMILARITY: BELONGS

TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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RESULT 4
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                    SEQUENCE OF 20-36.
TISSUE-Fibroblast;
MEDLINE-95009907; PubMed=7523108;
METRICK B.A., Patterson R.M., Wichter L.L., He C., Selki.
"Separation and sequencing of familiar and novel murine;
using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          differential screening."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96216731; PubMed=8645260;
Kajiwara K., Nagasawa H., Shimizu-Nishikawa K.,
Kimura M., Sugaya E.;
"Molecular characterization of seizure-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=C57BL/6; TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of immunoglobulin heavy chain binding protein as glucose-regulated protein 78 on the basis of amino acid sequence, immunological cross-reactivity, and functional activity."; J. Cell Sci. Suppl. 11:115-137(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF MEDLINE=90130686; PubMed=2559088; Kozutsumi Y., Normington K., Press I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heavy chain binding protein) (BiP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P20029; 035642; Q61630;
                                                                                                                                                                                                                                                                               Tillman J.B., Mote P.L., Walford R.L., "Structure and regulation of the mouse glucose and calcium ionophore.";
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-28 FROM N.A.
STRAIN=C3B10RF1; TISSUE=Liver;
MEDLINE=95331621; PubMed=7607546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Differential screening of a cDNA library win a heterologous host: isolation of murine serum-regulated low-abundance mRNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parfett C.L.J., Hofbauer R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 488-655 FROM N.A. MEDLINE=90060818; PubMed=2583523;
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  FUNCTION: Probably plays a role in facilitating the assembly multimeric protein complexes inside the ER. SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
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158:225-229(1995)
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GRP78 (BiP) promoter
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                       SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
STRAIN=S298C / AB972;
MEDLINE=S5400292; PubMed=7670463;
Murakami Y., Naitou M., Hagiwara H., Sh
Sasanuma S.-I., Sasanuma M., Tsuchiya Y
Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of
                                                                                                                                                  YEAST
YF13 YEAST
P43596;
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EMBL; U16277; AAA76734.1; -.
PIR; A37048; A37048.
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PIR; S27473; S27473.
HSSP; P17679; IGNF.
TRANSFAC; T02406; -
InterPro; IPR000679; Znf_GA
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                                                                                                                                                                                                                                                                                       the Buropean Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
SMART; SM00401; ZnF GATA; 2.

PROSITE; PS00344; GĀTA_ZN_FINGER_1; 2.

PROSITE; PS50114; GATA_ZN_FINGER_2; 2.

DNA-binding; Zinc-finger; Transcription regulation; Repressor;
                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor GATA-1.";

MO1. Cell. Biol. 13:7091-7100 (1993).

NO1. FUNCTION: INVOLVED IN THE REGULATION OF SECRETED FERRICHROME-TYPE SIDEROPHORES. ACTS DIRECTLY OR INDIRECTLY TO REPRESS THE BIOSYNTHESIS OF SIDEROPHORES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Voisard C.P., Wang J., McEvoy J.L., Xu P., Leong S.A.; "urbs1, a gene regulating siderophore biosynthesis in Ustilago maydis, encodes a protein similar to the erythroid transcripti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ustilago maydis (Smut fungus).
Ustilaginomycetes;
Bukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ustilaginomycetidae;
NCBI_TaxID=5270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              URB1 USTMA
P40349;
                                                                                                   Pfam; PF00320; GATA; 2.
PRINTS; PR00619; GATAZNFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94019380; PubMed=8413298;
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GO:0005634; C:nucleus; IPI.
GO:0005515; F:protein binding activity; IDA
GO:0006338; P:chromatin modeling; IPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 2 GATA-type zinc fingers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S56268; S56268
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6; Conserv
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787 AA;
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(Rel. 31, Last sequence up. (Rel. 40, Last annotation)
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PHSL IPUMA

CP27598;

AC P27598;

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-BUG-1992 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Alpha-1,4 glucan phosphorylase, L isozyme, chloroplast precursor

EEC 2.4.1.1) (Starch phosphorylase L).

OS Ipomoea batatas (Sweet potato) (Batate).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

DE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Solanales; Convolvulaceae; Ipomoea.
PRESCRIPTION OF THE PROPERTY O
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Best Local S
Matches 6
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                                                                                                                                                              EMBL; M64362; AAA63271.1; -.
PIR; T10947; T10947.
HSSP; P06738; 1YGP.
InterPro; IPR000811; Glyco_trans_35.
Pfam; PF00343; phosphorylase; 1.
PROSITE; P800102; PHOSPHORYLASE; 1.
Transferase; Glycosyltransferase; Carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: {(1,4)-alpha-D-glucosyl}(N) + phosphate {(1,4)-alpha-D-glucosyl}(N-1) + alpha-D-glucose 1-phosphate -!- COFACTOR: Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Its cDNA sequence.";

Plant Physiol. 95:1250-1253(1991).

-I- FUNCTION: PHOSPHORYLASE IS AN IMPORTANT ALLOSTERIC ENZYME IN

-ICARBOHYDBATE METABOLISM. ENZYMES FROM DIFFERENT SOURCES DIFFER
THEIR REGULATORY MECHANISMS AND IN THEIR NATURAL SUBSTRATES.

HOWEYER, ALL KNOWN PHOSPHORYLASES SHARE CATALYTIC AND STRUCTURA
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    -!- SUBCELLULAR LOCATION: Chloroplast; amyloplast.
    -!- SIMILARITY: BELONGS TO THE GLYCOGEN PHOSPHORYLASE FAMILY

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                                                                                            Amyloplast; Multigene
TRANSIT 1 4:
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955
                                                                                                                                        enzyme; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                       equires a license agreement (S email to license@isb-sib.ch).
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                                                                                                                       family.
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GATA-TYPE 2.
POLY-ALA.
POLY-SER.
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POLY-SER.
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                                         CHLOROPLAST (POTENTIAL),
ALPHA-1,4 GLUCAN PHOSPHORYLASE,
ISOZYME.
  PYRIDOXAL PHOSPHATE 
V; CCDB7CD5628A662A
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Pred. No.
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                                                                                                                                             peptide;
       (BY SIMILARITY) CRC64;
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MBL outstation -
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Best Local Similarity
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                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@alb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Bristol N2;
STRAIN-Bristol N2;
MEDLINE-89178677; PubMed-2926820;
MEDLINE-89178677; PubMed-2926820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myosin heavy chain A (MHC A).
MYO-3 OR K12F2.1.
Caenorhabditis elegans.
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01-OCT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P12844; Q21440;
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             HSSP; P08799; IMND.
Wormbep; K12F2.1; CE12204.
InterPro; IPR00048; IQ_region.
InterPro; IPR001609; myosin_head.
InterPro; IPR004009; myosin_N.
                                                                                                                                                   EMBL; X08067; CAA30856.1; -.
EMBL; Z78199; CAB01576.1; -.
PIR; T23622; S02771.
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"Sequence analysis of the complete
heavy chain gene family.";
J. Mol. Biol. 205:603-613(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harris B.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALHAH-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED STREEPLAMENT (C2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nitted (AUG-1996) to the EMBL/GenBank/DDBJ databases. FUNCTION: MUSCLE CONTRACTION.
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAW SIMILARITY: Contains 1 myosin-like globular head domain. SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: THERE C.ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPLIT FURTHER INT SUBFRAGMENT (S2).
                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
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Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BODY WALL THICK FILAMENT
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MBL outstation -
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RESULT 9
GLMS_LACLA
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                                                                                                                                       MEDLINE=21335186; PubMed=11337471;

A Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,

A Weissenbach J., Ehrlich S.D., Sorokin A.;

I weissenbach J., Ehrlich S.D., Sorokin A.;

"The complete genome sequence of the lactic acid bacterium Lactococcus

I lactis ssp. lactis IL1403.";

I Genome Res. 11:731-753(2001).

C -!- FUNCTION: CATALYZES THE FIRST STEP IN HEXOSAMINE METABOLISM,

C CONVERTING FRUCTOSE-6P INTO GLUCOSAMINE-6P USING GLUTAMINE AS A

C C CONVERTING FRUCTOSE-6P INTO GLUCOSAMINE-6P USING GLUTAMINE AS A

C NITROGEN SOURCE (BY SIMILARITY).

C -!- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-

G GUECELLULAR LOCATION: Cytoplasmic (By similarity).

C -!- SUMCELLULAR LOCATION: Cytoplasmic, Bellongs To THE SIS FAMILY.

C GEAT SUBFRMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLMS LACLA
Q9CGT6;
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
MOD_RES
MOD_RES
CONFLICT
use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Last annotation update)
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
(EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-
phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate
amidotransferase) (Glucosamine-6-phosphate synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                Lactococcus lactis (subsp. lactis) (our ramina: Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                    GLMS OR LL1006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50096; IQ; 1.
                                                                                                                            -!- SIMILARITY: Contains 1 type-2 glutamine amidotransferase
                                                                                                                                                                                                                                                                                                                                                STRAIN=IL1403
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1360;
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857
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770
130
707
717
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40, Last sequence update)
41, Last annotation update)
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1969
186
689
784
130
717
717
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                                                                                                                                                                                                                                                                                                                                                                                                                     lactis) (Streptococcus lactis)
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ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
Y -> YVRKLKLFKKKINTIQKLNRLNFQ
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Pred. No. 2.6e+02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64577BBAF7EAD80A CRC64;
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                         oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcaceae;
                                                    There are no restrictions on ng as its content is in no
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                                                                                  EMBL outstation
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                                                                                                collaboration
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-!- SIMILARITY: Contains 1 myosin-like globular head domain.
 -!- SIMILARITY: Contains 1 IQ domain.

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RESULT 10
MYS1_YEAST
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Best Local S
Matches 5
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HAMAP; MF_00164; -; 1.
InterPro; IPR00585; GATase 2.
InterPro; IPR005855; GImS.
InterPro; IPR001347; SIS.
Pfam; PF00310; GATase 2; 1.
Pfam; PF01380; SIS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYS1 YEAST ST7
P08964;
01-NOV-1988 (Rel.
01-FEB-1995 (Rel.
16-OCT-2001 (Rel.
Myosin-1 isoform
                                                                                                                                                                                                                                                                                                SEVUENCE:
STRAIN=5288c;
STRAIN=51088308; PubMed=2263482;
MEDLINE=91088308; PubMed=2263482;
Sweeney F.P., Watts F.Z., Pocklington M.J., Or
Sweeney F.P., Watts F.Z., Pocklington M.J., Or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMĀIN
SEQUENCE
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                                                                                                                                                         STRAIN-S288C / AB972;
MEDLINE-94378003; PubMed-8091229;
MEDLINE-94378003; PubMed-8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Du Z., Hillier L., Jier M., Johnston L., Langston Y.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L
Whan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
Vaudin M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; |
HSSP;
MEDLINE=88111539; PubMed=3322809; Watts F.Z., Shiels G., Orr E.; "The yeast MYO1 gene encoding a m division."; EMBO J. 6:3499-3505(1987).
                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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INIT MET 0
ACT_SITE 1
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PROSITE; PS00443; GATASE_TYPE_II;
Transferase; Aminotransferase; Gl
                                                                                                                           "Complete nucleotide sequence VIII.";
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             MYO1 OR YHR023W
                                                                           STRAIN=S288c;
                                                                                     SEQUENCE
                                                                                                              Science 265:2077-2082(1994).
                                                                                                                                                    Vaudin M.;
                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 18:7147-7147(1990).
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447
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5; Conservative
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                                                                                     OF 1-760
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(Rel. 31, Last seq
(Rel. 40, Last ann
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update)
annotation update)
 CELL DIVISION
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GATASE (BY SIMILARITY).

ISOMERIZATION FRU-6P (BY SIMILARITY).

GLUTAMINE AMIDOTRANSFERASE.

DFB7EDB1FFDE68A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 27; DB 1;
Pred. No. 2.1e+02;
                                    a myosin-like
                                                                                                                                       of Saccharomyces
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EMBL; X53947; CAA37894.1; -.
EMBL; X06187; CAA378550.1; -.
EMBL; U10399; AAB68872.1; -.
EMBL; U10399; AAB68872.1; -.
PIR; S46773; S46773.
HSSP; P08799; 1MND.
SGD; S0001065; MYOL.
GO; GO:0000142; C:contractile ring (sens GO; GO:0007120; P:axial budding; IMP.
GO; GO:0016288; P:cytokinesis; IMP.
GO; GO:0016288; P:cytokinesis; IMP.
GO; GO:0016288; P:cytokinesis; IMP.
GO; GO:0016288; D:cytokinesis; IMP.
GO; GO:0006970; P:response to osmotic st
InterPro; IPR001609; myosin head.
Pfam; PF00063; myosin head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00063; myosin head; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PR000355; myosin head; 1.
SMART; SM00015; 10; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
MYOSIN; Actin-binding; ATP-bindir
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                                                                                                                                                                           CONFLICT
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                                                                                                                                                          CONFLICT
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                                                                                                                                                                                                                     ATP-binding; Coiled coil; Alkylation.
MYOSIN HEAD-LIKE.
DDLVSE -> MTLFL (IN REF. 1).
AQN -> RKI (IN REF. 1).
EEAH -> KKLD (IN REF. 1).
S -> C (IN REF. 1).
L -> D (IN REF. 1).
C -> S (IN REF. 1).
C -> S (IN REF. 1).
M -> I (IN REF. 1).
A -> E (IN REF. 1).
A -> C (IN REF. 1).
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K -> I (IN I

I -> T (IN I

V -> S (IN I
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E -> R (IN REF. 1 AND 3).
NTKLFFKAGVLA -> ILTVFQKLEYWS (II
KL -> NV (IN REF. 1).
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ACTIN-BINDING (BY SIMILARITY).
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R -> S (IN REF. 1
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                                                                                                                                            NESLLNRVKTSSETLQ REF. 1).
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UN52_CAEEL STANDARD; PRT; 3375 AA.
C Q06561; O18261; O18263; Q9XTD2; Q9XTD5;
T 01-VUN-1994 (Rel. 29, Created)
T 15-SEP-2003 (Rel. 42, Last sequence update)
I 5-SEP-2003 (Rel. 42, Last annotation update)
Basement membrane proteoglycan precursor (Perlec UNc-52 OR ZC101.2.
CARRONSHEALITE - 1-1
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Best Local
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STRAIN=Bristol N2;
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                  Rogalski T.M., Williams "Products of the unc-52
                                                                                                                                                                                                                                                                                                 MEDLINE=93339574; PubMed=8393416;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                       Durbin
                                                                                         REVISIONS,
                                                                                                                                              Percy C.M.
                                                                                                                                                                                                               galski T.M., Williams B.D., Mullen roducts of the unc-52 gene in Caenc the core protein of the mammalian lfate proteoglycan."; nes Dev. 7:1471-1484(1993).
                    mitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. FUNCTION: Probable role in myofilament assembly and/or attachment of the myofilament lattice to the cell membrane. May be an
     extracellular anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             938
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Pred. No. 7e+0
1; Mismatches
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in Caenorhabditis elegans a
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ONSRNG -> NTTANGTKFKEW
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     receptors in
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7e+02;
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     EMBL; L13458; AAA28156.1; -.
EMBL; 293375; CAB07567.1; -.
EMBL; 293375; CAB07568.1; -.
EMBL; 293375; CAB07568.1; -.
EMBL; 293375; CAB07568.1; -.
EMBL; 293375; CAB07569.1; -.
EMBL; 293375; CAB07569.1; -.
EMBL; 293375; CAB07704.1; -.
EMBL; 293395; CAB07704.1; -.
EMBL; 293395; CAB07707.1; -.
EMBL; 293375; CAB07707.1; -.
EMBL; 293375; CAB07707.1; -.
EMBL; 293395; CAB07707.1; -.
EMBL; 293375; CAB07708.1; -.
EMBL; 293375; CAB0708; -.
EMBL; 293375; 
PRINTS; PR00261; LDLRECEPTOR PRODOM; PD003031; Laminin B; SMART; SM00181; EGF; 6.
SMART; SM00181; EGF CA; 2.
SMART; SM00180; EGF Lam; 6.
SMART; SM00409; IG; 17.
SMART; SM00409; IG; 17.
SMART; SM00408; IGc2; 17.
SMART; SM00281; LamB; 1.
SMART; SM00282; LamG; 3.
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                                                                                                                                                         Pfam; PF00047; ig; i6.
Pfam; PF00052; laminin
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InterPro;
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TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANE OF ALL CONTRACTILE TISSUES. IT IS CONCENTRATED OVER MUSCLE DENSE BO AND M-LINES WHICH ARE ASSOCIATED WITH BETA-INTEGRIN.
DEVELOPMENTAL STAGE: SYNTHESIZED EARLY IN EMBRYOGENESIS.
SIMILARITY: Contains 3 LDL-receptor class A domains.
SIMILARITY: Contains 16 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 7 laminin EGF-like domains.
SIMILARITY: Contains 3 amainin G-like domains.
SIMILARITY: Contains 3 laminin G-like domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Extracellular matrix. ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=Name=e;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note=No
Name=c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collal een the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q06561-3; Sequence=VSP_007191, VSP_007192;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q06561-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q06561-1; Sequence=Displayed;
Note=No experimental confirmation a
                                                                                                                        PRO0057; ldl_recept_a; 3.
PRO0261; LDLRECEPTOR.
PD003031; Laminin_B; 2.
                                                                                                                                                                                                                                            ; IPR006209; EGF like.
; IPR007110; Ig-like.
; IPR003599; Ig c2.
; IPR003006; Ig_MHC.
; IPR000314; Laminin B.
; IPR002049; Laminin_EGF.
; IPR001791; Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                     ZC101.2a; CE15028
ZC101.2b; CE15030
                                                                                                                                                                                                                            IPR002172; LDL_receptor_A.
                                                                                                                      Laminin_B;
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SMART; SM00192; LDLa; 3.

PROSITE; PS010022; EGF 1; 7.

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PROSITE; PS01285; IG LIKE; 17.

PROSITE; PS50025; LAM G DOMAIN; 3.

PROSITE; PS01204; LAMININ TYPE EGF; 7.

PROSITE; PS01204; LDLRA 1; 3.

PROSITE; PS01204; LDLRA 2; 3.

PROSITE; PS01206; LDLRA 2; 3.
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LDL-RECEPTOR CLASS A 2.
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LDL-RECEPTOR CLASS A 3.
IG-LIKE C2-TYPE 2.
LAMININ BGF-LIKE 1 (INCOMPLETE).
LAMININ BGF-LIKE 2 (C-TERMINAL).
LAMININ BGF-LIKE 3 (INCOMPLETE).
LAMININ BGF-LIKE 4 (C-TERMINAL).
LAMININ BGF-LIKE 5.
LAMININ BGF-LIKE 5.
LAMININ BGF-LIKE 7.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 10.
IG-LIKE C2-TYPE 11.
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IG-LIKE C2-TYPE 12.
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IG-LIKE C2-TYPE 13.
IG-LIKE C2-TYPE 14.
IG-LIKE C2-TYPE 15.
IG-LIKE C2-TYPE 16.
IG-LIKE C2-TYPE 17.
LAMININ G-LIKE 3.
BY SIMILARITY.
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EMBL; AF30325
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SEQUENCE 13
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This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Bristol N2;
Kohara Y., Shin'i T., Suzuki Y., Sugano S., Potdevin M.,
Thierry-Mieg Y., Thierry-Mieg D., Thierry-Mieg J.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
                                                      Z81515; CAB04194.3; -.
AF303250; AAG50208.1;
ep; F26H11.1; CE26712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
1 protein F26H11.1 in chromosome II.
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E3A3A7D2DB5FACBE CRC64;
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RA Mayer K.F.X., Schweller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N., RA Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Reger M., Mueller M., Rak Rak Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Mueller M., Rak Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., RA Reichert B., Dortetelle D., Perez-Alonso M., Boutry M., Bancroft I., RA Wos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., RA Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., RA Van der Schweren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., RA Wan der Schweren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., RA Mocijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R., RA Van Montagu M., Rogers J., Cronin A., Ouali M., Bray-Allen S., RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., Petett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., RA Clark L., Rojers J., Cronin A., Ouali M., Bray-Allen S., Haller R., Scharfe M., Gräm M., Loehnert T.-H., Dohe T., Johnson S., Argiriou A., Vitale D., Liguori R., Piravandi E., RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., RA Gaben F., Waller R., Schmidt W., Lecharny A., Aubourg S., RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E., Pieber R., Schmidt W., Lecharny A., Aubourg S., RA Chefdor F., Wandenbol M., Barques M., Terol J., Torres A., RA Peters P., Beak D., Lemcke K., Mewes H.-W., Stocker S., Beike C., RA Parnell L., Dedhia N., Gnoj L., Schwtz K., Huang E., Spiegel L., Ra Schon M., Mehren P., Cordes M., Abu-Threideh J., Schwarz S., Scholt P., Cordes M., Abu-Thre
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01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Auxin-binding protein 1 precursor (ABP).
ERABP1 OR ATAGO2980 OR T4I9.14.
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Palme K., Hesse T., Campos I
"Molecular analysis of an au
chromosome 4 of Arabidopsis
Plant Cell 4:193-201(1992).
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MEDLINE=20083488; PubMed=10617198;
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MEDLINE=94297934; FubMed=7517789;
MEDLINE=94297934; FubMed=7517789;
Shimomura S., Liu W., Inohara N., Watanabe S
"Structure of the gene for an auxin-binding
7SL RNA from Arabidopsis thaliana.";
Plant Cell Physiol. 34:633-637(1993).
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Bukaryota; Viridiplantae; Stresptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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P58-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

28-FEB-2003 (Rel. 41, Last annotation update)

Encyl-[acyl-carrier-protein] reductase [NADH] 1 ()

dependent encyl-ACP reductase 1).

dependent encyl-ACP reductase 1).

PABII OR R00898 OR SMC00005.

Rhizobium meliloti (Sinorhizobium meliloti).

Bacteria; Proteobacteria; Alphapproteobacteria; Rh.

Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorh.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X69901; CAA49526.1; ---
EMBL; S40550; AAB22612.1; ---
EMBL; X5111; CAA38909.1; ---
EMBL; AF069442; AAC79108.1;
EMBL; AF069442; CAB77783.1;
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  SEQUENCE FROM N.A.
                                         NCBI_TaxID=382;
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PROSITE; PS00014; ER_TARGET; 1
Receptor; Glycoprotein; Endopl
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A Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

A Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,

A Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,

A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,

A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,

Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;

"Analysis of the chromosome sequence of the legume symbiont

"Inorhizobium meliloti strain 1021.";

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

C. -! CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NADH.

C. -! SUBCELULAR LOCATION: Inner membrane-associated (By similarity).

C. -! SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN

DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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Best Local
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30-MAY-2000
30-MAY-2000
28-FEB-2003
                                                                                                    SEQUENCE FROM N.A.

MEDILINE=98363643; PubMed=9700063;

Southerton S.G., Strauss S.H., Olive M.R., Harcourt R.L., Decroocq

Southerton S.G., Strauss S.H., Olive M.R., Harcourt R.L., Decroocq

Zhu X., Llewellyn D.J., Peacock W.J., Dennis E.S.;

"Bucalyptus has a functional equivalent of the Arabidopsis floral

meristem identity gene LEAFY.";

Plant Mol. Biol. 37:897-910(1998).

-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Nuclear (Probable).

-!- TISSUE SPECIFICITY: Expressed strongly in the early floral
primordium and then successively in the primordia of sepals,

petals, stamens and carpels. Also in the leaf primordia and you
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a colbetween the Swiss Institute of Bioinformatics and the EMBL ou the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.ch or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eucalyptus globulus (Blue gum).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Myrtales; Myrtaceae; Eucalyptus.
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                                                      SIMILARITY: BELONGS TO THE FLO / LFY FAMILY.
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(Rel. 39, Last sequence update)
(Rel. 41, Last annotation update)
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A Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
A Mayer K.F.X., Schueller C., Wambutt R., Etian K.-D., Terryn N.,
A Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
A Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
A Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
A Kreis M., Delseny M., Puigdomenech P., Watson M., Sothmidtheini T.,
A Kreis M., Delseny M., Puigdomenech P., Watson M., Sothmidtheini T.,
A Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
A Kreis M., Wos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
A Langham S.-A., McCullagh B., Bilham L., Robben J.,
A Langham S.-A., McCullagh B., Bilham L., Robben J.,
A Langham S.-A., McCullagh B., Bilham L., Robben J.,
A Wan der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
B Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
A Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braum M.,
A Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
A Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
B Randt R., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
A Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
Van Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Dornelas M.C., Schwebel-Dugue N., Thomas M., Lecharny A., Strain-
"Three new cDNAs related to SGG/GSK-3 (SHAGGY/glycogen synthase kinase-3) from Arabidopsis thaliana.";

*** Plant Gene Register PGR97-008.
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Shaggy-related protein kinase eta (EC 2.7.1.-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dornelas M.C., Lejeune B., Dron M., Kreis M.; "The Arabidopsis SHAGGY-related protein kinase (ASK) gene family: structure, organization and evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98278841; PubMed=9611268;
Dornelas M.C., Lejeune B., Dron M
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RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Meumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Schnoh M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Schnoh M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Nelson J., Spieth J., Ryan E., Bandrews S., Geisel C., Layman D.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Mapper J., Courtney A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
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EMBL; AL035526; CAB37456.1; --
EMBL; AL161549; CAB78873.1; --
PIR; T04863; T04863
HSSP; P24941; 1AQ1.
ACT SITE CONFLICT CONFLICT
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-!- FUNCTION: MAY MEDIATE EXTRACELLULAR SIGNALS TO REGULATE TRANSCRIPTION IN DIFFERENTIATING CELLS (BY SIMILARITY).
                                                                                                                                                                                                                                                  Pfam; PF00069; pkinase; 1.

ProDom; PD000001; Prot_kinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00100; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X94939; CAA64409.1; -. EMBL; Y08947; CAA70144.1; -.
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InterPro; IPR002290; Ser thr pkinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE SER/THR FAMILY OF CDC2/CDKX SUBFAMILY; GSK-3 SUBSUBFAMILY.
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Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
Maarse A.C., Schaefer M., Mueller-Auer S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Endoplasmic reticulum
-!- INDUCTION: THE SYNTHESIS OF THIS ENOTEIN IS
FIBROBLASTS ARE DEPRIVED OF GLUCOSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Biol. 194:341-344(1987).
-!- FUNCTION: Molecular chaperone that functions in transport of secreted proteins (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRA1.
                                                                                                                                                                       SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENPL_MESAU
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InterPro; IPR001404; Hsp90.
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PS00014; ER TARGET; 1
PS00298; HSP90; PARTII
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(94 kDa glucose-regulated prote
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Pred. No. 2.1e+02;
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RA Habbrmann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,
RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,
RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,
RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,
RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,
RA Wagner-McDherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Wolckaert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,
RA Volckaert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,
RA Entlan K.-D., Terryn N., Hartley N., Bent E., Johnson S.,
RA Entlan K.-D., Terryn N., Hartley N., Bent E., Johnson S.,
RA Ramsperger U., Wedler H., Balke K., Wedler E., Peters S.,
RA Waltzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,
RA Weltzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,
RA Feldpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,
RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.F.;
Thalian "."
Sequence and analysis of chromosome S of the plant Arabidopsis
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STRAIN=CV. Columbia;
Dornelas M.C., Kreis !
"Plant homologues of !
Submitted (SEP-1997) !
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P43288; 004625;
01-NOV-1995 (Rel
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MEDLINE=21016721; PubMed=11130714;
Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S., Kohara M., Matsumoto M., Matsuno S., Takeuchi C., Wada Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M., Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R., Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston J., Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston J., Button J., Button J., Johnson D., Rohlfing T., Nelson J., Bec
                                                                                                    01-NOV-1995 (Rel. 32, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Shaggy-related protein kinase alpha (EC 2.7.1.-) (ASK-alpha).
ASK1 OR AT5G26751 OR F2P16.21.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                         -I- TISSUE SPECIFICITY: ROOTS, SHOOTS AND LEAVES.
-I- PTM: AUTOPHOSPHORYLATED MAINLY ON THREONINE A
-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF
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                    CDC2/CDKX SUBFAMILY; GSK-3 SUBSUBFAMILY CAUTION: Ref.2 and Ref.3 sequences diff:
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SGG/GSK-3 protein kinases.";
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EMBL; X68525; CAA48538.1; -N
EMBL; AJ000723; CAA04265.1; AN
EMBL; AF007270; AAB61055.1; AN
EMBL; AF428327; AAL16257.1; -
EMBL; AY046024; AAK76698.1; -
EMBL; AY142595; AAN13164.1; -
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                                                             STRAIN-cv. Columbia; TISSUE-Shoot;
MEDLINE-94150468; PubMed-7509023;
MEDLINE-94150468; PubMed-7509023;
Mianchi M.W., Guivarc'H D., Thomas M., Woodgett J.R., Kreis M.
"Arabidopsis homologs of the shaggy and GSK-3 protein kinases:
molecular cloning and functional expression in Escherichia col
Mol. Gen. Genet. 242:337-345(1994).
                                                                                                                                                                                    Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyra; Embry.
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Shaggy-related protein kinase gamma (EC 2.7.1.-)
ASK3 OR AT3G05840 OR F10A16.14
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ProDom; PD000001; Prot kinase; 1.

SMART; SM00220; S TKC; 1.

SMART; SM00219; TYTKC; 1.

PROSITE; PS001107; PROTEIN KINASE ST; 1

PROSITE; PS00111; PROTEIN KINASE DOM; PROSITE; PS00111; PROTEIN KINASE DOM;
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S41596.
S41596; P24941; 1AQ1.
srPro; IPR000719; Prot_kinase.
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RA Vezzi A. D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Rooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,

RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,

RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,

RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,

RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,

RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Talion L.J., Jenkins J.,

RA Rooney T., Haase B., Maiti R., Wu D., Peterson J., Van Aken S.,

RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,

RA Praser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,

RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,

RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,

**Sagamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,

RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,

**Fraiquan W., Wanda M., Yasuda M., Tabata S.;

**Traiquan W., Wanda M., Wanda M., Tabata S.;

**Traiquan W., Wanda M., Wanda M.,
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InterPro; IRR002290; Ser thr pkinase.
Pfam; PF00009; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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EMBL; X12710; CAA73247.1; -.
EMBL; AC012393; AAF26086.1; -.
PIR; S41597; S41597.
HSSP; P24941; 1AQ1.
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by non-profit institutions as long as its content
ified and this statement is not removed. Usage by ar
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TISSUE SPECIFICITY: ROOTS, SHOOTS AND LEAVES.
PTM: AUTOPHOSPHORYLATED MAINLY ON THREONINE AND SERINE RESIDUES.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CDC2/CDKX SUBFAMILY; GSK-3 SUBSUBFAMILY.
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PROSITE; PS00108; PROTEIN KINASE DOM; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
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SMART; SM00220; S_TKG; 1.
PROSITE; PS00107; PROTEIN KINASE ATP;
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Paz A., Jonak C., Boegre
Heberle-Bors E., Hirt H.
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ATP (BY SIMILARITY).
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InterPro; IPR002290; Ser thr_pkinase.
Pfam; PF00069; pkinase; I.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S_TKC; I.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATI
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Glycogen syni
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"The MsK family of alfalfa protein kinase genes encodes homologue shaggy/glycogen synthase kinase-3 and shows differential expressipatterns in plant organs and development.";
plant J. 3:847-856(1993).
-!- TISSUE SPECIFICITY: ABSENT IN LEAVES AND PETIOLES WHILE A MOI EXPRESSION IS SEEN IN THE STEMS, ROOTS, AND NODES.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CDC2/CDKX SUBFAMILY; GSK-3 SUBSUBFAMILY.
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MEDLINE-94004996; PubMed=8401615;
Tonak C., Boegre L., Meskiene I.,
                                                                                                                                                              MEDSA
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DOMAIN
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HSSP; P24941; 1AQ1.
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kinase-3 homolog MsK-2 (EC
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homolog MsK-3 (EC
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ATP (BY SIMILARITY).
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PHOSPHORYLATION (BY SIMILARITY).
BBBOCA647633989E CRC64;
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edons; core eudicots; Rosidae
oideae; Trifolieae; Medicago
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Pf00069; pkinase; I.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S TKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
Transferase; Serine/threonine-protein kinase; ATI
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P45679;
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SUN protein (FMU protein).
SUN OR FMU OR CBU1915.
Coxiella burnetii.
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entitles requires a license agreement (See http://www.isb
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago. NCBI_TaxID=3879;
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MEDLINE=94004996; PubMed=8401615;
                          Bacteria; Proteobacteria;
Coxiellaceae; Coxiella.
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SEEN IN THE NODES.
DEVELOPMENTAL STAGE: HIGH LEVELS
DEVELOPMENT, GRADUALLY DECREASES
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SIMILARITY: BELONGS TO THE SER/THR FAMILY CDC2/CDXX SUBFAMILY; GSK-3 SUBSUBFAMILY.
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TISSUE SPECIFICITY: P
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een the Swiss Institute of Bioinformatics and the EN
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ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (BY SIMILARITY)
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                                                                                            update)
                                                                                                                                                                                                                                                                                      2.3e+02;
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udicots; Rosidae;
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RESULT 24
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Best Local
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InterPro; IPR006174; NusB dom.
InterPro; IPR0006174; SAM bind.
InterPro; IPR001673; Sun.
InterPro; IPR001678; Sun. Nop1/Nop2.
Pfam; PF01189; No11 Nop2_Sun; 1.
Pfam; PF01189; NusB; 1.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SETRAIN=Nine Mile phase I / RSA 493;

MEDLINE=22608657; PubMed=12704232;

Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,

Seshadri R., Paulsen I.T., Eisen J.A., Madupu R., Dodson R.J.,

DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,

DeBoy R.T., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,

Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;

"Complete genome sequence of the Q-fever pathogen, Coxiella
                                                                                                                                                                                                                                                                                                                                                                                 ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD005242; NusB_dom; 1.
TIGRFAMs; TIGR00563; rsmB; 1.
PROSITE; PS01153; NOL1_NOP2_SU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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-!- SIMILARITY: BELONGS TO THE SUN (BACTERIAL) / NUCLEOLAR PROTEIN NOL1/NOP2 (EUKARYOTES) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and characterization of an from Coxiella burnetii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Nine Mile phase I / Bratislava; MEDLINE=94350801; PubMed=8071197;
STRAIN=cv. Columbia; TISSUE=Pollen;
                       SEQUENCE FROM N.A
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                                                                     NCBI_TaxID=3702;
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AE016966; AAO91406.1; -.
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176:5233-5243(1994).
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48949 MW; B264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.7%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                             Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                       core eudicots; Rosidae;
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Prodom; PD000001; Prot kinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;

InterPro; IPR000719; Prot kinase. InterPro; IPR002290; Ser thr pkinase Pfam; PF00069; pkinase; 1.

EMBL; AL137898; CAB7; PIR; T47908; T47908. HSSP; Q00534; 1BI8.

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RX. MEDLINE=2V: COLUMDIA;

RX MEDLINE=2V: COLUMDIA;

RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

RA Fartmann B., Valle G., Bloecker H., Perz-Alonso M., Obermaier B.,

RA Palseny M., Boutry M., Grivell L.A., Mache R., Puigdomencch P.,

RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomencch P.,

RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomencch P.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Wincker P., Cattolico L., Weissenbach N., Bangert S.,

RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

RA Wezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,

RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Rooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,

RA Rooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,

RA Mayer K.F.X., Kaul S., Town C.D., Koo H., Tallon L.J., Jenkins J.,

RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

RA Rooney T., Haas B., Malts A., Utterback T., Pujii C.Y., Shea T.P.,

RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,

RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,

RA Riyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Warana S., Nakazaki N., Shippo S., Takeuchi C., Wada T.,

"Sequence and analysis of chromosome 3 of the plant Arabidopsis
EMBL; AJ002280; CAA05292.1; -.
EMBL; AJ224338; CAA11903.2; -.
EMBL; AL137898; CAB71046.1; -.
                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fcentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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"Organization and structural evolution of four multigene families
Arabidopsis thaliana: AtLCAD, AtLGT, AtMYST and AtHD-GL2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
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MEDLINE=20267440; PubMed=10809443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE CDC2/CDKX SUBFAMILY; GSK-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: MAY MEDIATE EXTRACELLULAR SIGNALS TO REGULATE TRANSCRIPTION IN DIFFERENTIATING CELLS (BY SIMILARITY). PTM: AUTOPHOSPHORYLATED MAINLY ON THREONINE AND SERINE RESIDUES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. 42:703-717(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Columbia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SER/THR FAMILY OF SUBSUBFAMILY.
                                                                                                                                                                                                                                                                                                                                    There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mewes H.-W.,
                                                                                                                                                                                                                                                                                                                                                                               a collaboration
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RESULT 25
ARLY SULSO
ID ARLY
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
STRAIN=ATCC 35992 / DSM 1617 / P2;
STRAIN=ATCC 35992 / DSM 16177 P2;
She Q., Singh R.K., Confalonieri P., Zivanovic Y., Allard G.,
She Q., Singh R.K., Confalonieri P., Clausen I.G., Curtis B.A.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Exauso G., Fletcher C., Gordon P.M.K.,
De Moors A., Exauso G., Fletcher C., Kozera C.J., Medina N., P.
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., P.
Thi.Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstru
Charlebots R.L., Doolitttle W.F., Duguet M., Gassterland T.,
Charlebots R.L., Doolittle W.F., Duguet M., Gassterland T.,
Charlebots R.L., Doolittle W.F., Duguet M., Gassterland T.,
Charlebots R.L., Ragan M.A., Sensen C.W., Van der Oost J.,
Charlebots R.L., Ragan M.A., Sensen C.W., Van der Oost J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UX32;
15-SEP-2003
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00108; PROTEIN KINASE_ST; 1.

PROSITE; PS50011; PROTEIN KINASE_DOW; 1.

Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation; Multigene family.

Phosphorylation; Multigene family.

DOMAIN

102

386

PROTEIN KINASE.

DOMAIN

102

386

PROTEIN KINASE.

ATP (BY SIMILARITY).

BIND

BIND

108

116

BIND

BIND

108

116

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ARLY_S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAINATIC 35092 / DSM 1617 / P2;

MEDLINE=20165948; PubMed=10701121;

Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C.,

Confalonieri F., Curtis B., Duguet M., Erauso G., Faguy D.,

Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C.,

Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q.,

St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F.,

Ragan M.A., Sensen C.W.;

"Gene content and organization of a 281-kbp contig from the genome of

the extremely thermophilic archaeon, Sulfolobus solfataricus P2.";

Genome 43:116-136(2000).
                                                                             the European Bioinformatics Institute. Then use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                  Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J., "The complete genome of the crenarchaeon Sulfolobus solfataricus Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
-!- CATALYTIC ACTIVITY: N-(L-arginino)succinate = fumarate + L-
                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sulfolobus solfataricus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Argininosuccinate lyase
                                                                                                                                                                                                                                                                                PATHWAY: Arginine biosynthesis; eighth (last) step. SUBCELLULAR LOCATION: Cytoplasmic (Probable). SIMILARITY: Belongs to the lyase I family. Argining
                                                                                                                                                                                                                                                           subfamily.
                                                                                                                                                                                                                                                                                                                                                                          arginine.
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5; Conserv
                       requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 42, Lieute. up (Rel. 42, Last sequence up (Rel. 42, Last annotation related lyase (EC 4.3.2.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update.
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(Arginosuccinase)
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                                                                                                           There are no restrictions ng as its content is in
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                                                                                                                                                                          TRMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peng X
                                                                                                                                                                                                  a collaboration
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RESULT 26
TGN2 THUMAN
ID TGN2 THO 
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AC 0
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Best Local S
Matches 5
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EMBL; AE006692; AAK40947.1; ALT INIT.
PIR; DS0211; D90211.
HSSP; P24058; 1DCN.
HAMAP; MF 00006; -1 1.
HSSP; P24058; 1DCN.
HAMAP; MF 00006; -1 1.
FIRO0362; Fummarate_lyase.
Pfam; PF00206; lyase_1; 1.
PFAm; PF00206; lyase_1; 1.
PFAM; PF00206; PMRATELYASE; FALSE_NEG.
PRINTS; PR00149; FUMRATELYASES; FALSE_NEG.
PROSITE; PS00163; FUMRATELYASES; FALSE_NEG.
PROSITE; PS00163; FUMRATELYASE; Complete protecome.
Arginine biosynthesis; Lyase; Complete protecome.
SEQUENCE 444 AA; 50262 MW; 817B75F74C3C60CE CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98086273; PubMed=9422759;
MEDLINE=98086273; PubMed=9422759;
Kain R., Angata K., Kerjaschki D., Fukuda M.;
"Molecular cloning and expression of a novel human trans-Golgi !"
"Molecular cloning that contains multiple tyrosine-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trans-Golgi network integral membrane protein 2 precursor (Trans-Golgi network protein TGN51) (TGN46) (TGN48) (TGN38 homolog).
TGOLN2 OR TGN51 OR TGN46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGN2 HUMAN STANDARD; PRT; 480 AA. 043493; 015282; 043492; 043499; 043500; 043501; 16-0CT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: TYPE I MEI
GOLGI NETWORK. CYCLES BETWEEN TI
SURFACE RETURNING VIA ENDOSOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      functional implications.";

0. Cell Sci. 109:675-685(1996).

1. FUNCTION: MAY BE INVOLVED IN REGULATING MEMBRANE TRAFFIC TO FROM TRANS-GOLGI NETWORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ponnambalam S., Girotti M., Yaspo M.-L., Owen C.E., Perry A.C.,
Suganuma T., Nilsson T., Fried M., Banting G., Warren G.;
"Primate homologues of rat TGN38: primary structure, expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Fetal liver, and Fetal thy MEDLINE=97063845; PubMed=8907352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
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                                                                                                                                           TISSUE
                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                          Name=TGN51;
                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative
                                                                                                           TBOID=043493-3; Sequence=VSP 004455;
ISSUE SPECIFICITY: ISOFORM TGN46 IS WIDELY EXPRESSED. ISOFOR
RM51 IS MORE ABUNDANT IN FETAL LUNG AND KIDNEY, ISOFORM TGN4
ARELY EXPRESSED IN EMBRYONIC KIDNEY AND PROMYELOCYTIC CELLS.
                                                                                                                                                                                                                                                   IsoId=043493-2; Sequence=VSP_004454;
                                                                                                                                                                                                                                                                                                             IsoId=043493-1; Sequence=Displayed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273:981-988(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.7%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                 splicing; Named
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE I MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26; DB
Pred. No. 2.5e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; l
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEMBRANE PROTEIN.
THE TRANS-GOLGI
                                                                                                                                                                                                                                                                                                                                                                       isoforms=3;
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2.5e+02;
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                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.
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                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
-I- FUNCTION: NOT KNOWN; SUPPRESSOR OF SULFOXIDE ETHIONINE
-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- SIMILARITY: Belongs to the allantoate permease family.
                                                                                                                                                                                                                                                                                                             cerevisiae."
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                                                                                                                                                                                                                                                                                                                                     Clark M.W., Fortin
A.B., Su Y., Davies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces
                 Length 593;
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28-FEB-2003
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trafficking.
-!- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
-!- SIMILARITY: Contains 1 SH3 domain.
-!- SIMILARITY: Contains 1 phox homology (PX) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sorting nexin
                                                                                                                                                                                                                          Pfam; PF00787; PX; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                      EMBL; BC014814; AAH14814.1; MGD; MGI:1913866; Snx9.
                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                  PROSITE; PS50195; PX; 1. PROSITE; PS50002; SH3; 1.
                                                                                                                                                    ProDom; PD000066; SH3;
SMART; SM00312; PX; 1.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                     InterPro; IPR001683; PX. InterPro; IPR001452; SH3.
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(Rel. 41, Last sequence update)
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                                                                           Protein transport; SH3 domain.
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360 P.
66545 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
     3D5568476F2D816D CRC64;
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RESULT 29
KLP3_CAEEL
ID KLP3_C
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Matches 5; Conserv
TBB2_NEIMB STANDA
Q06988;
01-FEB-1995 (Rel. 31,
01-FEB-1995 (Rel. 31,
28-FEB-2003 (Rel. 41,
Transferrin-binding p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (kel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kinesin-like protein klp-3.
KLP-3 OR T09A5.2.
Caenorhabdic
                                                                                                                                                                                                                                                                                                                                                                               by non-profit institutions as long as its content is in no entities requires a license agreement '?
                                                                                                                                                                                          DOMAIN
NP BIND
SEQUENCE
                                                                NEIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomas K.;
Submitted (AUG-1994) to
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                    HSSP; P17119; 3KAR.
WormPep; T09A5.2; CE01083.
InterPro; IPR001752; kinesin_motor.
                                                                                                                                                                                                                                                                                                                                                     EMBL; Z36753; CAA853;
PIR; T24717; T24717.
                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                         Motor protein;
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PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
                                                                                                                                                                                                                                                                                        SMART; SM00129; KISc;
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                                                                                                                                                                                                                                                                                                            Pfam; PF00225; kinesin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAEEL
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                                                                                                          183 TEKDEL 188
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5; Conser
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89
170
242
328
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          (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 41, Last annotation updat
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248 C
496 K
335 A
67323 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the EMBL/GenBank/DDBJ databases.
TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                    ATP-binding; Coiled coil.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
KINESIN-MOTOR.
ATP (POTENTIAL).
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Pred. No. 3.4e
1; Mismatches
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Pred. No. 3.4e+02;
1; Mismatches 0
                                                                                                                                                                                             FBF971AD52905690 CRC64;
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3.4e+02;
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RESULT 31
SPO8_YEAST
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Matches 5
                                                                                                    P41833;
01-NOV-1995
01-NOV-1995
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cross-reactivity of antibodies to NH2-terminal peptides.";
FEMS Microbiol. Lett. 109:85-91(1993).
-i- FUNCTION: ACTS AS A TRANSFERRIN RECEPTOR AND IS REQUIRED FOR
TRANSFERRIN UTILIZATION.
-i- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Griffiths E., Stevenson P., Byfield P., Ala'Aldeen D.A., Borritello S.P., Holland J., Parsons T., Williams P., "Antigenic relationships of transferrin-binding proteins from "Antigenic relationships of transferrin-binding proteins from Neisseria meningitidis, N. gonorrhoeae and Haemophilus influenzae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-SCUG 37603 / B1686 / Serogroup B /
MEDLINE-93345825, PubMed-8344530;
Legrain M., Mazarin V., Irwin S.W., Bouche
Jacobs E., Schryvers A.B.;
       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932;
                                                                      Transcriptional regulator SPO8. SPO8 OR IME4 OR YGL192W OR G1337.
                                                                                                                                                                  SP08
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STRAIN=CCUG 37603 / B16B6 / Serogroup
MEDLINE=93307625; PubMed=8319886;
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Bacteria; Proteobacteria; Betapro
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                            Outer membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01298; Lipoprotein_5; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001677; Transferrin_bind
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                                                      Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- INDUCTION: By iron starvation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and characterization of Neisseria meningitidis genes encoding the transferrin-binding proteins Tbp1 and Tbp2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anchor (Probable).
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                                                                                                                                                               YEAST
                                                                                                                                                                                                                                           107 SERDEL 112
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599
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(Rel. 35, Last annotation
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65468 MW;
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Signal; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Betaproteobacteria; Neisseriales;
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Pred. No. 3.4e
1; Mismatches
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Best Local :
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                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
78 kDa glucose-regulated protein precursor (GRP heavy chain binding protein) (BiP).
HSPA5 OR GRP78.
                                                                                                                                                                              GR78 CHICK
Q90593;
15-DEC-1998
15-DEC-1998
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted [2]
                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                           CHICK
                                                                                                                                                                                                                                                                                                                                                                                                             SGD; S0003160; IME4.
GO; GO:0008174; F:mdNA methyltransferase activity; IDA
GO; GO:0007126; P:meiosis; IMP
GO; GO:0016556; P:mRNA modification; IMP.
Pfam; PF05063; MT-A70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D23721; BAA04938.1; --
EMBL; U30859; AAA74443.1; --
EMBL; X91837; CAA62952.1; --
EMBL; Z72714; CAA96904.1; --
PIR; S48509; S48509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
"78-kilodalton glucose-regulated protein is induced in Rous sarcoma virus-transformed cells independently of glucose deprivation;";
            Hanafusa H.;
"78-kilodalton
                                              SEQUENCE FROM N.A.
MEDLINE=88302183; PubMed=2841586;
                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; Activator; DNA-binding SEQUENCE 600 AA; 69395 MW; A99BETEBA76790BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequencing of a 40.5 kb fragment chromosome VII from Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                Stoeckle M.Y.,
                                                                                                         Archosauria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast 13:55-64 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bruschi C.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coglievina M., Klima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97197971;
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                                                                                 ICBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                        Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   non-profit institutions as long as its content and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                               SEKDEL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T03467; -.
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                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                         Aves;
                                 Sugano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FY1679;
                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=9046087;
                                                                                                         Neognathae;
                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.,
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83.3%;
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                                   Hampe A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                     Score 26;
Pred. No.
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                                   Vashishtha A.,
                                                                                                                                                                                                                                                                                                                                                                                                   DNA-binding; Nuclear
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and the EMBL outstation -
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PRODOM; PD000089; HSp70; 1.
PR05ITE; PS00297; HSP70_1; 1.
PR0SITE; PS00329; HSP70_2; 1.
PR0SITE; PS001036; HSP70_3; 1.
PR0SITE; PS001014; ER_TARGET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as loom has its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p11021; Q9NPF1; 01-JUL-1989 (Rel. 11, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
78 kDa glucose-regulated protein precursor (GRP heavy chain binding protein) (BiP) (Endoplasmic Ca(2+) binding protein grp78).
HSPAS OR GRP78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol.
                                                                                                                                                                                                                                                                                            Ting J., Lee A.S.; "Human gene encoding the 78,000-dalton glucose-regulated protein its pseudogene: structure, conservation, and regulation."; DNA 7:275-286(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000886; I
InterPro; IPR001023; I
Pfam; PF00012; HSP70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M27260; AAA4871
PIR; I50242; I50242.
SEQUENCE FROM N.A. TISSUE=Fibroblast; Hansen J.J., Niels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                   Submitted
                                                                                                                                                                                 TISSUE=Cervical carcinoma; Chao C.C.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88283347; PubMed=2840249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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FUNCTION: Probably plays a rote in facilitating the assembly multimeric protein complexes inside the ER (By similarity).
SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
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                                                                                                                                                   (DEC-1995)
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           Nielsen
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       Jorgensen
                                                                                                                                                   EMBL/GenBank/DDBJ databases
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Pred. No. 3.
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       Gregersen N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78) (Immunoglobulin reticulum lumenal
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           Bolund
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MBL outstation -
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PRINTS; PRO0301; HEATSHOCK70.
PRODOM; PD000089; H8970; 1.
PROSITE; PS00014; ER TARGET; 1
PROSITE; PS000297; HSP70_1; 1.
PROSITE; PS000329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Endoplasmic retic
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M19645; AAA52614.1; -.
EMBL; X87949; CAA61201.1; -.
EMBL; AZ71729; CAB71335.1; -.
EMBL; AZ71729; CAB72336.1; -.
EMBL; X59969; CAA42595.1; -.
EMBL; X59969; CAA42595.1; -.
PIR, A29821; A29821
HSSP; P19120; 3HSC.
SW15S-2DPAGE; P11021; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97295306; PubMed=9150948;
Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Eddes J.S., Burgess A.W., Simy Ji H., Reid G.E., Eddes J.E., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Grp78 is
Submitted
                                                                                                                                                                                                         GO; GO:0005788; C:endoplasmic reticulum lumen; NAS GO; GO:000524; F:ATP binding activity; NAS. GO; GO:0008577; F:Hsp70/Hsp90 organizing protein au InterPro; IPR00086; ER target. InterPro; IPR001033; Hsp70. Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                        PMMA-2DPAGE; P11021; -. PHCI-2DPAGE; P11021; -. Siena-2DPAGE; P11021; -. Genew; HGNC:5238; HSPA5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Two-dimensional electrophoretic analysis of human breast proteins: mapping of proteins that bind to the SH3 domain lineage kinase MLK2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97295304; PubMed=9150946; Rasmussen R.K., Ji H., Eddes J.S., Moritz R.L., Simpson R.J., Dorow D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bermudez-Fajardo A., Llewellyn D.H., Campbell A.K., Errington "Sequence differences between human grp78Lp isolated from He and previously reported human sequences.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                  MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A direct-repeat sequence of the A23187-mediated inducibility and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 19-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Electrophoresis 18:588-598(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.C.K., Lin-Chao S.;
                                                                                                                                                                                                                                                                                                                                                                     138120;
                                                                                                                                                                                 PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20:6481-6485(1992).
                                     reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human BiP gene is required for an inducible nuclear factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions ing as its content is in
                                                                                                                                                                                                                                                                                      protein activity; NAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL outstation
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Best Local S
Matches 5
    Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                     PRINTS; PR00301; HEATSHOCK70.

ProDom; PD000089; Hsp70; 1.

PROSITE; PS00297; HSP70 1; 1.

PROSITE; PS00299; HSP70 3; 1.

PROSITE; PS001036; HSP70 3; 1.

PROSITE; PS000014; ER_TARGET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE=96355436; PubMed=8702846;

Beggah A., Mathews P., Beguin P., Geering K.;

Beggah A., Mathews P., Beguin P., Geering K.;

"Degradation and endoplasmic reticulum retention of unassembled alpha-
and beta-subunits of Na,K-ATPase correlate with interaction of BiP.";

J. Biol. Chem. 271:20895-20902(1996).

J. FUNCTION: Probably plays a role in facilitating the assembly of

multimeric protein complexes inside the ER.

-i- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.

-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
CONFLICT
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                                                                                  SIGNAL
CHAIN
SITE
                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
78 kDag-1003 (Rel. 41, Last annotation update)
78 kDag-1000se-regulary (protein precursor (GRP 78) (Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q91883;
15-DEC-1998
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HSSP; P19120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSPA5
                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355;
                                                                                                                        ATP-binding; Endoplasmic
                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                             InterPro; IPR000886; ER_target.
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               89.7%;
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83.3%;
                                                                                reticulum; signal.

POTENTIAL.
78 kDa GLUCOSE-REGULATED PROTEIN.
PREVENT SECRETION FROM ER (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW.
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PREVENT SECRETION FROM ER.
MISSING (IN REF. 1 AND 2).
D -> H (IN REF. 1 AND 2).
R -> S (IN REF. 1 AND 2).
K -> N (IN REF. 1 AND 2).
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    Score 26; DB Pred. No. 3.8e
1; Mismatches
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Pred. No.
                                                                      SIMILARITY
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                                                         43E1468F532E80CF CRC64;
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DB 1; Le...
. 3.8e+02;
. 3. 0;
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3.7e+02;
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Best Local S
Matches 5
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PRODOM; PD0000089; HSp70; 1.
PROSITE; PS002297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
PROSITE; PS00014; ER_TARGET; 1.
-HTPG_BACFR
P58476;
28-FEB-2003
28-FEB-2003
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_APLCA
                                                BACFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the expression of BiP, the major protein chaperon of the ER.
J. Cell Biol. 119:1069-1076 (1992).
IPPUNCTION: Probably plays a role in facilitating the assermultimeric protein complexes inside the ER.
SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93077669; PubMed=1360013; Kuhl D., Kennedy T. Rayrin.
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z15041; CAA78759.1;
PIR; S24782; S24782.
HSSP; P08109; 1CKR.
                                                                                                                                                                                                                  SITE
                                                                                                                                                                                                                                           SIGNAL
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InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entities requires a license agreement (See http://www.isb-sib.ch/ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
Aplysioidea; Aplysiidae; Aplysia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q16956;
                                                                                                                                                                                                                                                    ATP-binding; Endoplasmic reticulum; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1603)
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                                                                                                                                                                                                     667 AA;
(Rel. 41, Created)
(Rel. 41, Last sequence
                                                                                                                                                   Conservative
                                      STANDARD;
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                                                                                                                                                               89.7%;
                                                                                                                                                                                                     MW; A59EC27AF188141D CRC64;
                                                                                                                                                Score 26; DB 1;
Pred. No. 3.8e+02;
1; Mismatches 0
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78 kDa GLUCOSE-REGULATED
PREVENT SECRETION FROM EF
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  (See http://www.isb-sib.ch/announce/
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ER.";
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RESULT 37
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                                                                                                                                                                                                                                                                                                                                            ENPL RABIT
018750;
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteroides fragilis.
Bacteria; Bacteroidetes;
Bacteroidaceae; Bacteroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_00505; -; 1.
InterPro; IPR003594; ATPbir
InterPro; IPR001404; Hsp90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
-!- FUNCTION: Molecular chaperone. Has ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smalley D., Smith C.J.,
An aerobic-type ribonucleotide reductase
                   MEDLINE=98264829; PubMed=9601063;
Vitadello M., Colpo P., Gorza L.;
"Rabbit cardiac and skeletal myocytes differ in constitutive and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chaperone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00775; HEATSHOCK90.
SMART; SM00387; HATPase_C; 1.
PROSITE; PS00298; HSP90; FALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02518; HATPase_c; 1. Pfam; PF00183; HSP90; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF404759; AAL02103.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=638R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                          Endoplasmin
inducible expression
                                                                                          STRAIN=New Zealand white;
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                        NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                               15-DEC-1998
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           618 AEKDEL 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEKDEL 6
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546
681 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Heat
1 326
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                                                                                                                                                                                                                                                                       (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 42, Last annotation updat
(94 kDa glucose-regulated prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteroides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           545 B
681 C
77951 MW;
                                                                                                                                                                                                       Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATPbind_ATPase.
of the glucose-regulated protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 26; DB 1;
Pred. No. 3.9e+02;
1; Mismatches 0
                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECA62D43009C03EB CRC64;
                                                                                                                                                                                  Leporidae;
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                                                                                                                                                                                                                                                                                                                                                                                              716
                                                                                                                                                                                                                                                                          protein)
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                                                                                                                                                                                                                                                                              (GRP94)
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                                                                                                                                                                                                                                                                            (Fragment).
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENPL MOUSE STANDARD;

P08113; P11427;

01-OCT-1989 (Rel. 12, Created)

01-OCT-1989 (Rel. 12, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

Endoplasmin precursor (Endoplasmic reticulum protein 99)

Endoplasmin precursor (Endoplasmic reticulum protein 99)

****Comparated protein) (GRP94) (ERP99) (Polymorphic variance regulated protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
SITE
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CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chaperone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- FUNCTION: Molecular chaperone that functions in the proctation of the process of transport of secreted proteins (By similarity).
-:- SUBUNIT: Homodimer; disulfide-linked (By similarity).
-:- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
-:- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00775; HEATSHOCK90.
SMART; SM00387; HATPase c; 1.
PROSITE; PS00298; HSP90; 1.
PROSITE; PS00014; ER TARGET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003594; ATPbir
InterPro; IPR00386; ER tal
InterPro; IPR001404; Hsp90
Pfam; PP02518; HATPase C; I
Pfam; PF00183; HSP90; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF001631; AAC48853.1; -. HSSP; P07900; 1YER.
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SEQUENCE OF 378-507 FROM N.A.
MEDLINE=87283933; PubMed=3612811;
Smith M.J., Koch G.L.E.;
"Isolation and identification of partial cDNA clones for endoplasmin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
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                                                                                                                                                                                                                                                   "ERp99, an reticulum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                        Mazzarella R.A., Green M.;
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87250515;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRA1 OR TRA-1
                                                                                                                                                                               Biol.
                                                                                                                                                                                                                       94-kDa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              711 AEKDEL 716
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IPR000886; ER_target.
                                                                                                                                                                        abundant, conserved glycoprotein of the endoplasmic is homologous to the 90-kDa heat shock protein (hsp: glucose regulated protein (GRP94)."; hem. 262:8875-8883(1987).
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                                                                                                                                                                                                                                                                                                                                                               PubMed=3036833;
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Rodentia;
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83.3%;
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Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PREVENT SECRETION FROM ER (POTENTIAL).
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N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7098C6442F0EC84B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
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(POTENTIAL).
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                                                                                                                                                                                                                                                              (hep90)
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RESULT 39
ENPL_HUMAN
ID ENPL_HUMAN S
AC P14625; Q96A97;
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Best Local S
Matches
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EMBL; M29652; AAA37743.1; -.
EMBL; M16370; AAA40023.1; -.
PIR; A29317; A29317.
HSSP; P07900; 1BYQ.
SWISS-2DPAGE; P08113; MOUSE.
MGD; MGI:98817; Tral.
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Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qu D., Mazzarella R.A., Green M.;
"Analysis of the structure and synthesis of GRP94, a protein of the endoplasmic reticulum.";
DNA Cell Biol. 13:117-124(1994).

-I- FUNCTION: Molecular Chaperone that functions in transport of secreted proteins (By similarity).

-I- SUBUNIT: Homodimer; disulfide-linked.
                                                                                                                                                                                                                                                          PRINTS; PRO0775; HEATSHOCK90.
SMART; SM00387; HATPASE C; 1.
PROSITE; PS00014; ER TARGET; 1.
PROSITE; PS00298; HSP90; 1.
                                                                                                                                                                                                                                                                                               InterPro; IPR003594; ATPbind AT:
InterPro; IPR000886; ER target.
InterPro; IPR001404; Hsp90.
InterPro; IPR001404; Hsp90.
Pfam; PF02518; HATPase C; 1.
Pfam; PF00183; HSP90; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Srivastava P.K., Chen Y.-T., Old L.J., "5'-structural analysis of genes encoding polymorphic antigens chemically induced tumors."; proc. Natl. Acad. Sci. U.S.A. 84:3807-3811(1987).
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                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Endoplasmic reticulum lumen. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
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Chen Y.-T., Old
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Pred. No.
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1.6e+02;
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Genew; HGNC:12028; TRA1.

MIM; 191175; -.

GG: GO:0005886; C:plasma membrane; TAS.
GG: GO:0005488; F:binding activity; TAS.
GG: GO:000573; F:heat shock protein activity; TAS.
GG: GO:0005211; F:plasma glycoprotein; TAS.
GG: GO:0005211; F:plasma glycoprotein; TAS.
GG: GO:000520; P:response to stress; TAS.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR00386; ER target.
InterPro; IPR00149; Hsp90.
                    InterPro; IPR000886; ER target.
InterPro; IPR001404; Hep90.
Pfam; PP02518; HATPase_C; 1.
Pfam; PF00183; HSP90; 1.
PRINTS; PR00775; HEATSHOCK90.
SMART; SM00387; HATPase_C; 1.
PROSITE; PS00014; ER TARGET; 1.
PROSITE; PS000298; HSP90; 1.
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EMBL; M33716; AAA68201.1; -.
EMBL; M26596; AAA58621.1; -.
EMBL; AY040226; AAK74072.1; -.
PIR; A35954; A35954.
HSSP; P07900; 1BYO.
Aarhus/Ghent-2DPAGE; 8602; IEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases -i- FUNCTION: Molecular chaperone that functions in the transport of secreted proteins.
-i- SUBUNIT: Homodimer; disulfide-linked.
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Mol. Cell. Biol. 9:2153-2162(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90332640; PubMed=2377606;
Maki R.G., Old L.J., Srivastava P.K.;
"Human homologue of murine tumor rejection antigen gp9
and coding regions and relationship to stress-induced
Proc. Natl. Acad. Sci. U.S.A. 87:5658-5662(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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Eukaryota; Metazoa;
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15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.

    -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
    -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.

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Glycoprotein; Calcium-binding;
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InterPro; IPR00386; ER target.
InterPro; IPR001404; Hsp90.
Pfam; PF02518; HATPase_C; 1.
Pfam; PF00183; HSP90; 1.
PFNITS; PR00775; HEATSHOCK90.
SMART; SM00387; HATPase_C; 1.
PROSITE; P800014; ER_TARGET; 1.
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Mammalia; Eutheria; Carnivora;
NCBI_TaxID=9815;
                                                                                                                                                        EMBL; U01153; AAA17708.1;
PIR; A53211; A53211.
HSSP; P07900; 1BYQ.
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5; Conservative
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precursor (94 kDa glucose-regulated
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Canis.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

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다	Q8BOW1; 01-MAR-2003 (TrEMBLrel. 23, Created)
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	(TrEMBLrel. 23, Last annotation
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	Infectious salmon anemia virus.
	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
	unclassified Orthomyxoviridae.
	NCBI_TaxID=55987;
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	SEQUENCE FROM N.A.
	STRAIN=Glesvaer;
_	Cook M., Vincent S., Griffiths S., Ritchie R.;
	"Development of a strain typing assay for infectious salmon anemia
	virus (ISAV).";
	(In) Unknown A. (eds.);
	PROCEEDINGS OF THE INFECTIOUS SALMON ANEMIA SPECIAL SESSION
	4TH INTERNATIONAL SYMPOSIUM ON AQUATIC ANIMAL HEALTH, pp.0-0,
	Unknown publisher (2003).
	EMBL; AY151801; AAN74857.1;
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L Ø	Best Local Similarity 100.0%; Pred. No. 78; Matches 6; Conservative 0; Mismatches 0;
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(In) Unknown A. (eds.);
PROCEEDINGS OF THE INFECTIOUS SIATH INTERNATIONAL SYMPOSIUM ON /
Unknown publisher (2003).
EMBL; AY151803; AAN74859.1; -.
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PROCEEDINGS OF THE INFECTIOUS SALMON ANEMIA SPECIAL SESSION,
4TH INTERNATIONAL SYMPOSIUM ON AQUATIC ANIMAL HEALTH, pp.0-0,
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EMBL; AX151802; AAN74858.1; -
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; unclassified Orthomyxoviridae.
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"Development of a strain
virus (ISAV).";
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Q8SR64;
01-JUN-2002
01-JUN-2002
01-MAR-2003
                                                                         STRAIN-Norway;

Clouthier S.C., Rector T., Brown N., Anderson E.D.;

Clouthier S.C., Rector T. Brown N., Anderson E.D.;

"Genomic organization of infectious salmon anemia virus.";

submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

SMBL; AF42999; AAN57725.1;

EMBL; AF42999; AAN57725.1;

SEQUENCE 256 AA; 28957 MW; 9108AEDDE63PB283 CRC64;
                                                                                                                                                                                                                                 Q8BDV2;
Q8BDV2;
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM
SEQUENCE
                                                                                                                                                                 Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; unclassified Orthomyxoviridae. NCBI_TaxID=55987;
                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 414:450-453(2001).
EMBL; AL590449; CAD25760.1;
InterPro; IPR003903; UIM.
Pfam; PF02809; UIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=GH-mi,
MEDLINE=21576510; PubMed=11719806;
MEDLINE=21576510; PubMed=11719806;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thor
Prensier G., Barbe V., Peyretaillade E., Brottier P., W.
Prensier G., Barbe V., Peyret P., Saurin W., Gouy M.,
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NCBI_TaxID=6035;
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Weissenbach J., Vivares C.P.
                                                                                                                                                                                                    Infectious salmon anemia virus
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(C STRAIN=C2A / ATCC 35395 / DSM 2834;

RX MEDLINE=21929760; PubMed=11932238;

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

RA Springer T.A., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
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PRINTS; PR00035; HTHGNTR.
SMART; SM00345; HTH GNTR; 1.
PROSITE; PS00043; HTH GNTR FAMILY; 1.
DNA-binding; Transcription regulation; Complete SEQUENCE 279 AA; 31997 MW; 47D710A53CC4F5B1
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MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwi
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson
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TIGR; VC1900;
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Vibrionaceae; Vibrio.
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Archaea; Euryarchaeota; Methanococci;
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SMART; SMOOSO7; HNHC; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
Endonuclease; Complete proteome.
SEQUENCE 279 AA; 32509 MW; 840
                                              NCBI_TaxID=55987;
                                                                                   Infectious salmon anemia virus Viruses; ssRNA negative-strand unclassified Orthomyxoviridae.
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Genome Res. 12:532-542(2002).
EMBL; AE011058; AAM06859.1;
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SEQUENCE 300;
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Virus Res. 84:161-170(2002).
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Pfam; PF01844; HNH; 1.
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Metcalf W.W., Birren B.;
"The genome of Methanosarcina
   SEQUENCE FROM N.A.
                                                                                                                                                                                                           Matrix
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Viruses; ssRNA negative-strand
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InterPro; IPR002711; HNH.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutron G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutron G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Wan K.H., Doyle C., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Dietz S.M.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Davielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Lasko P., Lei Y., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Melson D.R., Nelson K.A., Nixon K., McSherri D.R., Paceleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paceleb J.M.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q95T08;
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21898794; PubMed=11900848; Ritchie R.J., Bardiot A., Melville K., Snow M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
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Virus Res. 84:161-170(2002).
EMBL; AJ306487; CAC80624.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
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A Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

A Formalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Formalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Formalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A Pacleb J., Paragas V., Park S., Patel S., Pfeifer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 6
                                                                                                                  Q9P8R5;
01-OCT-2000
01-OCT-2000
01-OCT-2002
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EMBL; AE003678; AAN14308.1;
FlyBase; FBgn0037556.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Matthews B.B., Bayraktaroglu L., Campbell K Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronneller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                  Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Asperg
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304 AA; 34
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Pred. No. 1.9e+02;
Mismatches 0;
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nith C.D.,
er S.E.,
                      Aspergillus.
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RESULT 12
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"The Aspergillus niger transcriptional activator XlnR, which is involved in the degradation of the polysaccharides xylan and cellulose, also regulates D-xylose reductase gene expression.";
MOI. Microbiol. 36:193-200(2000).
EMBL; AP219625; AAF61912.1; -.
                                                                                                                                                                                    WormPep; K09C
Hypothetical
SEQUENCE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Creat 01-JAN-1998 (TrEMBLrel. 05, Last 01-MAR-2003 (TrEMBLrel. 23, Last Hypothetical 38.0 kDa protein. K09C6.2
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SEQUENCE
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Pfam; PF00248; aldo ket red; I.

PRINTS; PR00069; ALDKETEDPASE.

ProDom; PD000288; Aldo/ket red; 1.

PROSITE; PS00062; ALDKETO REDUCTASE 2; 1.

PROSITE; PS00063; ALDKETO REDUCTASE 3; 1.

PROSITE; PS00063; ALDKETO REDUCTASE 3; 1.
                                                                                                                                                                                                                         "Direct Submission.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; AF022975; AAB70669.1; -.
Wormhep; K09C6.2; CE11990.
                                                                                                                                                                                                                                                                                                                                                                                                                     Goela D., Harper M.;
"The sequence of C. of Submitted (SEP-1997)
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Hasper A.A., Visser J., de Graaff L.H.;
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Science 282:2012-2018(1998).
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44
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344 AA; 3
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C. elegans Sequencing Consortium.";
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EMBL/GenBank/DDBJ databases.
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RESULT 14
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Q9VHU9; Q9VHU8;
01-MAY-2000 (TTEMBLrel. 1
01-MAY-2000 (TTEMBLrel. 1
01-CCT-2002 (TTEMBLrel. 2
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Q97LX1;
01-OCT-2001 (TremBLrel. 1
01-OCT-2001 (TremBLrel. 1
01-MAR-2003 (TremBLrel. 2
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MEDLINE=21359325; PubMed=11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.C.

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hrazapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=BERKELEY;
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PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2;
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EMBL; AE007558; AAK78413.1; -.
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
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Pred. No.
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Soucaille P., Daly M.J.,
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017735
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SORRETT A REPRESENTATION OF THE SORREST OF THE SORR
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Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000)

1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.
EMBL; AE003678; AAF54200.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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01-JAN-1998 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                               EMBL; Z81052; CAB02876.1; -. WormPep; D2023.6; CE09076. InterPro; IPR004147; ABC1.
                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=99069613;
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Submitted (OCT-1996)
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1     9     MISSING (IN SHORT )
462 AA; 52097 MW; E24B9B128BA14F69
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58043 MW;
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Pred. No. 2
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RESULT 16
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ da.
DR EMBL, AC024766; AAF59489.1; -.
R Wormbep; Y39G10AL.2; CE25267.
Hypothetical protein.
SEQUENCE 607 **
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01-OCT-2000 (TrEMBLrel. 15, Lasi
01-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical 69.0 kDa protein.
Y39G10AL.2.
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STRAIN-Bristol N2;
Bradshaw-Cordum H., D
"The sequence of C. e
Submitted (MAR-2000)
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Q8YSS4;
01-MAR-2002
01-MAR-2002
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Q9N403;
01-OCT-2000
SEQUENCE FROM N.A.
MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P.,
Watanabe A., Iriguchi M., Ishikawa
                                                                                                                                                                                             Anabaena sp. (strain PCC Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. investigating biology. The C. eleganized 282:2012-2018(1998).
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MEDLINE=99069613;
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(TrEMBLrel. 23, La
(IremBLrel. 33, La
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D; Mismatches
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Pred. No. 3.2e+02;
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         Kuritz T., Sasamoto S.,
A., Kawashima K., Kimura T.,
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Best Local S
Matches
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Q9DC41;
01-JUN-2001
01-JUN-2001
01-MAR-2003
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Kreis M., Kavanagh T., Entian K.D., Rieg
Puigdomenech P., Hatzopoulos P., Obermai
Jones J., Palme K., Ansorge W., Delseny
Schueller C., Chalwatzis N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical 70.1
AT4G16810.
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"Complete genomic sequence of the f
cyanobacterium Anabaena sp. strain
DNA Res. 8:205-213(2001).
Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing pr
Submitted (MAR-2000) to the
EMBL; Z97342; CAB10454.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Pfam; PF00515; TPR; 1.
Hypothetical protein; GSEQUENCE 613 AA; 688
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Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 623 AA; 70062 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
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                                                                                           shock
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                                                                                         70kD
                                                                                    (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
70kD protein 5 (Glucose-regulated protein,
                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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13 AA; 68822 MW;
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  Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         project;
ne EMBL/GenBank/DDBJ
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K.D., Rieger M., James R.,
P., Obermaier B., Duesterhoft
., Delseny M., Bancroft I., Me
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 10; Length 623; Pred. No. 4e+02;
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Pred. No.
Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Asato T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Gustincich S., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Wynshaw-Boris B., Ringwald M., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local S
Matches 6
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PRODOM; PD000089; HSp70; 1.
PROSITE; PS000014; ER TARGET; 1.
PROSITE; PS00027; HSF70_1; 1.
PROSITE; PS000329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Endoplasmic reticuli
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Q92E24;
01-DEC-2001
01-DEC-2001
01-MAR-2002
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-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
HSSP; P19120; 3HSC.
                Baquero F., Berche P., Blo
Charbit A., Chetouani F.,
                                                                    SEQUENCE FROM N.A. STRAIN=CLIP 11262 / PubMed=11679669;
                                                                                                                                                          Listeria innocua.
Bacteria; Firmicutes;
                                                                                                                                                                                               Hypothetical LIN0637.
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MEDLINE=21085660; PubMed=11217851;
                                                    Glaser P., Frangeul L.,
                                                                                                                                         NCBI_TaxID=1642;
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InterPro; IPR001023; Hsp70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
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l (TrEMBLrel. 19, La
2 (TrEMBLrel. 20, La
al protein lin0637.
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ilarity 100.0%;
Conservative
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, Buchrieser C., Rusniok C., Amend A.,
Bloecker H., Brandt P., Chakraborty F.,
F., Couve E., de Daruvar A., Dehoux P.,
ernal G., Duchaud E., Durant L., Dussur
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2 MW; 69E2C0A2C896DE6C
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Last annotation updat
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Pred. No. 4.2e+02;
; Mismatches 0;
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QRESULT QRYSAA ID DT O11 DT O12 DT O1
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A Gautier L., Goebel W., Gomez-Lopez N., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

A Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

A Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

A Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

"Comparative genomics of Listeria species.";

ENBL; AL596165; CAC55869.1; -.

DI Stillst; LIN00637; -.

M Hypothetical protein; Complete proteome.

SEQUENCE 91 AA; 9878 MW; SABBCC7D530B96AB CRC64;
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XX MEDLINE-21537279; pubMed=11679669;

XA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

A Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

A Domann E., Dominguez-Bernal G., Durant L., Dussurget O.,

A Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

A Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

"Comparative genomics of Listeria species.";

Science 294:849-852(2001).

BELL, ALS91976; CAC98706.1; -.
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01-MAR-2002
01-MAR-2002
01-MAR-2002
Q9TW79;
Q9TW79;
01-MAY-2000
01-MAY-2000
01-JUN-2001
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Bacteria; Firmicutes; I
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Hypothetical protein; Complete
SEQUENCE 91 AA; 9862 MW; 3D
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2 (TrEMBLrel. 20, La
al protein lmo0628.
(TrEMBLrel. (TrEMBLrel.
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83.3%;
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1; Mismatches 0
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Pred. No. 1.6e+02;
1; Mismatches 0
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3DEDB6DDF31E90E1 CRC64;
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annotation update)
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RESULT
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=MAL-KP26, and MAL-E15;
Ravichandran M., Doolan D.L., Cox-Singh J., Hoffin Ravichandran M., Doolan D.L., Cox-Singh J., Hoffin Ravichandran M., Doolan D.L., Cox-Singh J., Hoffin Ravichandran M., Doolan B.L., Cox-Singh J., Hoffin Plant I was a stage-specific antigen-1 (LSA-1) are complementation of the stage-specific antigen-1 (LSA-1) are complementation of the stage of the s
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Submitted (AUG-1998) to the EMBL
EMBL; AR086801; AAC42998.1;
EMBL; AF086799; AAC42979.1;
EMBL; AF086799; AAC42991.1;
EMBL; AF086799; AAC42981.1;
EMBL; AF086799; AAC42982.1;
EMBL; AF086799; AAC42983.1;
EMBL; AF086800; AAC42984.1;
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132
AF3 15564 MW; 11
Q26028
Q26028;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001.
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Q9TW78;
Q9TW78;
Q1-MAY-2000
Q1-MAY-2000
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Eukaryota; Alveolata;
NCBI_TaxID=5833;
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Eukaryota; Alveolata;
NCBI_TaxID=5833;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Liver stage-specific antigen-1 (Fragment).
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"Class I HLA degenerate
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1; Mismatches
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MEDLINB=96065765; PubMed=7477115;
MEDLINB=96065765; PubMed=7477115;
Yang C., Shi Y.P., Udhayakumar V., Alpers M.
Hawley W.A., Collins W.E., Lal A.A.;
"Sequence variations in the non-repetitive specific antigen-1 (LSA-1) of Plasmodium fa
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Plasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID=5833;
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Liver stage-specific antigen 1 (Fragment).
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                               Eukaryota;
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Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.,
"Sequence variations in the non-repetitive regions of the liver
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STRAIN=Kenyan;
SEQUENCE FROM N.A.
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01-NOV-1996
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MEDLINE=96065765; PubMed=7477115;
MEDLINE=96065765; PubMed=7477115;
MEDLINE=96065765; PubMed=7477115;
MEDLINE=96065765; PubMed=7477115;
MARINE M.P., POVOR M.M.,
Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.;
Hawley W.A., Collins W.E., Lal A.A.;
"Sequence variations in the non-repetitive regions of the liver stage-
"Sequence variations in the non-repetitive regions of the liver stage-
"Sequence variations in the non-repetitive regions of the liver stage-
"Sequence variations in the non-repetitive regions of the liver stage-
"Sequence variations in the non-repetitive regions of the liver stage-
"Sequence variations in the non-repetitive regions of the liver stage-
"Sequence variations in the non-repetitive regions of the liver stage-
"Sequence variations in the non-repetitive regions of the liver stage-
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Eukaryota; Alveolata;
NCBI_TaxID=5833;
SEQUENCE FROM N.A.
STRAIN=Kenyan;
MEDLINE=96065765; PubMed=7477115;
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01-NOV-1996 (TrEMBLrel 01, Last sequence update)
01-NOV-1998 (TrEMBLrel 08, Last annotation update)
Liver stage-specific antigen 1 (Fragment).
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EMBL; L40917; AAC41587.1; -.
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MEDLINE=96065765; PubMed=7477115;
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Eukaryota; Alveolata;
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EMBL; L40945; AAC41581.1; -.
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                                                                                                                                      NCBI_TaxID=5833;
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5; Conservative
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Last annotation update)
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Pred. No. 2.8e
1; Mismatches
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Pred. No.
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01-NOV-1996
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                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
Liver stage-specific antigen
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Yang C., Shi Y.F., Udhayakumar V., Alpers M.P., Povo
Hawley W.A., Collins W.E., Lal A.A.;
"Sequence variations in the non-repetitive regions o
"Securitic antigen-1 (LSA-1) of Plasmodium falciparum
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01.NOV-1996 (TrEMBLrel. 1), Last sequence update)
01.DEC-2001 (TrEMBLrel. 19, Last annotation updat
Liver stage-specific antigen 1 (Fragment).
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MEDLINE=96065765; PubMed=7477115;
Yang C., Shi Y.P., Udhayakumar V.,
                                          SEQUENCE FROM N.A. STRAIN=Kenyan;
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                                                                                                                              Eukaryota;
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Last annotation updat
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    Alpers M.P.,
                                                                                                                              Haemosporida;
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Best Local S
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Q25896;
Q1-NOV-1996 (TrEMBLrel. 01, Cr
01-NOV-1996 (TrEMBLrel. 19, La
01-DEC-2001 (TrEMBLrel. 19, La
Liver stage-specific antigen 1
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01-NOV-1996
01-NOV-1996
01-NOV-1998
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SEQUENCE
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MEDLINE-96065765; PubMed-7477115;
Yang C., Shi Y.P., Udhayakumar V., Alpers M
Yang C., Shi Y.P., Udhayakumar V., Alpers M
Hawley W.A., Collins W.E., Lal A.A.;
"Sequence variations in the non-repetitive
specific antigen-1 (LSA-1) of Plasmodium fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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STRAIN=Brazilian;
MEDLINE=96065765; PubMed=7477115;
Yang C. Shi Y.P. Udhayakumar V.
Hawley W.A., Collins W.E., Lal A.
                                                                                                                                                                                                                                                                                                    Q25897
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                                                                                                                  Eukaryota; Alveolata;
NCBI_TaxID=5833;
                                                                                                                                                                                                01.NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Liver stage-specific antigen 1 (Fragment).
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                                                                              SEQUENCE FROM N.A.
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160 AA;
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160 AA;
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Last annotation update)
n 1 (Fragment).
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of Plasmodium falciparum from field
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Pred. No. 2.8e
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                Alpers
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                    м.р.,
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Q25904;
01-NOV-1996
01-NOV-1996
01-MAY-1999
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STRAIN-Kenyan;
MEDLINE-96065765; PubMed=7477115;
MEDLINE-96065765; PubMed=7477115;
Yang C., Shi Y.P., Udhayakumar V., Alpers M
Hawley W.A., Collins W.E., Lal A.A.;
"Sequence variations in the non-repetitive
"Sequence variations in the non-repetitive
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Q25899;
01-NOV-1996
01-NOV-1996
01-NOV-1998
SEQUENCE FROM N.A.
STRAIN=PAPUA NEW GUINEA;
MEDLINE=96065765; PubMed=7477115;
Yang C., Shi Y.P., Udhayakumar V., Alpers
Hawley W.A., Collins W.E., Lal A.A.;
                                                                                    (Fragment).
LSA-1.
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Eukaryota; Alveolata;
NCBI_TaxID=5833;
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EMBL;
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Eukaryota; Alveolata;
NCBI_TaxID=5833;
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AAC41589.1;
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                                                                  Apicomplexa;
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n 1 (Liver stage-specific
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Pred. No. 2.8e
1; Mismatches
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STRAIN-Papua New Guinea;
MEDLINE-96065765; PubMed=7477115;
MEDLINE-96065765; PubMed=7477115;
Yang C., Shi Y.P., Udhayakumar V., Alpers M
Yang C., Shi Y.P., Udhayakumar V., Alpers M
Hawley W.A., Collins W.E., Lal A.A.;
"Sequence variations in the non-repetitive
"Sequence variations in the non-repetitive
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01-NOV-1996
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01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence variations in the non-repetitive regions of the liver stage-
specific antigen-1 (LSA-1) of Plasmodium falciparum from field
isolates.";
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Eukaryota; Alveolata;
NCBI_TaxID=5833;
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Submitted (AUG-1998)
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Plasmodium falciparum
                      Liver stage-specific antigen
                                                                                   Q25898
                                                                                                                                                                                                                                                                               EMBL; L40943; AAC41595.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liver stage-specific antigen
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             LSA-1
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RESULT Q25887 ID Q2 AC Q2 DT 01

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InterPro; IPR003439; ABC_transporter.
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SMART; SM00382; AAA; 1.
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Q8YTX9;
01-MAR-2002
01-MAR-2002
01-MAR-2003
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Kaneko T., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL, AP003590; BAB194283.1; -.
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Hawley W.A., Collins W.E., Lal A.A.,
"Sequence variations in the non-repetitive
specific antigen-1 (LSA-1) of Plasmodium fa
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NCBI_TaxID=5833;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

:	22	100.0	100.0 5 21 A	121	AAY90827	Linker amino acid
ωį	22	100.0	ט נ	21	AAB74581	Context-dependent
4	22	100.0	5	23	AAE20415	Ser4Gly spacer use
ហ	22	100.0	10	22	AAG97963	Human complementar
6	22	100.0	10	22	AAG97964	Human complementar
7	22	100.0	10	22	AAG85127	Saccharomyces cere
8	22	100.0	10	22	AAG85129	Saccharomyces cere
9	22	100.0	10	22	AAG85131	Saccharomyces cere

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	AR570	AB57	AB55'	AW25'	BP47:	AW649	AE16	AW19	AR55:	A017	AY679	AY27!	BG733	AE09(BU076	BU086	AG80:	AU049	AE09:	AU086	AY908	AW531	AW65	AR39!	BG686	AW194	AE16	AE16	AW989	86MY	AW989	AR55:	AR27	AG85	AG85	UI.
ì	7	547	700	774	134	992	539	402	185	004	939	544	392	9	645	677	185	949	161	883	828	278	570	572	623	403	540	526	967	966	953	180	243	651	4	4.
Carboxit			le asso	brain	Human BLyS binding	Bromelain protein	tissue f	Tissue factor pept	huTFh antigenic pe	Linker peptide use	EPOa-hSA fusion pr	듣	Rat SSeCKS cyclin		Epstein-Barr virus	chai	Fusion construct h	Humanised anti-p18	arr	Antibody L19-Fibro	ino a	ptide	4	ום בם		ч.	tissue fact	tissue fact	tissue	tissue fact	n tissue f	D) O)	ez	accharomyces c	accharomyces ce	Saccharomyces cere

ALIGNMENTS

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Ring DB;	(CHIR) CHIRON CORP.	11-AUG-1994; 94US-0288981.	••	08-FEB-1984; 84US-0577976.	08-MAY-1988; 88US-0190778.	21-MAR-1986; 86US-0842476.		07-JUN-1995; 95US-0483749.		25-APR-2000.	US6054561-A.		Synthetic.		toxin targeting; imaging; genetic; therapeutic.	specific binding assay; affinity purification; drug targeting;	Ϋ́	Antigen binding site; immunoglobulin; cancer antigen; immunological;	٠	Linker amino acid sequence SEQ ID NO:30.		29-AUG-2000 (first entry)		AAY90827;		AAY90827 standard; Peptide; 5 AA.	LT 1

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RESULT 2
AAY67938
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The present invention describes erythropoietin analogue-human serum albumin (EPOa-hSA) fusion proteins having at least one amino acid residue of the EPOa moiety altered such that a site, which serves as a site for glycosylation in EPO does not serve same purpose in the EPOa. The present sequence represents a specifically claimed peptide linker for use in the construction of an EPOa-hSA fusion protein. The EPOa-hSA fusion protein can be used in treatment of a subject in need of EPO, e.g. for a patient suffering from anaemia associated with renal failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding assays, affinity purification, drug or toxin targeting, imaging and genetic or immunological therapeutics for various cancers. The present sequence represents a linker amino acid sequence which is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPOa-hSA fusion protein; peptide lir anaemia; renal failure; blood loss;
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                                                                                                                                                                                                                                                       Claim 18; Page 53; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-1998;
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9.3e+05;
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                                                                            cancer, arthritis, infections, neovascular glaucoma, inflammatory conditions, dermatitis, endometriosis, atherosclerosis, vascular restenosis and conditions associated with granulation tissues, suburns and pyogenic granuloma. The present sequence is an example spacer peptide for use in the invention.
                                                                                                                                               The present invention describes a method of enhancing the efficacy of agent by coadministering the agent and a context-dependent functional entity. The latter comprises a substructure with thrombogenic potentia and a selective recognition domain. This is useful in the treatment of
                                                                                                                                                                                                                                               Enhancing the efficacy of active and diagnostic agents and treating pathological conditions in a subject by administering the agent with a context-dependent functional entity, useful for treating e.g. malignant neoplasms -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chronic disease, HIV infection, blood loss or cancer. The EPOa-hSA fusion protein can be included in a nutraceutical, such as an infant feeding formula. The EPOa-hSA constructs can be used as part of a gene therapy protocol to delivery nucleic acids encoding an EPOa-hSA fusion
                                                    Sequence
                                                                                                                                                                                                                   Disclosure; Page 23; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-2000; 2000WO-US27794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Context-dependent selective recognit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Context-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB74581 standard; peptide; 5 AA
                                                                                                                                                                                                                                                                                                               WPI; 2001-258295/26
                                                                                                                                                                                                                                                                                                                                        Houston
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ependent functional entity; efficacy enhancement; in-
recognition domain; thrombogenic potential; cancer;
; atherosclerosis; burn.
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             100.0%;
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Score 22; DE
Pred. No. 9.3
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entity
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spacer peptide
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. 9.3e+05;
                             DB
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                          Length
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RESULT 4
AAE20415
RESULT 5
AAG97963
ID AAGS
XX
AC AAGS
DT 18-8
XX
DE Huma
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                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                             Matches:
          Human complementary peptide,
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                              The invention relates to gene-delivery compound comprising a single-chain binding polypeptide (SCBP) having at least one effector segment having a cysteinyl residue, and a nucleic acid-binding moiety (NBM) or a lipid-associating moiety (IAM) coupled to SCBP by the residue. Gene-delivery compound is useful for targetted gene delivery for treating diseases by
                                                                                                                                                                                                                                                                                                                                                        Gene-delivery compound for targeted gene delivery, comprises single-chain binding polypeptide having effector segment with cysteinyl residue and nucleic acid-binding/lipid-associating moiety coupled to polypeptide by residue -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200200914-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene-delivery compound; single-chain binding polypeptide; SCBP; nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM; gene therapy; targetted gene delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ser4Gly spacer
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Huston JS, Wils P,
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                                 18-SEP-2001
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                                                                           AAG97963 standard;
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                                                                                                                                                                                                                                             fusion
                                                                                                                                                                                                                                                       therapy. The present peptide sequence is a spacer used to prepare
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) QUAN Z.
) LAURENT O.
) MARASCO W A.
) SCHERMAN D.
                                                                                                                                                                           Similarity
5; Conserv
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                                                                                                                                   SSSSG
                                                                                                                                                                                                                        5 AA;
                                                                                                                                                                                                                                             construct.
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                                (first entry)
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                                                                           Peptide; 10
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           SEQ ID
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Pred. No.
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thes 0;
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RESULT 6
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ID AAG9
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interact with their relevant target proteins encoded in the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs -
                                                                                                                                                                                                                                                    Human complementary peptide,
                                                                                                                                                                                                                                                                                                     AAG97964;
                                                                                                                                                                                                                                                                                                                            AAG97964 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roberts GW, Heal JR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; complementary peptide; ligand; drug discovery; drug design.
                                WPI; 2001-408419/43.
                                                                                                                                                        14-JUN-2001.
                                                                                                                                                                             WO200142277-A2
                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                             Human; complementary peptide; ligand; drug discovery; drug design.
                                                                                                                                                                                                                                                                             18-SEP-2001
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                                                                                (PROT-) PROTEOM LTD.
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ilarity 100.0%;
Conservative 0
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                                                        Heal JR
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                                                                                                                                                                                                                                                    SEQ ID NO: 4159.
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Pred. No. 1.3e+02;
); Mismatches 0;
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A
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A set of peptide ligands consisting to proteins encoded by genes of the

of specific complementary peptides human genome, useful in an assay

FFXSXSSSSSSXX

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RESULT 7
AAG85127
ID AAGE
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Matches 5
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                                                                                                                                                 The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for screening and identifying of drug candidates or pro-drugs -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides
                                                                                                    Sequence
                                                                                                                                    Saccharomyces
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                                                                                                                                                                                                                                                                                                                            Identifying complementary peptides by nucleotide sequence databases, useful
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-367863/38.
                                                                                                                                                                                                                                                                                                                                                                                                                Roberts GW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae; complementary peptide; peptide identification;
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                              Local Similarity nes 5; Conserv
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                                                                                                    A,
                                                                                                                                    cerevisiae.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                          analysis of protein in drug design -
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1.3e+02;
                                              1.3e+02;
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Saccharomyces cerevisiae; drug discovery; drug desig

drug design.

complementary peptide;

peptide identification;

Saccharomyces cerevisiae

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RESULT 8
AAG85129
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AC AAG8
                                                                                                                              RESULT 9
AAG85131
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Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              grug
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                                                          Saccharomyces
                                                                              11-SEP-2001
                                                                                                 AAG85131;
                                                                                                                     AAG85131 standard;
                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 40; 488pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                     Roberts GW, Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG85129 standard;
                                                                                                                                                                                                                                                                                                                                                                                   Identifying complementary peptides by analysis of protein and nucleotide sequence databases, useful in drug design -
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PROT-) PROTEOM LTD.
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                                                                                                                                                                                                             Similarity 5; Conser
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                                                          cerevisiae peptide,
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Pred. No. 1.3
0; Mismatches
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                                                          SEQ
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PD 14-JU
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Best Local S
Matches 5
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                                                                                                                                                                                                                                       Saccharomyces cerevisiae
                                                                                                                                                                                                                                                             Saccharomyces cerevisiae; complementary peptide; peptide identification; drug discovery; drug design.
                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying complementary peptides by analysis of protein nucleotide sequence databases, useful in drug design -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roberts
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           Example 3; Page 112; 488pp; English
                                 Identifying complementary peptides by nucleotide sequence databases, useful
                                                                                                                                                                                                                WO200142276-A1.
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                                                                                                                                                                                                                                                                                                                                                                       AAG85647 standard;
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                                                                                                                                                                                          14-JUN-2001
                                                                                                                    (PROT-) PROTEOM LTD.
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                                                                     2001-367863/38
                                                                                             GW,
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5; Conser
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                                                                                             Heal JR;
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                                                                                                                                                                                                                                                                                                 peptide,
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Pred. No.
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                                 analysis of protein
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RESULT 11
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Best Local
                                                                                                                    The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                Roberts GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces
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                                                                                                                                                                                                                                Example 3; Page 112; 488pp; English.
                                                                                                                                                                                                                                                           Identifying complementary peptides by analysis of protein and nucleotide sequence databases, useful in drug design -
                                                                                                                                                                                                                                                                                                                                                                                                                 13-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug discovery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae; complementary peptide; peptide identification;
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                                                                                                            Saccharomyces
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                            Conservative
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                                                                                                          cerevisiae.
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Pred. No. 1.3
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Pred. No. 1.3e+02;
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                                         1.3e+02;
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RESULT 12
AAG85651
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AAR27243
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                                                                                                                                                                                                                                                                   Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG85651 standard; Peptide; 10
         Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying complementary peptides by analysis of protein nucleotide sequence databases, useful in drug design -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae; complementary peptide; peptide identification;
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                                                              Fusion
                                                                                  Sequence of
                                                                                                       25-MAR-2003
25-FEB-1993
                                                                                                                                                          AAR27243 standard;
                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 112; 488pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-367863/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-DEC-1999;
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                                                             protein;
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                                                                                 serine-rich peptide linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heal JR;
                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                   AA;
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(first entry)
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Location/Qualifiers
3..7
/label= repeat unit
                                                              serine-rich
                                                                                                                                                          peptide;
                                                                                                                                                                                                                                                                  100.0%;
                                                              peptide linker;
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                                                                                                                                                                                                                                                                   Score 22;
Pred. No.
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ches 0;
                                                                                                                                                                                                                                                                              DB 22;
                                                               protease resistant
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RESULT 14
AAR55180
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Best Local S
Matches 5
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19-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               media, re
lysis by
                                                                                                                                                                         Human; tissue factor; TF; heavy chain; pre-protein; pre-huTFh; breast; soluble; huTFh; hydrophobic; transmembrane; anchor region; monoclonal; aggregation; factor VII; factor VIIa; coagulation; antibody; MAb; assay; thrombus; detection; cancer; lung; carcinoma; anticoagulant; heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resistant to proteolysis. In particular it is used to tuse domain mimicking Vh and Vl from monoclonal antibody, to produce single chain binding site proteins (sFV) which dissolve in physiological media, retain their activity at high concentrations, and resist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR27243 is a prefd. linker of the invention. The advantage of such linkers is that they can improve the refolding properties of the fusion protein expressed in procaryotes. The linker itself is resistant to proteolysis. In particular it is used to fuse domains resistant to proteolysis.
         (SCRI )
(UYPE-)
(UTEM )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                     huTF binding site peptide analogue
                                                                                                                                                                                                                                                                                                 AAR55180;
                                                                                                                                                                                                                                                                                                                       AAR55180 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteolysis
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                                                                               16-NOV-1993;
                                                                                                       26-MAY-1994.
                                                                                                                            WO9411029-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pusion proteins comprising serine-rich peptide linkers improved solubility in physiological media, resistance proteolysis and enhanced regolding properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CREA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Updated on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1992-331728/40
        ) SCRIPPS RES INST.
) UNIV PENNSYLVANIA.
) UNIV TEMPLE.
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endogenous protesases.
on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                 SSSSG
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(first entry)
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                                                                                93WO-US11239.
                                                        92US-0977281.
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Pred. No. 1.7
0; Mismatches
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1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  new sequences given in AAR55179-80 represent peptide analogues of the human tissue factor (huTF) binding site. These peptides may be used to competitively inhibit the binding of huTF to blood coagulation factor VII/VIIa, pref. without forming an activated complex, ie. without initiating coagulation.

(Updated on prevent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting coagulation during extracorporeal circulation - by admin of monoclonal antibody preventing binding of tissue factor to coagulation factor 7 or 7a
A method has been developed for inhibiting tissue factor (TF) mediated cerebral reperfusion tissue damage in a subject with cerebral ischaem (or one in which blood flow to the cerebral vesets has been occluded during a surgical procedure) by the administration of monoclonal antibodies similar to those produced by the cell lines ATCC HB9381, HB9382 and/or HB9383 to inhibit blood coagulation reactions initiated
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                                                                                                             Inhibiting tissue factor mediated reperfusion tissue damage following cerebral ischaemia or myocardial infarction - by the administration of tissue factor specific monoclonal antibodies to inhibit binding of the tissue factor to the Factor VII/VIIA complex
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13-JAN-1995;
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                                                                                      Disclosure; Column
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Pred. No. 1.7e+02;
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A method has been developed for inhibiting tissue factor (TF) mediated cerebral reperfusion tissue damage in a subject with cerebral ischaemia (or one in which blood flow to the cerebral vessels has been occluded during a surgical procedure) by the administration of monoclonal antibodies similar to those produced by the cell lines ATCC HB9381, HB9382 and/or HB9383 to inhibit blood coagulation reactions initiated be the binding of TF to a Factor VII/VIIa complex. The method can be used to prevent damage caused by the reperfusion of blood into tissues following, for example, a stroke, myocardial infarction or a surgical procedure that resulted in the occlusion of blood flow to the tissue. Reperfusion damage may be a result of TF mediated fibrin formation (i.e the beginning of the clot formation reaction), which contributes to the no-reflow phenomenon by producing smaller secondary clots in capillarie
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                                                                                                                                                                                                                                                                                     Inhibiting tissue factor mediated reperfusion tissue damage following cerebral ischaemia or myocardial infarction - by the administration of tissue factor specific monoclonal antibodies to inhibit binding of the tissue factor to the Factor VII/VIIA complex
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13-JAN-1995;
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Best Local S
Matches 5
                                                                                                               during a surgical procedure) by the administration of monoclonal antibodies similar to those produced by the cell lines ATCC HB9381, HB9382 and/or HB9383 to inhibit blood coagulation reactions initiated by the binding of TF to a Factor VII/VIIa complex. The method can be used to prevent damage caused by the reperfusion of blood into tissues following, for example, a stroke, myocardial infarction or a surgical procedure that resulted in the occlusion of blood flow to the tissue. Reperfusion damage may be a result of TF mediated fibrin formation (i.e. Reperfusion damage may be a result of TF mediated fibrin formation to the beginning of the clot formation reaction), which contributes to the no-reflow phenomenon by producing smaller secondary clots in capillaries downstream from the original obstruction in response to vascular damage.
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13-JAN-1995;
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                                                              Treatment with the antibody prevents these clots from forming. AAW98951 to AAW98968 represent human TF binding site peptide analogues.
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actor VIIa; coagulation; anticoagulant; vasotropic;
rdial infarction; cerebral ischaemia.
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Query Match

100.0%;

Score 22;

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Length 13;

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ARE16 ID ARE16
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Matches 5
The invention relates to a method for diagnosis of a disease or susceptibility to a disease associated with abnormal cell-cell adhesion between epithelial cells, comprising detecting a mutation in a nucleic acid encoding an adhesion protein, a protease or a protease inhibitor, modulated level of adhesion protein, protease or protease inhibitor, or its fragment polypeptide. The method is useful for diagnosing a disease
                                                                                                                                                                                                                                                                   Diagnosing a disease or susceptibility to a disease associated with abnormal cell-cell adhesion between epithelial cells, by detecting mutation in nucleic acid encoding adhesion protein, protease or protease inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    basal cell carcinoma; cutaneous lymphoma; skin cancer; lung malignancy; gastrointestinal tract malignancy; acne vulgaris; psoriasis vulgaris; antipsoriatic; dermatological; antinflammatory; antiallergic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crohn's disease; ulcerative colitis; coeliac disease; peptic ulceration; impetigo; meningitis; skin melanoma; squamous cell carcinoma; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stratum corneum chymotryptic enzyme; envoplakin; desmoplakin; pig; SCCE desmocollin 1; adhesion protein; protease; protease inhibitor; eczema; contact dermatitis; lung atopic asthma; post viral asthma; viral warts; bronchial hyper-reactivity; chronic obstructive pulmonary disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                              Example A5; Page 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tazi-Ahnini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corneodesmosin peptide #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG68623 standard; Peptide; 14
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                                                                                                                                                                                                                                                                                                                                                                                                                         2002-557554/59
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2000GB-0029879.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; 22pp;
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                                                                                                                                                                                                              English.
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1.8e+02;
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               c-erbB-2 refers to a protein antigen expressed on the surface of tumour cells. such as breast and ovarian tumour cells, which is an approx. 200,000 mol. wt. acidic glycoprotein having an isolelectric pt. of about 5.3 (see AAQ46083, AAR39568). A single chain Fv (sFv) is a covalently linked VH-VL heterodimer which is expressed from a gene fusion including VH- and VL- encoding genes connected by a peptide-encoding linker. Such linker sequences are set forth in AA residues 116-135 in AAR39569, which includes part of the 16 AA linker sequences in AAR39572. Using AAQ46084 for the 520C9 monoclonal antibody, a single chain polypeptide can be produced having a binding affinity for a c-erbB-2 related antigen.
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07-FEB-1994
                                                                                                                                                                                                                                                                                                                                                            New single chain Fv polypeptide binding antigen - for imaging or treating breast
                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ46087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houston
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                                                                                                                                                                                                                                                                                                               Example; page 70; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CREA-)
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(Updated on 25-MAR-2003 to correct
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(first entry)
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Pred. No. 1.8e+02;
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  field.)
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t or ovarian cancer
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Query Match

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22; DB 19;

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                                       The invention relates to a vaccine for alleviating or preventing cautoimmune disorders induced by infection with Epstein-Barr virus (EBV). CI tomprises EBV or a component in a carrier for administration of the virus or viral component to alleviate or prevent the autoimmune disorder. Also claimed are: (1) a diagnostic test kit comprising: (a) reagents control samples from individuals not at risk of developing an autoimmune disorder control samples from individuals not at risk of developing an autoimmune disease; and (c) a device for determining the differences in levels of a developing an autoimmune disease from those at lower risk of developing an autoimmune disease; and (2) a method for screening for genetic markers or risk factors for development of autoimmune disorders induced by comprising comparing the responses of different strains of the same species of an animal vaccinated with EBV or a component to induce an autoimmune response in at least one of the strains of identify potential genetic markers or risk factors. The methods can be cused for the prevention, diagnosis, and treatment of autoimmune diseases having EBV as an etiological agent. The autoimmune diseases may be e.g. systemile onset diabetes mellitus, Wegener's syrantiomatosis, etc.

The present sequence represents a peptide derived from Epstein-Barr or virus. Reagents are used to detect antibodies to this peptide in a control control disease to the diagnostic rest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of Epstein-Barr virus or component(s) - for developing product(s) which can be used for preventing, diagnosing, t determining risk of developing autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Epstein-Barr virus; diagnostic test; autoimmune disease; vaccine; infection; antibody; screening; genetic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW65570 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Epstein-Barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-399062/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harley JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JAN-1997;
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Page 64; 81pp; English.
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                                  diagnostic test.
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RESULT 24
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                                                                                                                                   The present sequence represents a peptide used in an example of the present invention. The present invention describes an antiviral agent capable of combatting herpes virus replication. The antiviral agent is capable of disrupting herpes virus replication. The antiviral agent is capable of disrupting the association between ULB and POL (UL30), where ULB and POL are respectively defined as ULB and POL of herpes simplex virus type 1 (HSV-1) together with homologues in other herpes viruses. The present invention also describes an assay to determine the ability of a test substance to interfere with the association of ULB and POL. The assay comprises: (a) exposing a lst viral component to a test substance followed by a 2nd viral component, or exposing a 1st viral component to a 2nd viral component followed by a test substance; (b) washing to cremove any 2nd viral component and/or test substance, and optionally determining the amount, of 2nd viral component associated with the 1st viral component. The antiviral agent can be used to combat herpes virus
                                                 Query Match
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Matches
                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 36; 83pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Marsden HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herpes simplex virus type 1; replication; UL8; POL.
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                                                                                                                             replication
11
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5; Conserv
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 SSSSG
                        SSSSG
                                                                                                                                                                                                                                                                                                                                                                              l agent capable of inhibiting herpes virus replication association between herpes simplex virus type 1 UL8 ar
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                                                                                                                             or infection.
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                                                             Score 22;
Pred. No.
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                                                          2e+02;
                                                                         DB 19;
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RESULT 25 AAY90828

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RESULT 26
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Matches 5
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08-MAY-1988;
08-FEB-1984;
11-JAN-1985;
11-AUG-1994;
                                                                                                                                                                                                                                                                                                                                         The present invention describes a monoclonal antibody (MAb) (I) that binds to a human breast cancer antigen that is also bound by MAb 454Cl1 and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). All described is a hybridoma that produces (I). (I) is useful in specific binding assays, affinity purification, drug or toxin targeting, imaging, and genetic or immunological therapeutics for various cancers. The present sequence represents a linker amino acid sequence which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ring
Angiogenesis; extracellular matrix; ED-B domain; fibronectin; lesion; IL-2; doxorubicin; interleukin-12; Interferon-gamma; IL-12; IFN-gamma Tumour Necrosis Factor alpha; TNF alpha; tissue factor protein; angion electrochemical potential; tumour; cancer; rheumatoid arthritis;
                                                                                                                                             AAU08688
                                                                 Antibody
                                                                                           18-DEC-2001
                                                                                                                     AAU08688;
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody capable of binding useful for affinity purification, drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-338508/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen binding site; immunoglobulin; cancer antigen; immunolo; antibody; tumour; human; mucin; cancer; cytostatic; hybridoma; specific binding assay; affinity purification; drug targeting; toxin targeting; imaging; genetic; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2000
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                                                                                                                                                                                                                                                                              Similarity
                                                                 L19-Fibronectin-2 (IL-2)
                                                                                                                                            standard;
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                                                                                          (first entry)
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88US-0190778.
84US-0577976.
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94US-0288981
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                                                                                                                                            Peptide;
                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                            Score 22; DB 21;
Pred. No. 2e+02;
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                                                                 fusion protein amino acid linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or toxin
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targeting, imaging, a
                                                                                                                                                                                                                                                                                       Length
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                           IFN-gamma;
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                                                                                                                                                                                                                                                                                                                                                                                 imaging,
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RESULT 27
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XX IS-NC
DT 15-NC
DT 15-NC
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XX Vacci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a conjugate comprising a molecule that exerts a biocidal or cytotoxic effect on target cells in lesions of pathological angiogenesis and an antibody (L19) directed against an extracellular matrix component (the ED-B domain of fibronectin) which is present in the lesions. Examples of biocidal or cytotoxic molecules include fibronectin-2 (II-2), doxorubicin, interleukin-12 (II-12), Interferon-gamma (IFN-gamma), Tumour Necrosis Factor alpha (TNF alpha) tissue factor protein. These proteins may interact with a membrane-bound receptor on the target cell or perturb the electrochemical potential of the cell membrane. The treatable disorders include tumours, rheumatoid arthritis, diabetic retinopathy, age related muscular degeneration and angiomas. This sequence represents an amino acid linker encoded by a PCR primer used in the construction of an L19-IL-2 fusion protein.
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Halin C;
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             demyelinating disease; Hashimoto's thyroiditis; autoimmune infertility; hypoparathyroidism, primary biliary cirrhosis; ankylosing spondylitis; inflammatory bowel disease; Addison's disease; thyroiditis; filariasis; Graves' disease; ulcerative colitis; dermatomyositis; myasthenia gravis; Crohn's disease; CREST syndrome; autoimmune cystitis; glomerulonephritis; polyarteritis nodosa; hepatitis; atopic rhinitis; Goodpasture's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-FEB-2000; 2000US-184767P.
21-DEC-2000; 2000US-257192P.
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                                                                                                                       Vaccine; therapy; autoimmune disorder; Epstein-Barr virus; EBV; anaemia; polymyositis; systemic lupus erythematosus; SLE; rheumatoid arthritis; sjogren's syndrome; diabetes mellitus; adrenalitis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    member specific for and a molecule that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-596713/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-2001; 2001WO-IB00382.
                                                                                                                                                                                                                                         15-NOV-2001
                                                                                                                                                                                                                                                                                                             AAE09161 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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polyarteritis nodosa; r
sarcoidosis; rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                   virus (EBV) peptide #6 used in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for treating lesions, comprises a specific binding for extra-cellular matrix component present in lest that exerts biocidal/cytotoxic effect on target cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; 88pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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Pred. No.
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pyoderma gangrenosum; fibromyalgia; Kawasaki's disease; cardiomyopathy; Sampter's syndrome; asthma; polymyalgia rheumatica; psoriasis; arteritis; erythroblastosis foetalis; cyclitis; IgA nephropathy; Hodgkin's lymphoma; renal cell carcinoma; eosinophilia; immunosuppressive; ophthalmological; thyromimetic; neuroprotective; cytostatic; nephrotropic; antiallergic; dengue; antiulcer; vasotropic; antipyretic; hepatotropic.
                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-2001; 2001WO-US04191
                                                                                                                                                                                                                                                                                                                                                                                                                                    Epstein-Barr virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cushing's syndrome; bird-fancier's lung; alveolitis; erythema nodosum;
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09-FEB-2000; 2000US-0500904

(OKLA-) OKLAHOMA MEDICAL RES FOUND

Novel vaccine for alleviating or preventing autoimmune disorders induced Epstein-Barr virus (EBV) infection e.g. systemic lupus erythematosus, juvenile induced Epstein-Barr rus (EBV) infection e.g. systemic lu onset diabetes mellitus, comprises

WPI; 2001-522437/57.

Harley JB,

James JA,

Kaufman KM

Claim 8; Page 61; 114pp; English.

inflammatory bowel disease, polymyositis, dermatomyositis, multiple chalure, Schmidt's syndrome, autoimmune uvestis, Addison's disease, adrenalitis, primary biliary cirrhosis, Graves' disease, thyroiditis, Hashimoto's thyroiditis, autoimmune thyroid disease, thyroiditis, Hashimoto's thyroiditis, autoimmune thyroid disease, autoimmune and haemolytic anaemia, lupoid hepatitis, demyelinating thypoparathyroidism, Dressler's subacute cutaneous lupus erythematosus, hypoparathyroidism, Dressler's syndrome, myasthenia gravis, autoimmune pemphigus vulgaris, pemphigus, bullous pemphigoid, dermatitis herpetiformis, alopecia careata, autoimmune cystitis, pemphigoid, soleroderma, progressive systemic sclerodactyly and telanglectasia), adult onset diabetes dysmotility, sclerodactyly and telanglectasia), adult onset diabetes mellitus (Type II diabetes), male or female autoimmune infertility, connective tissue disease, polyarteritis, nodosa, systemic necrotising consective tissue disease, polyarteritis, nodosa, systemic necrotising conseculitis, glomerulonephritis, atopic dermatitis, areourrent abortion, anti-phospholipid syndrome, farmer's lung, archarem multiforme, costaraformy sundrome, Castaformy sundrome, fashinc's sundrome. erythema multiforme, postcardotomy syndrome, Cushing's syndrome, autoimmune chronic active hepatitis, bird-fancier's lung, allergic encephalomyelitis, toxic necrodermal lysis, alopecia, Alport's syndrome, allergic alveolitis, fibrosing alveolitis, interstitial lung disease, erythema nodosum, pyoderma gangrenosum, transfusion reaction, chronic fatigue syndrome, fibromyalgia, Takayasu's arteritis, Kawasaki's disease, polymyalgia rheumatica, temporal arteritis, giant cell arteritis, dengue, sampter's syndrome (triaditis, nasal polyps, cosinophilia) and Behcet's disease, Caplan's syndrome, encephalomyositis, erythema elevatum et disease, Caplan's syndrome, encephalomyositis, Shulman's syndrome, is sisteme, portiasis, erythroblastosis foetalis, Shulman's syndrome, is enchronic cyclitis, heterochromic cyclitis, Fuch's cyclitis, Hodgkin's and non-Hodgkin's lymphoma, cardiomyospathy, Henoch-Schonlein purpura, post vaccination syndromes, renal cell carcinoma, Eaton-Lambert syndrome or The present invention relates to a vaccine for alleviating or preventing autoimmune disorders induced by infection with Epstein-Barr virus (EBV), comprising EBV or its component in a carrier. The vaccine is useful for preventing or alleviating autoimmune disorders induced by EBV, e.g. systemic lupus erythematosus (SIB), Sjogren's syndrome, juvenile onset diabetes mellitus, rheumatoid arthritis, Wegener's granulomatosis, polychondritis. The present sequence 18

DB 22;

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RESULT 28
AAU04949
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RESULT 29
AAG80185
ID AAG80
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AC AAG80
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                                                                                                                                                                                                         The sequence represents a linker peptide used to make a humanised antipuls (520C9) single chain antibody/human interleukin-2 (IL-2) fusion protein. The fusion protein (or immunoconjugate) is used to inhibit the growth of tumours or cancers particularly those characterised by overexpression of p185 e.g. human adenocarcinomas and malignant and/or benign tumours of the breast, renal system, salivary gland,
                                                                                                                                                                                                                                                                                                      Novel immunoconjugate useful for inhibiting tumour cell growth in vivo comprises a humanized anti-p185 antibody linked to an Interleukin-2 polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised; antibody; p185; 520C9H; interleukin-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04949 standard; Peptide; 15
                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                   Disclosure; Page 16; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                   Austin R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200153354-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; tumour; adenocarcinoma; fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU04949
  21-JAN-2002
                      AAG80185
                                          AAG80185 standard;
                                                                                                                                                                                                  gastrointestinal tract or
                                                                                                                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON CORP.
(HAMI-) HAMILTON CIVIC HOSPITALS
(HAMI-) HAMILTON REGIONAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JAN-2000; 2000US-0177258.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-p185
                                                                                                                                                                                                                                                                                                                                                                    Kwok CS,
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                                                                                                                                    100.0%;
ilarity 100.0%;
Conservative 0
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  (first entry)
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                                         peptide; 15
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                                                                                                                                                                                                  tumours.
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Active agent conjugate; intracellular signalling cascade; cytostatic; antiinflammatory; nootropic; neuroprotective; immunosuppressive; cancer inflammation; cellular storage disease; Alzheimer's disease; infection;
                                                                                                                                                                                                                                                                                                   Fusion construct human STAT3/CD4 linker peptide.
                                                                                                                                                                                                                                                                      autoimmune disease; degenerative disorder.
                                                                                                                                                                                                                                                                                        intracellular signalling cascade;
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Conjugate for treatment targeting domain, where
cascade
                                                           WPI; 2002-025972/03.
                                                                                       Duebel S,
                                                                                                                                                                                                                25-OCT-2001.
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                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                       (BIOT-)
                                                                                                                                                    18-APR-2000; 2000DE-1019157.
                                                                                                                                                                                 18-APR-2001; 2001WO-DE01495.
                                                                                                                       BIOTECTID GMBH.
                                                                                       Emmrich F;
            the
            diagnosis of cancer,
e ligand modulates an
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comprises a ligand and intracellular signalling

Example 2; Page 28; 45pp; German.

autoimmune disease; infections and degenerative disorders), also for modifying differentiation and growth of cells; (ii) for elucidating the functional significance of individual stages in signal transduction; (iii) for introducing ligands into cells; (iv) as diagnostic reagents; and (v) for inducing immunological tolerance. (A) act specifically on a particular cellular target, can be delivered to specific cells and are toxicologically acceptable. They are universally specificable, by appropriate selection of their modular components. This sequence represents a peptide linker fragment used in the construction of a fusic construct composed of a fragment of the human STAT3 protein and CD4. an intracellular signalling cascade within the target cell. The products of the invention have cytostatic, antiinflammatory, nootropic, neuroprotective and immunosuppressive activity. (A) are useful, in human or veterinary medicine: (i) for treating diseases associated with abnormal physiological function and proliferation of specific cell types or populations (cancer; local or systemic inflammation; cellular storage diseases, e.g. amyloidosis, hemochromatosis or Alheimer's diseases; This invention describes a novel active agent conjugate (A) which comprises at least one each of: (i) a ligand (I); and (ii) a targeting domain (II) that binds specifically to a surface structure on a target cell in a non-human mammal, where the new feature is that (I) modulates in the construction of a fusion uman STAT3 protein and CD4.

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Sequence
15 AA;
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RESULT 30
ABU08677
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                                         ABU08677 standard; Peptide; 15
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Pred. No.
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Human single chain MHC class I polypetide associated linker

10-JUN-2003

(first entry)

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RESULT 31
ABU07645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a chimeric polypeptide (I) comprising an antigenic peptide capable of binding a human major histocompatibility complex (MHC) class I, a functional human beta-2 microglobulin and a functional human MHC class I heavy chain. The chimeric polypeptide is useful in generating large quantities of pure single chain MHC class I polypeptides which can be used in monomeric or multimeric form to. present antigenic peptides to cytotoxic T-lymphocyte (CTL) clones. They may also be used in rapid, sensitive and reliable MHC peptide binding assay to identify high affinity MHC binding T cell epitopes, in in vitro primary CTL induction studies to define those peptides that are immunogenic, and to generate antibodies. This is the amino acid sequence of a linker peptide used in the creation of a chimeric polypeptide capable of binding human major histocompatibility complex (MHC) class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New chimeric polypeptide useful for generating antibodies, comprisantigenic peptide that binds a human major histocompatibility comp(MHC) class I, a human beta-2 microglobulin and a human MHC class heavy chain -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2002; 2002US-0073300.
                                            autoimmune disorder; Epstein-Barr virus arthritis; multiple sclerosis; dermatiti
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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Epstein-Barr virus
                                                                               EBV; viral;
                                                                                                         Epstein-Barr virus nuclear antigen peptide #18.
                                                                                                                                            10-MAY-2003
                                                                                                                                                                                                         ABU07645 standard; Peptide; 15
                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence differs from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Page 9; 37pp; English.
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                                                                                                                                                                                                                                                                                                                      1 SSSSG 5
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                               allergy.
                                                                                                                                                                                                                                                                                          SSSSG 6
                                                                                                                                                                                                                                                                                                                                                                                                                   15
                                              Epstein-Barr virus nuclear antigen; vaccine;
disorder; Epstein-Barr virus infection; diabetes mellitus;
multiple sclerosis; dermatitis; psoriasis; asthma;
                                                                                                                                                                                                                                                                                                                                                    Conservative
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RESULT 32
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AC AAE09
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TIS-NC
DT 15-NC
XX
DE Epste
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KW Vacci
KW polym
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprising an Epstein-Barr virus or a component in a carrier for administration to alleviate or prevent the autoimmune disorders. The methods and compositions of the present invention are useful for diagnosing, preventing, treating and/or alleviating autoimmune disorders, such as diabetes mellitus, rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic arthritis, multiple sclerosis, encephalomyelitis, mysthenia gravis, systemic lupus erythematosus, autoimmune thyroiditis, atopic dermatitis, eczematous dermatitis, psoriasis, Sjogren's Syndrome, Crohn's disease, aphthous ulcer, iritis, conjunctivitis, keratoconjunctivitis, ulcerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-1996;
30-NOV-1993;
13-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                              colitis, asthma, allergic asthma, cutaneous lupus erythematosus, soleroderma, vaginitis, procritis, drug eruptions, leprosy reversal reactions, erythema nodosumleprosum, autoimmune uveitis, allergic encephalomyelitis, acute necrotising haemorrhagic encephalopathy, idiopathic bilateral progressive sensorineural hearing loss, aplastic anaemia, pure red cell anaemia, idiopathic thrombocytopenia, polychondritis, Wegener's granulomatosis, chronic active hepatitis, polychondritis, Wegener's granulomatosis, chronic active hepatitis, Stevens-Johnson syndrome, idiopathic sprue, lichen planus, Graves', disease, sarcoidosis, primary bilary circhosis, uveitis posterior, interstitial lung fibrosis, graft-versus-host disease, and allergy. The present sequence represents an Epstein-Barr virus nuclear antigen peptide used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New vaccine preventing or alleviating autoimmune disorders induced by the Epstein-Barr virus, such as diabetes mellitus, rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, atopic dermatitis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a vaccine for alleviating or preventing autoimmune disorders induced by infection with Epstein-Barr virus, comprising an Epstein-Barr virus or a component in a carrier for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 28; Page 28; 41pp; English.
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97US-0781296.
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Pred. No. 2e+02;
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Vaccine; therapy; autoimmune disorder; Epstein-Barr virus; EBV; anaemi polymyositis; systemic lupus erythematosus; SLE; rheumatoid arthritis;

EBV; anaemia;

Epstein-Barr virus (EBV) nuclear antigen-1 (EBNA-1) peptide #12

AAE09089;

(first

AAE09089 standard; peptide; 16

0

demyelinating disease; Hashimoto's thyroiditis; autoimmune infertility; hypoparathyroidism, primary biliary cirrhosis; ankylosing spondylitis; inflammatory bowel disease; hdisease; thyroiditis; filariasis; Graves' disease; ulcerative colitis; dermatomyositis; myasthenia gravis; Crohn's disease; CREST syndrome; autoimmune cystitis; glomerulonephritis; polyarteritis nodosa; hepatitis; atopic rhinitis; Goodpasture's syndrome; sarcoidosis; rheumatic fever; anti-phospholipid syndrome; farmer's lung; cushing's syndrome; bird-fancier's lung; alveolitis; erythema nodosum; pyoderma gangrenosum; fibromyalgia; Kawasaki's disease; cardiomyopathy; Sampter's syndrome; asthma; polymyalgia rheumatica; psoriasis; arteritis; erythroblastosis foetalis; cyclitis; IgA nephropathy; Hodgkin's lymphoma; renal cell carcinoma; eosinophilia; immunosuppressive; ophthalmological; thyromimetic; neuroprotective; cytostatic; nephrotropic; antiallergic; dengue; antiulcer; vasotropic; antipyretic; hepatotropic. Sjogren's syndrome; diabetes mellitus; adrenalitis; multiple sclerosis;

Epstein-Barr virus

16-AUG-2001

09-FEB-2001; 2001WO-US04191

09-FEB-2000; 2000US-0500904.

(OKLA-) OKLAHOMA MEDICAL RES FOUND.

James JA, Kaufman KM

Novel vaccine for alleviating or preventing autoimmune disorders induced Epstein-Barr virus (EBV) infection e.g. systemic lupus erythematosus, juvenile onset diabetes mellitus, comprises EBV vits component EBV virus

Example 9; Page 52; 114pp; English

CC inflammatory bowel disease, polymyositis, deermatomyositis, multiple CC endocrine failure, Schmidt's syndrome, autoimmune uveitis, Addison's CC disease, adrenalitis, primary billary cirrhosis, Graves' disease, CC disease, adrenalitis, primary billary cirrhosis, Graves' disease, CC thyroiditis, Hashimoto's thyroiditis, autoimmune thyroid disease, CC pernicious and haemolytic anaemia, lupoid hepatitis, demyelinating CC disease, multiple sclerosis, subacute cutaneous lupus erythematosus, CC pernicious and haemolytic anaemia, lupoid hepatitis, demyelinating CC didopathic thrombocytopenic purpura, autoimmune pemphigus vulgaris, CC pemphigus, bullous pemphigoid, dermatitis herpetiformis, altoimmune cystitis, pemphigoid, scleroderna, progressive CC mellitus (Type IT diabetes), male or female autoimmune infertility, CC ankylosing spondylitis, ulcerative colitis, Crohn's disease, mixed CC connective tissue disease, polyarteritis nodosa, systemic necrotising CC vasculitis, glomerulonephritis, atopic dermatitis atopic rinnitis, CC asthma, recurrent abortion, anti-phospholipid syndrome, farmer's lung, CC antoimmune chronic active hepatitis, bird-fancier's lung, allergic calveman multiforme, postcardotomy syndrome, Cushing's syndrome, CC allergic alveolitis, fibrosing alveolitis, interstitial lung disease, corphalomyelitis, fibrosing alveolitis, interstitial lung disease, corphalomyelitis, postcarnal lysis, alopecia, Alport's syndrome, CC sampter's syndrome (triaditis, nassl polyps, eosinophilia) and Behcet's disease, Caplan's syndrome, enrophalomyositis, crythema elevatum et tradicum en order and service for a store content of contents of the conten autoimmune disorders induced by infection with Epstein-Barr virus (EBV) comprising EBV or its component in a carrier. The vaccine is useful for preventing or alleviating autoimmune disorders induced by EBV, e.g. systemic lupus erythematosus (SLE), Sjogren's syndrome, juvenile onset disbetes mellitus, rheumatoid arthritis, Wegener's granulomatosis, infiliates mellitus, rheumatoid arthritis, Wegener's granulomatosis, The present invention relates to a vaccine for alleviating or preventing

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Matches 5
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                  New monoclonal antibodies which specifically bind to the tumour suppressor gene, SSeCKS, useful for binding or modulating SSeCKS
                                                                                                                                                                                                                                    WPI; 2003-298674/29
                                                                                                                                                                                                                                                                                                18-JUN-1996;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                10-JUL-2001; 2001US-0902432
                                                                                                                                                                                                                                                                                                                                                                          US2002160002-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat, tumour suppressor gene; SSeCKS; substrate of protein kinase C; mitogenic regulator; tumour suppressor; mitosis; tumour; cancer; cell proliferation disorder; fertility; nervous system development; cytostatic; CY domain; cyclin D binding domain; penetratin; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat SSeCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG73392,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG73392 standard; peptide; 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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97US-0978277.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CY) domain mutated peptide
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Pred. No. 2.1e+02;
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Example; Page 28; 124pp; English

suppressor gene, designated SSeCKS, that encodes a substrate of protein kinase C, and that functions as a mitogenic regulator and as a tumour suppressor. The invention also discloses a monoclonal antibody which specifically binds to an epitope of SSeCKS. The monoclonal antibody may be used to modulate the SSeCKS protein. The SSeCKS gene and protein are useful in diagnostic and therapeutic methods, particularly in regulating mitosis, suppressing tumours and treating cell proliferation disorders such as cancer. SSeCKS may be used as a marker for aberrations in fertility and/or nervous system development. The present sequence represents rat SSeCKS cyclin D binding (CY) domain mutated peptide which is linked to a penetratin peptide in the examples of the present invention. The present invention relates to the isolation of a novel rat tumour

Sequence 16

DB 24;

Length 16

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RESULT 34
AAY27544
ID AAY27544
ID AAY27544
AC AAY2
XX MOON
KW MOON
KW WOON
KW VASK
XX PSet
XX PSet
XX AAY2
PN WOO!
YN ADE
XX AAY2
PF 10-1
XX NEW
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PF 10-1
XX NEW
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CCC FOO
  RESULT 35
AAY67939
ID AAY67
XX
AC AAY67
XX
DT 27-MA
XX
DE EPOa-
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Best Local Similarity
Matches 5; Conserv
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides an isolated, mutated Monoamine Oxidase B (MAO B) enzyme having at least one amino acid substitution for wild-type amino acids in a MAO B active site, the wild-type amino acid residues selected from Phe423, Glu427 and Thr428. A plasmid containing the DNA encoding the mutated MAO B and regulatory elements can be used for the recombinant expression of the enzyme. The mutated MAO B enzyme is useful for indirect regulation of cellular neurotransmitters and vasoamines, as the substitutions reduce MAO B's activity and alters its pH profile. The present sequence represents a Pseudomonas P-450terp peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY27544 standard; peptide; 17
EPOa-hSA fusion protein peptide linker
                                                                                                     AAY67939
                                                                                                                                                          AAY67939 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mutant
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5; Conserv
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                                                                                                                                                                                                                                                                                  SSSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lewis DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 1; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme useful for regulation of neurotransmitters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
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                                                    (first entry)
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                                                                                                                                                    peptide; 17
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                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                Score 22; DB zv;
Pred. No. 2.2e+02;
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RESULT 36
AAO17004
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Best Local (
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                                                      Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis; alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthmacirrhosis; dermatitls; psoriasis; inflammatory bowel disease; immunosuppressive; antiinflammatory; antirheumatic; antiarthritic; antiasthmatic; antibacterial; dermatological; antipsoriatic; antidiabetic; ophthalmological; neuroprotective; multiple sclerosidiabetes; uveitis; coeliac disease; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An erythropoietin analog-human serum albumin fusion protein, used e.g. treatment of HIV infection - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erythropoietin analogue human serum albumin fusion protein; infection; EPOa-hSA fusion protein; peptide linker; HIV; cytostatic; antianaemic; anaemia; renal failure; blood loss; cancer; nutraceutical; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein.
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                           Synthetic
                                                                                                                                                                            Linker
                                                                                                                                                                                                       29-MAY-2002
                                                                                                                                                                                                                                  AAO17004;
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                                                                                                                                                                            ť
                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 22; Di
100.0%; Pred. No. 2.:
cive 0; Mismatches
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                                                                                                                                                                            construct alpha-MSH concatamer
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2.2e+02;
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WO200206316-A2

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RESULT 37
AAR55185
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Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concatamer. The sequences are useful for treating an individual suffering from, or at risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatoid arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The present sequence is a linker peptide described in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUL-2000; 2000US-218381P.
18-AUG-2000; 2000US-226382P.
06-OCT-2000; 2000US-238380P.
29-DEC-2000; 2000US-258764P.
14-JUN-2001; 2001US-298317P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 16; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-2002
                                                                                                                                                                                                                                         huTFh antigenic peptide P159-169.
                                                                                                                                                                                                                                                                   25-MAR-2003
19-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JUL-2001; 2001WO-US22263
                                                                                            26-MAY-1994
                                                                                                                                                                        thrombus;
                                                                                                                                                                                                  Human; tissue fa
soluble; huTFh;
                                                                                                                                                                                                                                                                                                            AAR55185
                                                                                                                                                                                                                                                                                                                                      AAR55185 standard; Protein; 18 AA.
(SCRI ) SCRIPPS RES INST. (UYPE-) UNIV PENNSYLVANIA.
                                        16-NOV-1992;
                                                                                                                      WO9411029-A1
                                                                                                                                                                      Human, tissue factor; TF; heavy chain; pre-protein; pre-huTFh; breast; soluble; huTFh; hydrophobic; transmembrane; anchor region; monoclonal; aggregation; factor VII, factor VIIa; coagulation; antibody; MAb; assay; thrombus; detection; cancer; lung; carcinoma; anticoagulant; heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZYCO-) ZYCOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention.
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(first entry)
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                                                                 93WO-US11239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fusion protein comprising alpha-melanocyte mer or its analog, for treating inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen
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2.2e+02;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAR55181-93 represent antigenic peptides derived from human tissue factor (huTF) heavy Chain (huTFh). These are peptide analogues of the huTFh binding site. These peptides may be used to competitively inhibit the binding of huTF to blood coagulation factor VII/VIIa, pref. without forming an activated complex, ie. without initiating coagulation. Active huTFh has the capacity to induce factor VII/VIIa-dependant coagulation. Monoclonal antibodies (MAb) raised against these huTFh fragments, may be used to assay for huTFh, for in vivo thrombus detection and for treating cancers which express TF on the surface, eg. breast and lung carcinoma. These MAb may be used to eliminate the need for large doses of conventional anticoagulants such
                                                                                                                                                                                                                                                                                                                      TF; factor X; factor VIIa; inhibitor; blood clotting;
                                                                                                                                                                                                                                                                                                                                                 Tissue factor
                                                                                                                                                                                                                                                                                                                                                                                                                               AAW19402 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting coagulation during extracorporeal circulation - by admin of monoclonal antibody preventing binding of tissue factor to coagulation factor 7 or 7a
        Disclosure; Page 7; 22pp; English
                                                                                                                                                                        07-JUN-1995;
                                                                                                                                                                                                                           19-DEC-1996.
                                                                                                                                                                                                                                                     WO9640779-A1
                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                        coagulation; human.
                                                                                                                                                                                                                                                                                                                                                                          04-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      AAW19402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 6; 152pp; English.
                                   Rabbit and mouse Tissue Factor-derived inhibiting blood coagulation in humans
                                                                             WPI; 1997-052236/05.
                                                                                                       Arbo
                                                                                                                                                                                               07-JUN-1996;
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NYCOMED IMAGING AS
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                                                                                                   Fischer P,
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                                                                                                                                                                                                                                                                                                                                                peptide Hu#152-169 from human.
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                                                                                                                                                                        95US-0479223
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Pred. No. 2.3e+02;
; Mismatches 0;
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RESULT 39
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Matches 5
                                                   Matches
                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a peptide fragment Hu#152-169 corresponding to residues 152-169 of human tissue factor (TP). The peptide sequence contains a putative Factor X binding site. The peptide is an inhibitor of TF-dependent coagulation in humans, specifically the binding of TF-factor VIIa to factor X. It is useful for treating or preventing blood clotting disorders or associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                        The present invention relates to tissue factor (TF) mediated reperfusion tissue damage in mammal, e.g. human is inhibited by administering to the mammal a TF inhibitor. The invention is used for inhibiting TF mediated reperfusion tissue damage in mammal, e.g. human. The TF inhibitor blocks the formation of the TF:factor VII/VIIa complex thus inhibiting the initiation of the coagulation cascade. The present sequence is human TF
                                                                                                                                                                                                                                                              Use of tissue factor inhibitor to inhibit tissue factor mediated reperfusion tissue damage in mammal, e.g. human -
                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2001048924-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human tissue factor (TF) protein binding site analogue #16.
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                                                                                                                                                                                                                                      Disclosure;
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                                                                                                    Sequence
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                         SSSSG 5
SSSSG
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                                                                                                                                                                                                                                    Page 5; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                        ZOPPO G J.
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                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reperfusion tissue damage; coagulation cascade;
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Pred.
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Pred. No. 2.3e+02;
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RESULT 40

Query Match Best Local Similarity

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DB 19; 2.5e+02;

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                                                                                                                                                                                                        The sequence is an internal peptide from a new protein, designated CC CXX2, which is a component of bromelain. The protein has a molecular CC weight of 22.2 to 25.08 kD (as determined by SDS-PAGE) and an CC isoelectric point of 3.8-4.79. It is obtainable by: (a) dissolving CC bromelain in acetate buffer at pH 5; (b) separating the components of CC bromelain by fast flow high performance liquid chromatography on CC S-Sepharose (RTM), eluting with a linear gradient of 0 to 0.8M Nacl CC in acetate buffer over 300 ml; (c) collecting the fraction corresponding CC to the second sharp peak off the column, and (d) isolating the major CC protein from the fraction collected in (c) by anion chromatography and hydrophobic interaction chromatography.

CC CX2 is able to activate macrophages and natural killer cells and also CC increase interferon-gamma-mediated nitric oxide (NO) production. It is largely responsible for the anticancer activity of bromelain. It can be used for the treatment or prevention of solid cancers (such as covarian, colon, breast or lung cancer, or melanoma), non-solid tumours, CC leukaemia, or virus-induced tumours (such as hepatocellular carcinoma, CC Kaposi's sarcoma, T-cell leukemia or cervical carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-1997;
25-FEB-1997;
25-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated bromelain component protein - used for e.g. treating cancers, immunodeficiency or diseases which respond to increased nitric oxide production, or as a vaccine adjuvant or antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bromelain protein fraction CCX2,
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                                                          tumours, trauma, medical treatment, diabetes and old age), and as a vacc an antiparasitic, antifungal, antiba
                                                                                                                                                                                        Kaposi's marcoma, T-cell Leukemia or cervical carcinoma).

CCX2 can also be used as an immunostimulant (e.g. for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                        immunodeficiencies arising from malnutrition, infection,
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                                                          tment, protein loss, genetic abnormalities, a vaccine adjuvant. It can also be used as antibacterial and antiviral agent.
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Oy 1 SSSG 5 Db 3 SSSG 7 Search completed: December 11, 2003, 09:55:21 Job time : 28.2 secs	Matches	5	5; Conservative	0;	0; Mismatches	0;	0; Indels	0;	0; Gaps	<u>.</u>
Db 3 SSSSG 7 Search completed: December 11, 2003, 09:55:21 Job time : 28.2 secs	8	1 88	111 1886 5		4					
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                                          ; TOPOLOGY: 1i; MOLECULE TYPE: US-08-665-202-2
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US-08-665-202-2
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                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUNDER: CS/000
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                             TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
                                                                                                                                                                       REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                    TYPE: amino STRANDEDNESS:
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COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                  LENGTH: 5 amino acids
TYPE: amino acid
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US-08-297-330-2
US-08-451-240-3
US-08-451-240-2
US-08-461-598-3
US-08-461-598-3
US-08-954-915A-1
US-08-954-915A-1
US-08-954-915A-1
US-08-942-332B-1
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US-09-154-390-3
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Result No.

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Database :

Minimum DB Maximum DB

COMPUTER READABLE FORM:

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US-09-315-574-2
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                                                                                        GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: NO. 651
TITLE OF INVENTION: Tumor A
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-UW-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,914
DEFENSION FORTER 108
                                                                                                                                                                                                           Sequence 2, Application US/09315574 Patent No. 6512097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6054561
GENERAL INFORMATION:
APPLICANT: RING, I
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TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
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ZIP: 94662-8097
                                 STATE:
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                COUNTRY:
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                                               San Francisco
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INTELLECTUAL PROPERTY - R440,
                USA
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Query Match
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Watches 5; Conserve
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                 APPLICATION NUMBER: UIFILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UIFILING DATE:
                                                                                                                              ZIP: 01748

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IF C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 15-UUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-UUN-1996
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APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OPPERMANN, HERMANN
APPLICANT: TIMASHEFF, SERGE N
TITLE OF INVENTION: SERINE RICH PEPTIDE LINKER
                                                                                                                                                                                                                                                                                         CITY:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US FILING DATE: 20-MAY-99
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APPLICATION NUMBER: US 07/662,226
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100.0%; Pred. No. 2.5e+05
Ltive 0; Mismatches 0
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Best Local Similarity
Matches 5; Conserv
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                              TELEFAX: (619) 455-5110 NFORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: CRE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., Johr
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-2416
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,637
FILING DATE: 09-DEC-1992
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  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
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OTHER INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1880 Centi
CITY: Los Angeles
                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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FEATURE:
NAME/KEY:
LOCATION:
US-08-372-887-16
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Best Local Similarity
Whiches 5; Conserve
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                                Query Match
Best Local Similarity 100.
Thes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Applicat Patent No. 5879677 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph. IREGISTRATION NUMBER: 31,67
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                         TELEPHONE:
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                         1 SSSSG 5
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                                                                                                                                                                                                                                                            (619) 455-5110
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                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                             Ph.D., John
                                                                                                                                                                                                                                                                                                     PD-2416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB
Pred. No. 67;
0; Mismatches
                                                                  Score 22;
Pred. No.
                                                    Mismatches
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                                                                              Length 13;
                                                    Indels
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RESULT 7
US-08-372-887-17
; Sequence 17, Application US/08372887

GENERAL INFORMATION:

Gregory J.

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Patent No. 6162902
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIPICATION: 424
PRIOR APPLICATION NUMBER: US 07/987
APPLICATION NUMBER: US 07/987
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., ph.D.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1855-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (619) 455-5110 INFORMATION FOR SEQ ID NO: :
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: METHOD
TITLE OF INVENTION: DAMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                       APPLICANT: MISCHAK, RONALD P.
APPLICANT: LIM, GARRETT A.
APPLICANT: SCARDINA, JAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                          TLE OF INVENTION:
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STATE: California
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                                                                  COUNTRY:
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                                                         94304-1018
                                                                                                          PALO ALTO
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1880 Century Park East, Suite 500
                                                                                                                        755 PAGE MILL
                                                                         USA
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RESULT 9
US-09-510-721-4
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REFERENCE/DOCKET NUMBER: 2190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAC: (415) 494-0792
TELEZAS: (415) 494-0792
TELEZAS: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09510721 Patent No. 6376207
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site LOCATION: 1
OTHER INFORMATION: /labe!
OTHER INFORMATION: /note
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 5; Conserv
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OTHER INFORMATION:
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SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lehnhardt, Sus
REGISTRATION NUMBER:
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COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/510,721
                                                                                               COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                             SCARDINA, JAN M.
TITLE OF INVENTION: ASSAY AND REAGENTS FOR QUANTIFYING HENP NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MISCHAK, RONALD P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SSSSG 5
                                                                                                                                                                                STATE: CA
                                                                                                                                                                                                  CITY: PALO ALTO
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                         GARRETT A
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/note= "Either hydrogen-, lysine-, arginine-lysine-
glycine-arginine-lysine "
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/note= "Bither -hydroxyl, -cysteine(C), -C-lysine(K),
-C-K-valine(V), -C-K-V-leucine(L), -C-K-V-L-arginine(R),
-C-K-V-L-R-R or -C-K-V-L-R-R-histidine(H) "
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PRIOR APPLICATION DATA:

CLASSIFICATION: <Unknown>

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 4:
                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Biosynt)
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                                                                                                                                                                                                                                                                                                                                                                              PPLICANT:
                                                                                                                                                                                                                                                  STREET:
                                                    APPLICATION NUMBER:
                                                                                                                                                                                COUNTRY: UZIP: 02109
                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                       DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /label= X5
/note= "Either -hydroxyl, -cysteine(C), -C-lysine(K),
-C-K-valine(V), -C-K-v-leucine(L), -C-K-v-L-arginine(R),
-C-K-v-L-R-R or -C-K-v-L-R-R-histidine(H) "
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/610,172 FILING DATE: 04-MAR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        8, Application US/08133804
5. 5534254
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/note= "Bither hydrogen-, lysine-, arginine-lysine- or
glycine-arginine-lysine "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 21900-20280.00
                                                                                                                                                                                                                  Massachusetts
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Exchange Place,
                                                                                                                                                                                                 USA
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Houston, L. L.
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Place, 53 State Street
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                                                    US/08/133,804
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Pred. No.
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US-08-461-838-8
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                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION UNBER: 34,637
REFERENCE/DOCKET NUMBER: 2054
TBLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                        TELEFAX: 617-248-7100 INFORMATION FOR SEQ ID NO:
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FEATURE:
NAME/KEY:
LOCATION:
                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Biosyntheritle OF INVENTION: Imaging
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                        STRANDEDNESS:
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                                                             CPOLOGY:
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5. 5753204
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Exchange Place, 53 State Street
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Protein
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; OTHER INFORMATION: US-08-461-838-8
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               US-08-356-786-12; Sequence 12, A
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                                                RESULT 13
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Best Local Similarity
Matches 5; Conserv
Sequence 12, Application US/08356786 Patent No. 5877305
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NAMME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Ring, David
TITLE OF INVENTION: Biosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                             LENGTH: 15 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                     NAME/KEY: Protein
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Exchange Place, 53 State Street
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                                                                                                                                                                100.0%; Score 22; DE 100.0%; Pred. No. 77;
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Pred. No.
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; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-356-786-12
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                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08665202
Patent No. 5977322
COUNTRY: US...
ZIP: 94111-3834
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPATITER: IBM PC COMPATIBLE
TOWNSTITER: TOWNS PC-DOS/MS-DOS
TOWNSTITER: TOWNS PC-DOS/MS-DOS
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Best Local Similarity
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REGISTRATION NUMBER: 27,847
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TTT.EPHONE: (617) 248-7000
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ADDRESSEE: Edmund R. Pitcher, Tes
STREET: Exchange Place, 53 State
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8
FILING DATE: 06-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
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TITLE OF INVENTION: Biosy.
TITLE OF INVENTION: Marke.
NUMBER OF SEQUENCES: 16
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                                                                                                                                                                             NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
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                                                                                                                                                                                                                                  TITLE OF INVENTION:
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         PatentIn Release #1.0, Version #1.30
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Pred. No.
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

13-JUN-1996

US/08/665,202

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Patent No. 6054561
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REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                       TELEPHONE: (510) 601-2585
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 31
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local :
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                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 05:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                           ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 07-JUN-199
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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              STRANDEDNESS:
                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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linear
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Pred. No.
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RESULT 17
US-09-315-574-3
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SEQ ID NO 14
LENGTH: 15
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Patent No. 6337074
GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
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CURRENT FILLING DATE: 199-01-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Medical Research Council TITLE OF INVENTION: ANTI-VIRAL AGENT FILE REFERENCE: P17970C
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
            APPLICATION NUMBER: US/0
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:peptide derived OTHER INFORMATION: from herpes simplex virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                          ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DG/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marks, James D. APPLICANT: Schier, Robert
                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION:
                                                                                                                                                                                                                                                                    STREET: run_ CITY: San Francisco
                                                                                                                                                                                                                                                   COUNTRY:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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5. 6512097
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                                                                                                                                                                                                                                                      USA
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100.0%; Pred. No.
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 0 FILING DATE: 13-JUN-1996

US 08/665,202

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US-09-265-653-19
                                                                                                                                                                                                          US-09-333-213-4
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CURRENT FILING DATE: 1999-03-10
EARLIER APPLICATION NUMBER: US 60/077,482
EARLIER FILING DATE: 1998-03-11
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 19
LENGTH: 17
                                                  Sequence 4, Application US/09333213
Patent No. 6548653
GENERAL INFORMATION:
APPLICANT: Young, Michael
APPLICANT: Weade, Harry
APPLICANT: Krane, Ian
TITLE OF INVENTION: ERYTHROPOIETIN ANALOGY-HUMAN
FILE REFERENCE: 10275/041001
                                                                                                                                                                                                                                                                                                                                                                             Best
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Patent No. 6451570
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/333,213
CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Abell, Creed W.
APPLICANT: Lewis, Duame A.
TITLE OF INVENTION: Mutants of Monoamine Oxidase
FILE REFERENCE: D6048
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Amino acid sequence containing conserved site of OTHER INFORMATION: Pseudomonas P-450terp
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ATTORNEY/AGENT INFORMATION:
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Conservative 0
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Pred. No.
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                                                                           SERUM ALBUMIN FUSION
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Query Match
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; OTHER INFORMATION: Synthetically generated linker sequence US-09-333-213-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-382-689A-8
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PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: GB 97
PRIOR APPLICATION NUMBER: GB 97
PRIOR APPLICATION NUMBER: GB 97
PRIOR FILING DATE: 1997-02-25
PRIOR PRIOR PRIOR DATE: 1997-02-25
PRIOR APPLICATION NUMBER: GB 97
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                                                                                                                                                      Sequence 4, Application US/08942332B Patent No. 6124430
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                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 8
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                                                           GENERAL INFORMATION:
APPLICANT: MISCHAK, RONALD P.
APPLICANT: LIM, GARRETT A.
APPLICANT: SCARDINA, JAN M.
TITLE OF INVENTION: ASSAY AND REAGENTS
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 0623.0760001
CURRENT APPLICATION NUMBER: US/09/382,689A
CURRENT FILING DATE: 1999-08-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified site LOCATION: 17; 19 OTHER INFORMATION: "Amino acid nos. 17 and 19 are unidentified amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 19
TYPE: PRT
ORGANISM: Ananas comosus
FEATURE:
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                                        CORRESPONDENCE ADDRESS:
                           ADDRESSEE:
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PALO ALTO
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              755 PAGE MILL
                                                                                                                                                                                                                                                                                                                    Conservative
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              MORRISON & FOERSTER
5 PAGE MILL ROAD
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100.0%; Pred. No.
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Pred. No.
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97;
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Query Match
Best Local Similarity
Matches 5; Conserve
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US-07-924-030-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 21900-20280.00

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600

TELEPAX: (415) 494-0792

TELEPAX: (415) 494-0792

TELEPAX: 106141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                Sequence 2, Application US/07924030
Patent No. 5403716
GENERAL INFORMATION:
APPLICANT: Kimihiko MATSUZAWA e
                                                                                                                            APPLICANT: Kimihiko MATSUZAWA et al.
TITLE OF INVENTION: METHOD FOR MEASUREMENT OF TISSUE FACTOR IN
TITLE OF INVENTION: HIGH SENSITIVITY AND MEASUREMENT KIT THEREFOR NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 04-MAR-1996
ATTORNEY/AGENT INFORMATION:
  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1-3
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                     STREET: 805 Fifte
CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                      COUNTRY: U.S.A. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 436
                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site
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                                                                                             E: Wenderoth,
805 Fifteenth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Either -cysteine, -cysteine-lysine, -cysteine-lysine-valine-leucine, -cysteine-lysine-valine-leucine, -cysteine-lysine-valine-leucine-arginine, -cysteine-lysine-valine-leucine-arginine-arginine or -cysteine-lysine-valine-leucine-arginine-arginine-histidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= X4
/note= "Either lysine-, arginine-lysine- or
glycine-arginine-lysine- or missing "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= X5
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Street, N.W., #700
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Pred. No. 1.1e+02;
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US-07-924-030-2
                            Query Match
Best Local Similarity
Matches 5; Conserv
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CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/07/924,03
FILING DATE: September 3, 1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA;
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
LOCATION: 1-22
LOENTIFICATION METHOD:
OTHER INFORMATION: /not
OTHER INFORMATION: res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 11
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
                                                                                                    FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                               UNITS:
                                                                                                                                                                                                                                                                                                                                                                                             MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MS-DOS
                                                                                                                                                   DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                            VOLUME:
                                                                                                                                                                                                                                                       AUTHORS:
                                                                                                                                                                                              ISSUE:
                                                                                                                                                                                                                            JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY:
SSSSG 5
                             Conservative
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                            100.0%; Score 22; DB 1;
100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                    residues
                                                                                                                                                                                                                                                                                    /note = "146th to 167th amino acid
residues of human tissue factor"
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US-08-372-887-5
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US-09-466-268B-7
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                                                                                      Sequence 7, Application US/09466268B
Patent No. 6407211
GENERAL INFORMATION:
APPLICANT: Burnett, Jr., John C.
APPLICANT: Lisy, Ondrej
TITLE OF INVENTION: Chimeric natriuretic peptides
FILE REFERENCE: 150.199US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08372887 Patent No. 5879677
                                                                                                                                                                                                                                                                                                                                                                 Matches
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APPLICANT: del Zoppo,
TITLE OF INVENTION: M
TITLE OF INVENTION: D
                                 CURRENT APPLICATION NUMBER: US/09/466,268B
CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION UDATA:
APPLICATION NUMBER: 00 7/987,637
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-2416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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5; Conserv
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1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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1..22
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METHOD FOR INHIBITION OF REPERFUSION
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                                                                                                                                                                                                                                                                                                                                                                                    Score 22; DB 2;
Pred. No. 1.1e+02;
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RESULT 25
US-08-850-910A-1
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                                                                                                 US-08-850-910A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT AFFULCATION NUMBER: US/08/850,5
APPLICATION NUMBER: US/08/850,5
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/477,226
                                                                                                                                                                                                                                                    NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                              TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y MATCH 100.0%;
Local Similarity 100.0%;
Local Similarity 00.0%;
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/299,880 FILING DATE: 19-JAN-1989 APPLICATION NUMBER: 07/206,470 FILING DATE: 14-JUN-1988 APPLICATION NUMBER: 07/200,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 08-FEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 SSSSG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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    1 SSSSG 5
                                                                                                                                                        amino acid
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SCARBOROUGH, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEILHAMER, J.J.
                                                                                                                                                                                                                                       202-822-0168
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                                   Conservative
                                                                                                                            ss: single
linear
                                                                                                              peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRODUCTION OF BRAIN NATRIUETIC PEPTIDE
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                                   100.0%; S
100.0%; F
tive 0;
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Pred. No. 1.3e+02;
D; Mismatches 0;
                                                   Score 22;
Pred. No.
                                     Mismatches
                                                  1.3e+02;
                                                                    DB 2;
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Best Local Similarity
Watches 5; Conserve
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      COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS
SOFTWARE: WOrdperfect
SOFTWARE: WORDPERST
SOFTWARE: WORDPERST
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,525
FILING DATE: 28-FEB-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/0249;
FILING DATE: 16-MAR-1993
PRIOR APPLICATION NUMBER: 851,732
FILING DATE: 16-MAR-1993
PRIOR APPLICATION NUMBER: 851,732
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5547940man D.
REGISTRATION NUMBER: LUD 5265
TELEFONMUNICATION INFORMATION:
TELEPHONE: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/027,108C CURRENT FILING DATE: 1998-02-20 PRIOR APPLICATION NUMBER: 60/63,622 PRIOR FILING DATE: 1997-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: Melanocortin Receptor Ligands and Methods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 27
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Nice, Edouard C., James, R., Simpson, R., APPLICANT: Burgess, A. W., Whitehead, Robert H. TITLE OF INVENTION: METHOD FOR STIMULATING PROLIFERATION TITLE OF INVENTION: OF COLON CELLS USING POMC76-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
TELEPHONE: (21
TELEFAX: (212)
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CITY: New York City
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                NUMBER: US/08/202,525
28-FEB-1994
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                                                           LUD 5265.2
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Pred. No. 1.4e+02;
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US-07-828-450-41
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Best Local Similarity 100.0%;
Matches 5; Conservative 0
                                                               Matches
                                                                                           Query Match
                                                             Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/828,450
FILING DATE: 19920131
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 9437/94133
                                                                                                                                                                                                                                       TELEX: 6714627 CUSH INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PARTICATION UNDER 10/07/000 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TANAKA, SHOUL APPLICANT: MINAMITAKE, YOSH APPLICANT: KITAJIMA, YASUO MAYUMI
                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FURUYA, MAYUMI
APPLICANT: MATSUO, HISAYUKI
TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: lir
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19
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                               1 SSSSG 5
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USA
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                                                               Conservative
                                                                                                                                                         linear
23
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                                                                                                                                                                                                                                                                                                                       9437/94133
                                                                            Score 22; DB 1; Pred. No. 1.6e+02;
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Pred. No. 1.4e+02;
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                                                             Mismatches
                                                                                           Length 32;
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                                                             Indels
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RESULT 29 US-08-297-330-2

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/025,935
PILING DATE: 03-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: WOESSNEY, WALTEN D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 1016.99-US01
TELEPHONE: 612-332-5300
TELEPHONE: 612-332-5300
TELEPHONE: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
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Matches
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Patent No. 5665704
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                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Lowe, David
APPLICANT: Cunningham, Brian
APPLICANT: Oare, David
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, John
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
TITLE OF INVENTION: PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:

"IPE amino acide STRANDEDNESS: 81"
TOPOLOGY:
"OLECULE"
"TOPOLOGY:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wei, Chi-Ming
APPLICANT: Burnett, John C.
TITLE OF INVENTION: Vasonatrin Peptide and Analogs
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: N
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                                                                                                                                                            JMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSSSG 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 22; DB 1;
100.0%; Pred. No. 1.6e+02;
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RESULT 31
US-08-451-240-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/08451240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/362552
APPLICATION UNMBER: 08/362552
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/152994
APPLICATION NUMBER: 08/152994
PRICHES DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
TOTAL TOTA
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICATION NUMBER: US/08/
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362
FILING DATE: 06-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,240
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Burnier, John
TITLE OF INVENTION: RECEPTOR
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lowe, David
APPLICANT: Cunningham, Brian
APPLICANT: Oare, David
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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TOPOLOGY: linear
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TELEPHONE: 415/952-9881
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REGISTRATION NUMBER: 36,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 22; DB 1; 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR SPECIFIC ATRIAL NATRIURETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inch,
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                                          08/362552
                                                                                                                                                                                        US/08/451,240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P0844P1C1
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

08/152994

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Query Match
Best Local Similarity
Watches 5; Conserve
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         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/322,137
FILING DATE: 13-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,431
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
ATTORNEY/ACENT INFORMATION:
NAME: COOPER, IVET P.
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,531
FILING DATE: 05-UN-1995
CLASSIFICATION: 435
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APPLICANT: FOWLKE
APPLICANT: BROACH
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INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P084
TELECOMMUNICATION INFORMATION:
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LENGTH: 32 amino acids
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ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PAUL, Jeremy
APPLICANT: TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415/952-9881
REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLEIN, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOWLKES, Dana M.
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                                                                                                                                                                                                                                                                                                                                                         Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative (
                                   TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                       FILING DATE: 06-Jun-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419877
FILING DATE: 11-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362552
APPLICATION NUMBER: 08/362552
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                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                   REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: POI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                      FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                      FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                               TELEPHONE: 415/62-9881
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                                                                                                                                      NAME: Kubinec, Jeffre REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/470,846A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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5, 5846932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McDowell, Robert 5.
Burnier, John
RUENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES
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linear
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                                                                                          415/225-8228
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                                                                                                                                                        Jeffrey S
                                                                                                                                                                                                           08/152994
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Pred. No. 1.6e+02;
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                                  US-08-461-598-34
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Query Match
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                                                                                                                                                 INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/041,431 FILING DATE: 31-MAR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 01 FILING DATE: 31-JAN-1994 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 1
FILING DATE: 20-SEP-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/322,137
FILING DATE: 13-OCT-1994
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                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                 TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                               TELEFAX: 248633
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                                                                                                                                                                                                                               REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOLWKES=2F
                                                                              STRANDEDNESS:
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419 Seventh Street, N.W.,
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TRUEHEART, Joshua
TRUEHEART, Joshua
VENTION: YEAST CELLS ENGINEERED TO PRODUCE
VENTION: YEAST CELLS ENGINEERED TO PRODUCE
                                                                                                                                                                                 202-737-3528
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 Score 22;
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 DB 2;
Length 32;
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RESULT 35
US-08-954-915A-1
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                                                                                                                                                     Sequence 48, Application US/08954915A Patent No. 6028055
                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                                                       GENERAL INFORMATION:
APPLICANT: Lowe, David
APPLICANT: Schoenfeld, Jill
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/954, FILLING DATE: 21-Oct-1997 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/028854 FILING DATE: 22-Oct-1996
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APPLICANT: Schoenfeld, Jill
                                          TITLE OF INVENTION: Receptor Selective BNP
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 650/225-8228
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                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kubinec, Jeffrey S. REGISTRATION NUMBER: 36,5 REFERENCE/DOCKET NUMBER:
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                           STREET:
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South San Francisco
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100.0%; Pred. No.
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າສະ P1017R1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
                                         URRENT APPLICATION NUMBER: US/08/322,11,
APPLICATION NUMBER: US/08/322,11,
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/309,313
                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
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APPLICATION NUMBER: US/0
FILING DATE: 21-Oct-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PAUL, Jeremy
APPLICANT: TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/028854
FILING DATE: 22-Oct-1996
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P10
TELECOMMUNICATION INFORMATION:
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             APPLICATION NUMBER: US 08 FILING DATE: 20-SEP-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                  STATE: C
COUNTRY:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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BROACH, Jim
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KLEIN, Christine
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US 08/190,328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08942332B Patent No. 6124430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/942,332B
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/610,172
FILING DATE: 04-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                 TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                    NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 2190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
                               SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MISCHAK, RONALD P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 248633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 202-628-51:
TELEPAX: 202-737-3528
STRANDEDNESS: 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLE OF INVENTION:
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                   single
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Pred. No. 1.6e+02;
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Sequence 1, Application US/08942456
Patent NO. 6162902
GENERAL INFORMATION:
APPLICANT: MISCHAK, RONALD P.
APPLICANT: LIM, GARRETT A.
APPLICANT: SCARDINA, JAN M.
TITLE OF INVENTION: ASSAY AND REAC
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US-08-942-456-1
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                                                                             RESULT 40
US-09-510-721-1
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Best Local Similarity
Matches 5; Conserv
                        Sequence 1, Application Patent No. 6376207 GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 21900-20280.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                   ENGTH:
APPLICANT: MISCHAK, RONALD P.
LIM, GARRETT A.
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                                                                                                                                                                                                         Similarity 5; Conserv
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                                                              Application US/09510721
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100.0%; Pred. No. 1.6e+02;
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TOPOLOGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US+09-510-721-1
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Search completed: December 11, 2003, 09:59:52 Job time : 10.4 secs
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                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/610,172
FILING DATE: 04-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REGISTRATION NUMBER: 21900-20280.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/510,721
FILING DATE: 23-Feb-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PETENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ASSAY AND REAGENTS FOR QUANTIFYING HENP NUMBER OF SEQUENCES: 4
                                                                              19 SSSSG
                                                                                                                  1 SSSSG 5
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STATE: CA
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                                                                                                                                                       Conservative
                                                                              23
                                                                                                                                                                       100.0%;
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                                                                                                                                                     Score 22; DB 4;
Pred. No. 1.6e+02;
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                                                                                                                                                                                          Length 32;
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Maximum DB
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                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 2000000000
       Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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Match Length
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1 SSSSG 5
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Listing first 45 summaries
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   10 US-09-144-886-2
11 US-09-572-404B-4158
11 US-09-572-404B-4159
11 US-09-103-067-3
12 US-09-103-067-17
12 US-10-217-387A-13
12 US-10-217-387A-17
10 US-09-144-886-3
10 US-09-187-853-8
11 US-10-012-756-21
11 US-09-887-853-8
12 US-10-077-213-4
13 US-10-077-213-4
14 US-10-077-213-4
15 US-10-077-213-4
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Sequence 2, Appli
Sequence 4158, Ap
Sequence 4159, Ap
Sequence 3, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 3, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 34, Appli
Sequence 4, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 4, Appli
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45	44	43	42	41	40	39	38	37	36	<u>3</u> 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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US-09-864-761-47008	US-09-864-761-37541	US-10-029-386-31992	US-10-106-806-1	US-10-029-386-32430	US-10-125-540-403	US-09-864-761-42449	US-09-764-870-403	US-09-864-761-40941	US-10-029-386-30954	US-10-029-386-32835	US-10-197-954-24	US-10-106-806-6	US-10-029-386-33882	US-09-902-517-49	US-09-309-196-34	US-09-864-761-42463	US-09-752-724-4	US-09-996-069-12	US-09-864-761-34039	US-10-106-806-7	US-09-902-517-1	US-10-029-386-30482	US-10-217-387A-5	_	US-10-029-301-8	US-09-880-748-3145	-217-387	US-09-103-067-16	US-10-119-604C-19
Sequence 47008, A	Sequence 37541, A				Sequence 403, App	4	Sequence 403, App	Sequence 40941, A	Seguence 30954, A	328	Sequence 24, Appl			Seguence 49, Appl	æ	Sequence 42463, A	Sequence 4, Appli			7,	Sequence 1, Appli	30	o o	5	Sequence 8, Appli	31	e 16	16, 2	Sequence 19, Appl

ALIGNMENTS

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RESULT 2
US-09-572-404B-4158
; Sequence 4158, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
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US-09-144-886-2
                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize TITLE OF INVENTION: Botulinum Neurotoxins FILE REFERENCE: 2500.117USO CURRENT APPLICATION NUMBER: US/09/144,886 CURRENT FILING DATE: 1998-08-31 NUMBER OF SEQ ID NOS: 98 SOFTMARE: Patentin Ver. 2.0 SEQ ID NO 2 atentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09144886
Patent NO. US20020153114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                          Matches
APPLICANT: Proteom Ltd
                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: [(Ser)4Gly]
OTHER INFORMATION: linker
                                                                                                                                                                         1 SSSSG
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                                                                                                                                                                                                                          Conservative
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100.0%; Pred. No. 6.:
:ive 0; Mismatches
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RESULT 4
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CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOPTWARE: ProtPatent version 1.0
SEQ ID NO 4158
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Best Local Similarity
Matches 5; Conserv
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CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 4159
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Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
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Best Local S
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SEQ ID NO 3
                                   CURRENT APPLICATION NUMBER: US/09/103,067
CURRENT FILLING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: 08/372,887
EARLIER FILING DATE: 1995-01-13
EARLIER APPLICATION NUMBER: 07/987,637
EARLIER FILLING DATE: 1992-12-09
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                       APPLICANT: del Zoppo, Gregory J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF REPERFUSION DAMAGE
FILE REFERENCE: scr2018s
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                   NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver.
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OTHER INFORMATION: sequence located in
OTHER INFORMATION: in this patent.
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ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
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nes 5; Conserv
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100.0%; Pred. No.
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Sequence 3, Application US/10217387A
Publication No. US20030138420A1

GENERAL INFORMATION:
APPLICANT: Del Zoppo, Gregory J
ITILE OF INVENTION: METHOD FOR INHIBITION OF CEREBRAL TISSI
ITILE OF INVENTION: FACTOR MEDIATED REPERFUSION DAMAGE
FILE REFERENCE: TSR1 327.0 Con.2

CURRENT APPLICATION NUMBER: US/10/217,387A

CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 99/103,067
PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-32
PRIOR FILING DATE: 1995-01-13
PRIOR FILING DATE: 1995-01-13
PRIOR FILING DATE: 1992-12-09
NUMBER OF SCT TO NOCE. 20
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CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: 08/372,887
EARLIER FILING DATE: 1995-01-13
EARLIER APPLICATION NUMBER: 07/987,637
EARLIER APPLICATION NUMBER: 07/987,637
EARLIER FILING DATE: 1992-12-09
NUMBER OF SEQ ID NOS: 20
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 17
LENGTH: 13
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                                                                                NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: del Zoppo, Gregory J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF REPERFUSION DAMAGE
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TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                              ENGTH: 13
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Pred. No. 1.5
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Pred. No. 1.5e+02;
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APPLICANT: Del Zoppo, Gregory J
TITLE OF INVENTION: METHOD FOR INHIBITION OF CEREBRAL TISSUE
TITLE OF INVENTION: FACTOR MEDIATED REPERFUSION DAMAGE
FILE REFERENCE: TSRI 327.0 Ccn. 2
CURRENT APPLICATION NUMBER: US/10/217,387A
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 09/103,067
PRIOR APPLICATION NUMBER: US 09/103,067
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: US 08/372,887
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1995-01-13
PRIOR FILING DATE: 1992-12-09
NUMBER: US 07/987,637
PRIOR FILING DATE: 1992-12-09
NUMBER: DESC ID NOS: 20
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                                                             US-09-144-886-3
                                                                                                                                                                                   APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3 15
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09144886 Patent No. US20020155114A1 GENERAL INFORMATION:
Query Match
Best Local Similarity
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Best Local
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LENGTH: 13
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                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                             OTHER INFORMATION: Description of Artificial Sequence: [(Ser)4Gly]3 OTHER INFORMATION: linker
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                                                                                                                      FEATURE:
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100.0%; Pred. No. 1.5e+02;
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Pred. No.
Score 22;
Pred. No.
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DB 10;
1.8e+02;
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                  Length 15;
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RESULT 10
US-10-012-756-21
US-10-012-756-21; Sequence 21, Application US/10012756; Publication No. US20020164355A1; GENERAL INFORMATION:
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US-09-887-853-8
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Patent No. US20020168375A1
GENERAL INFORMATION:
                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-248-7100 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            LOCATION: 1..15
OTHER INFORMATION: /note= "LINKER SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/133,804
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible operating system: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, V CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887,853 FILING DATE: 21-Jun-2001 CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Huston, James S.
                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Biosynthetic Binding Proteins
                                                                                                                                                                              1 SSSSG 5
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                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 617-248-7477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Exchange Place,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
STREET: Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                   Conservative
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Houston, L. L.
Ring, David B.
                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                   Protein
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0;
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GENERAL INFORMATION:

APPLICANT: ITWIN H. Gelman
APPLICANT: SUBAN G. Jaken
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
FILE REFERENCE: A30558-A-FWC-A 070156.0597
CURRENT APPLICATION NUMBER: US/99/902,432
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: 08/978,277
PRIOR FILING DATE: 1997-11-25
PRIOR FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: 08/655,401
PRIOR APPLICATION NUMBER: 08/655,401
PRIOR APPLICATION NUMBER: 08/655,121
PRIOR APPLICATION NUMBER: 08/635,121
PRIOR APPLICATION NUMBER: 08/635,121
PRIOR APPLICATION NUMBER: 08/635,121
PRIOR APPLICATION NUMBER: 08/635,121
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US-09-902-432-34
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                                                                                                                                                                                                                                                                                                                         Sequence 34, Application US/09902432 Patent No. US20020160002A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 5; Conserv
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/012,756
FILING DATE: 24-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: OMRF161
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
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ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: John B. Harley and Judith A. James
TITLE OF INVENTION: Diagnostics And Therapy Of Epstein-Barr
Virus In Autoimmune Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SSSSG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/160,604 FILING DATE: 30-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/019,053 FILING DATE: 16-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Georgia
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Pred. No. 1.8e+02;
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Sequence 19, Application US/10074956

Publication No. US20020193332A1

GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
FILE REFERENCE: 08191-022001
CURRENT APPLICATION NUMBER: US/10/074,956
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/268,175
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 29
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                                 US-10-074-956-19
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US-10-074-956-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4
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Best Local Similarity
                                                                                                       SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Young, Michael
APPLICANT: Meade, Harry
APPLICANT: Krane, Ian
TITLE OF INVENTION: ERYTHROPOIETIN ANALOGY-HUMAN SERUM ALBUMIN FUSION
FILE REFERENCE: 10275/041001
CURRENT APPLICATION NUMBER: US/10/081,400
CURRENT FILING DATE: 2002-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 35
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PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 4
                                                                    LENGTH: 17
TYPE: PRT
                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetically generated linker sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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ORGANISM: Artificial Sequence
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100.0%; Pred. No. 2e+02;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Length 17;
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Query Match

100.0%; Score 22;

DB 14;

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US-10-077-210-4
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                                                                                                                                    OTHER INFORMATION: Linker sequence US-10-077-210-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-077-213-4
                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/077,210 CURRENT FILING DATE: 2002-06-13 PRIOR APPLICATION NUMBER: 60/318,474 PRIOR FILING DATE: 2001-09-10 NUMBER OF SEQ ID NOS: 4 SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0%; Matches 5; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4
                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Wu, Chung-Hsiun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10077210 Publication No. US20030049801A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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APPLICANT: Wu, Chung-Hsiun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10077213
Publication No. US20030049694A1
                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lin, Rong-Hwa
APPLICANT: Hsu, Pet-Ling
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT PROTEINS IN VIVO AND
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 13062-004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/077,213
CURRENT FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: 60/318,474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lin, Rong-Hwa
APPLICANT: Hsu, Pei-Ling
TITLE OF INVENTION: PRODUCTION OF FUSION PROTEINS AND USE
TITLE OF INVENTION: FOR IDENTIFYING BINDING MOLECULES
FILE REFERENCE: 13062-002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 4
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Linker sequence
                                                                                                                                                                      FEATURE:
                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity hes 5; Conserv
   1 SSSSG 5
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                                                         Similarity
5; Conserv
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                                                                          100.0%; Score 22; DB 15
100.0%; Pred. No. 2e+02;
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Pred. No.
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); Mismatches
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                                                             Mismatches
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                                                                                             DB 15; Length 17;
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RESULT 18
US-10-217-387A-16
; Sequence 16, Application US/10217387A
; Publication No. US20030138420A1
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                                                                                                                                                                      Query Match
Best Local Similarity
Thes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 17
US-09-103-067-16
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APPLICANT: del Zoppo, Gregory J.
APPLICANT: del Zoppo, Gregory J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF REPERFUSION DAMAGE
FILE REFERENCE: scr2018s
CURRENT APPLICATION NUMBER: US/09/103,067
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: 08/372,887
EARLIER FILING DATE: 1995-01-13
EARLIER APPLICATION NUMBER: 07/987,637
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. SEQ ID NO 16
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SEQ ID NO 19
LENGTH: 17
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APPLICANT: Abell, Creed W. APPLICANT: Lewis, Duane A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lewis, Duane A.
TITLE OF INVENTION: Mateants of Monoamine Oxidase
FILE REFERENCE: D6048/D
CURRENT APPLICATION NUMBER: US/10/119,604C
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: US 09/265,653
PRIOR FILING DATE: 1998-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1992-12-09 NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Amino acid sequence of active site OTHER INFORMATION: p-450terp enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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Pred. No.
                                                                                                                                                                                       Score 22; DB 9;
Pred. No. 2.1e+02;
; Mismatches 0;
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APPLICANT: Del Zoppo, Gregory J
ITITLE OF INVENTION: METHOD FOR INHIBITION OF CEREBRAL TISSUE
ITITLE OF INVENTION: METHOD FOR INHIBITION OF CEREBRAL TISSUE
ITITLE OF INVENTION: METHOD FOR INHIBITION OF CEREBRAL TISSUE
ITITLE OF INVENTION METHOD FOR TO INHIBITION OF CEREBRAL TISSUE
ITITLE OF INVENTION INHER: US.10/10/217,387A
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US.09/103,067
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: US.08/372,887
PRIOR FILING DATE: 1995-01-13
PRIOR APPLICATION NUMBER: US.07/987,637
PRIOR APPLICATION NUMBER: US.07/987,637
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RESULT 20

US-10-029-301-8

; Sequence 8, Application US/10029301

; Publication No. US20020188107A1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3145
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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SEQ ID NO 3145
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Best Local
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Best Local
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ruben et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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5; Conserv
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Pred. No. 2.2e+02;
); Mismatches 0;
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TITLE OF INVENTION. Component of Stem Bromelain (as amended)
FILE REFERENCE: 0623.0760002
CURRENT APPLICATION NUMBER: US/10/029,301
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/382,689
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 09/382,689
PRIOR PILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: CGT/GB98/00592
PRIOR APPLICATION NUMBER: GB 9704252.7
PRIOR APPLICATION NUMBER: GB 9704252.7
PRIOR APPLICATION NUMBER: GB 9703850.9
PRIOR APPLICATION NUMBER: GB 9703850.9
PRIOR APPLICATION NUMBER: GB 9703850.7
PRIOR APPLICATION NUMBER: GB 9703827.7
PRIOR FILING DATE: 1997-02-25
PRIOR FILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIAL OF SEQ ID NOS: 11
SOFTWARE: PATENTIAL OF SEQ ID NOS: 11
TYPE: PRT
TYPE: PRT
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Matches
                                                                                                                                                                                                             SEQ ID NO 5
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Human tissue
OTHER INFORMATION: factor binding site polypeptide analog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09103067
Patent No. US20010048924A1
GENERAL INFORMATION:
                                                                                                Matches
                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: del Zoppo, Gregory J.

TITLE OF INVENTION: WETHOD FOR INHIBITION OF REPERFUSION DAMAGE
FILE REFERENCE: SCZC10189
CURRENT APPLICATION NUMBER: US/09/103,067
CURRENT FILING DATE: 1998-06-22
EARLIER PILING DATE: 1998-01-13
EARLIER FILING DATE: 1995-01-13
EARLIER FILING DATE: 1992-12-09
NUMBER OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
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Local Similarity 100.0%; Pred. No. 2.2e+02;
hes 5; Conservative 0; Mismatches 0;
15 SSSSG 19
                                                 1 SSSSG 5
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Peek, Keith
                                                                                                Conservative
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da, Christian
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                                                                                                  Mismatches
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Best Local Similarity
Matches 5; Conserve
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RESULT 24
US-09-902-517-1
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 30482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
                                                                                                                                                                                 Query Match
Best Local :
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TITLE OF INVENTION: METHOD FOR INHIBITION OF CEREBRAL TISSUE
TITLE OF INVENTION: FACTOR MEDIATED REPERFUSION DAMAGE
FILE REFERENCE: TSRI 327.0 Con.2
CURRENT APPLICATION NUMBER: US/10/217,387A
CURRENT FILING DATE: 2002-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SECID NOS: 20 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/103,067 PRIOR FILING DATE: 1998-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 08/372,887 PRIOR FILING DATE: 1995-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 07/987,637
                                                                                                                                                                                                                                                           OTHER INFORMATION: MAP TO ACO13718.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW,
OTHER INFORMATION: EXPRESSED IN FETAL LIVER,
OTHER INFORMATION: EXPRESSED IN FETAL LIVER,
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                            Local Similarity
nes 5; Conserv
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                                                                                SSSSG 22
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100.0%; Pred. No. 2.8e+02;
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100.0%; Pred. No. 2.:
tive 0; Mismatches
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, SIGNAL = 0.62
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Query Match
Best Local Similarity
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US-10-106-806-7
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                                                                                                                                           US-10-106-806-7
                                                                                                                                                                                                            SOFTWARE: FASTSEQ SEQ ID NO 7
                                                                                  Query Match
Best Local Similarity
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Publication No. US20030109430A1
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Publication No. US20030069186A1
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                                                                     Matches
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CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 09/466,268
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Burnett, Jr., John C.
APPLICANT: Lisy, Ondrej
TITLE OF INVENTION: Chimeric natriuretic peptides
FILE REFERENCE: 150.199US2
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SOFTWARE: FastSEQ for
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PRIOR APPLICATION NUMBER: 07/206,470
PRIOR FILING DATE: 1988-06-14
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PRIOR APPLICATION NUMBER: 07/477,226
PRIOR FILING DATE: 1990-02-08
PRIOR APPLICATION NUMBER: 07/299,880
PRIOR APPLICATION NUMBER: 07/299,880
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CURRENT APPLICATION NUMBER: US/09/902,517
CURRENT FILING DATE: 2001-07-09
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PRIOR APPLICATION NUMBER: 08/850,910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN TITLE OF INVENTION: NATRIURETIC PEPTIDE
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                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Unknown
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19 SSSSG
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23
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100.0%; Pred. No.
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Pred. No. 3e+02;
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RESULT 26

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US-09-864-761-34039
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SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 34039
LENGTH: 29
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
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PRIOR APPLICATION NUMBER: US 06/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/774,203
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00664
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R INFORMATION:
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FILING DATE: 2001-01-30
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R INFORMATION:
R INFORMATION:
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    INFORMATION
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EXPRESSED IN BT474,
EST_HUMAN
                          EST_HUMAN
SWISSPROT
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                                                              EXPRESSED
                                                                                                   D IN HEART, SIGNAL = 1.5
D IN BRAIN, SIGNAL = 1.1
D IN ADULT LIVER, SIGNAL =
D IN LUNG, SIGNAL = 8.4
D IN HBL100, SIGNAL = 3
D IN PLACENTA, SIGNAL = 8.9
                                       IN HELA, SIGNAL = 1.8
IN FETAL LIVER, SIGNAL = 20
HIT: AA147887.1, EVALUE 2.00e-10
    HIT: BF338316.1, EVALUE 3.00e-10
                                                                                                                                                                                                                               IN BONE MARROW, SIGNAL
                          AA147887.1,
P36784, EVA
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                          EVALUE 8.30e+00
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RESULT 27
US-09-996-069-12
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                                          RESULT 29
US-09-864-761-42463
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US-09-752-724-4
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US-09-752-724-4
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SEQ ID NO 12
LENGTH: 31
TYPE: PRT
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SEQ ID NO 4
LENGTH: 32
TYPE: PRT
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Best Local
            Sequence 42463, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: KITAKAZ
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Patent No. US20010027181A1
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Best Local Similarity
GENERAL INFORMATION:
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TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKI
TITLE OF INVENTION: AND COMPOSITIONS AND
FILE REFERENCE: M01015/70071
CURRENT APPLICATION NUMBER: US/09/996,069
CURRENT FILING DATE: 2001-11-27
NUMBER OF SEQ ID NOS: 35
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                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR USE IN TREATMENT OR PROPHYLAXIS TITLE OF INVENTION: ISCHEMIC HEART DISEASE FILE REFERENCE: FP/S-38-252US
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/752,724
CURRENT FILING DATE: 2001-01-03
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                           PatentIn version 3.0
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Conservative
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SITIONS AND METHODS
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Pred. No. 3.3e+02;
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Pred. No. 3.
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FOR TREATMENT OF CANCER
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RESULT 30
US-09-309-196-34
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OTHER INFORMATION: EXPRESSED IN BRAIN,
OTHER INFORMATION: EXPRESSED IN PLACEN'
OTHER INFORMATION: EXPRESSED IN BONE MI
OTHER INFORMATION: EXPRESSED IN HELA,
OTHER INFORMATION: EXPRESSED IN PETAL I
OTHER INFORMATION: EXPRESSED IN FETAL,
OTHER INFORMATION: EXPRESSED IN FETAL,
OTHER INFORMATION: EXPRESSED IN HEART,
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Best Local
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR FILING DATE: 2000-08-03
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: US 60/236,359
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Chen, Wensheng
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100.0%; Pred. No. 3.6e+02;
                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                IN BONE MARROW, SIGNAL = 2.7
IN ADULT LIVER, SIGNAL = 2.6
IN HELA, SIGNAL = 4
IN FETAL LIVER, SIGNAL = 4
IN HEART, SIGNAL = 4
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Query Match
Best Local Similarity
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                                                                                          RESULT 31
US-09-902-517-49
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Sequence 49, Application US/09902517
Publication No. US20030109430A1
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Lewicki, John
APPLICANT: Scarborough, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: FOWLKES
APPLICANT: BROACH,
APPLICANT: MANFRED
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                                                                                                                                                                                                                                                                                                                                              TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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TOPOLOGY: linear
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MURPHY, Andrew J.
PAUL, Jeremy
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MANFREDI, John
                                                                                                                                                                                                                     Conservative
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100.0%; Pred. No.
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Scarborough, Ro Porter, Gordon

, Robert don J.

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RESULT 33
US-10-106-806-6
; Sequence 6, Application US/10106806
; Publication No. US20030069186A1
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US-10-029-386-33882
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CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 09/287,892
PRIOR FILLING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: 08/850,910
PRIOR FILLING DATE: 1997-05-05
PRIOR FILLING DATE: 1997-05-05
PRIOR PILLING DATE: 1997-05-08
PRIOR FILLING DATE: 1990-02-08
PRIOR FILLING DATE: 1990-02-08
PRIOR APPLICATION NUMBER: 07/299,880
PRIOR APPLICATION NUMBER: 07/299,880
PRIOR FILLING DATE: 1999-01-19
PRIOR FILLING DATE: 1999-01-19
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Best Local S
Matches 5
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL DAVID K.
APPLICANT: HANZEL DAVID K.
APPLICANT: HANZEL DAVID K.
APPLICANTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TILLE REFERENCE: AEOMICA.Y-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33882
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LENGTH: 32
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Best Local
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                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 50 SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 07/206,470 PRIOR FILING DATE: 1988-06-14
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                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: MAP TO AC007059.1 OTHER INFORMATION: EXPRESSED IN HELA,
                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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ORGANISM: Unknown
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Similarity 100.0%;
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Pred. No. 3.6e+02;
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Pred. No. 3.6e+02;
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APPLICANT: Burnett, Jr., John C.
APPLICANT: Lisy, Ondrej
FILE OF INVENTION: Chimeric natriuretic peptides
FILE REFERENCE: 150.199US2
CURRENT APPLICATION NUMBER: US/10/106,806
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 09/466,268
PRIOR PILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
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US-10-197-954-24
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US-10-029-386-32835
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CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 60/306,019
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/314,123
PRIOR APPLICATION NUMBER: 60/314,123
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 60/363,433
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 149
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LENGTH: 32
TYPE: PRT
Sequence 32835, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, DAVI
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Matches 5; Conservat
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Publication No.
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APPLICANT: Siddiqi, Suhaib
APPLICANT: Little, Daniel
APPLICANT: Little, Daniel
TITLE OF INVENTION: Capture Compounds,
TITLE OF INVENTION: And Methods For An
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Compositions
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Pred. No.
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Pred. No.
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US-09-864-761-40941
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                                                                                                                Sequence 40941, Application Patent No. US20020048763A1 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HANZEL, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.57
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.81
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL =
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL
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TYPE: PRT
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.92
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: SWISSPROT HIT: P15269, EVALUE 8.60e+00
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Pred. No.
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Pred. No. 4.1e+02;
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ADULT LIVER, SIGNAL =
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                    PROBES USEFUL
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RESULT 38 US-09-764-870-403

Sequence 403, Application US/09764870 Patent No. US20020042386A1 GENERAL INFORMATION:

APPLICANT:

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Best Local S
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                                                                             Matches
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SOFTWARE: Annomax Sequence
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PRIOR APPLICATION NUMBER: US 60/236,359
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PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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CURRENT FILING DATE: 2001-05-23
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00661
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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N: EXPRESSED IN LING, SIGNAL = 3.9

N: EXPRESSED IN ADULT LIVER, SIGNAL = 2.6

N: EXPRESSED IN HEART, SIGNAL = 2.6

N: EXPRESSED IN FETAL LIVER, SIGNAL = 4.7

N: EXPRESSED IN BRAIN, SIGNAL = 4.7

N: EXPRESSED IN PLACENTA, SIGNAL = 4.7

N: EXPRESSED IN BOME MARROW, SIGNAL = 4.5

N: EXPRESSED IN HELA, SIGNAL = 5

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4.3e+02;
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Prior application data removed - cc
NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 403
LENGTH: 39
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-870-403
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PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR PILING DATE: 2000-02-04

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-08-03

PRIOR PILING DATE: 2000-18-03

PRIOR PILING DATE: 2000-10-04

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                                               PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
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PRIOR PPLICATION NUMBER: PCT/US01/00662
PRIOR PPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: US01-01-30
PRIOR APPLICATION NUMBER: US01-01-30
PRIOR APPLICATION NUMBER: US07-034,687
PRIOR APPLICATION NUMBER: US07-08,408
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US09/608,408
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-08-30
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CURRENT FILING DATE: 2001-01-17
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CURRENT FILING DATE: 2001-05-23
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
APPLICATION NUMBER: US 09/774,203 FILING DATE: 2001-01-29
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Chen, Wensheng
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US-10-125-540-403
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NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 403
                                                                                                                                                                                                                                                                                                                                                                              Sequence 403, Applic Publication No. US20 GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ14C1
CURRENT APPLICATION NUMBER: US/10/125,540
                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-04-19
                                                                                                                                                          LENGTH: 39
TYPE: PRT
ORGANISM: Homo sapiens
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ON: EXPRESSED IN HEART, SIGNAL = 7.2
ON: EXPRESSED IN BRAIN, SIGNAL = 7.5
ON: EXPRESSED IN PLACENTA, SIGNAL = 8.1
ON: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
ON: EXPRESSED IN ADDLT LIVER, SIGNAL = 2.4
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ALIGNMENTS

C;Species: Streptococcus gordonii C;Date: 10-Mar-1993 #sequence_revision C;Accession: A4.896 R;Jenkinson, H.F.

76K cell surface lipoprotein SarA - Streptococcus gordonii (fragment)

18-Nov-1994 #text_change 15-Oct-1999

A43896

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Query Match
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                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-60 <PAR>
A;Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73644.1; PID:g696907
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                            C;Accession: F81262
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, I.C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: F81262
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A; Residues: 1-55 < JEN's
A; Cross-references: GB: $85398; NID: 9246451; PIDN: AAB21606.1; PID: 9246452
A; Note: sequence extracted from NCBI backbone (NCBIN: 85398, NCBIP: 85399)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Infect. Immun. 60, 1225-1228, 1992
A;Title: Adherence, coaggregation, and hydrophobicity of Streptococcus gordonii associat
A;Reference number: A43896; MUID:92175970; PMID:1339408
A;Contents: Challis
A;Accession: A43896
                                                                                             A;Gene: Cj1656c
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Pred. No. 1.2e+02;
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C; Bron, S; Erouillet, S; Bruschi, C.V.; Caldwell, B; Capuano, V.; Carter, N.M.; Cha, A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Lin, H.; Masuda, S.; Maueelly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Saddaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, A; Minters, P.; Mipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A; Herrick, R.; Yoshikawa, H.; Danchin, A.
A; Reference number: A69580; MUID:98044033; PMID:9384377
A; A; Terpstra, Timeleta, A; Ti
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: G69747
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AB3284
hypothetical protein BMEI0255 [imported]
C;Species: Brucella melitensis
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A;Title: Characterization and nucleotide sequence of a novel gene fixW upstream of the A;Reference number: JQ0311; MUID:90066358; PMID:2555670
A;Accession: JQ0311
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A;Experimental source: strain 168
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C;Species: Rhizobium leguminosarum
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A; Residues: 1-71 < HON>
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100.0%; Pred. No. 1.4e+02;
^ Mismatches 0;
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R.DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letese Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliteners A;Reference number: AD3252; PMID:11756688
A;Accession: AB3284
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A;Experimental source: strain 16M
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A; Residues: 1-79 < KUR>
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C;Species: human herpesvirus 3, varicella-zoster virus
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
C;Accession: E27344
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                                                                                                                                                                            R;Davison, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
A;Title: The complete DNA sequence of varicella-zoster virus
A;Reference number: A27345; MUID:86306657; PMID:3018124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-80 <BRO>
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C; Superfamily: varicella-zoster virus
                                                                           A;Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27932.1; PID:g60038
                                                                                                   A; Molecule type: DNA
A; Residues: 1-81 < DAV >
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Pred. No. 1.6e+02;
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submitted to the EMBL Data Library, November 1995 A; Description: The sequence of C. elegans cosmid R13A1 A; Reference number: Z18569
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T16739
                 hypothetical protein B0391.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T18731 R;Gardner, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein AT4g30740 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
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A; Residues: 1-85 < DUZ >
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A; Residues: 1-91 <STO>
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R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprir
Nature 402, 769-777, 1999
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 submitted to the EMBL
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Best Local S
Matches
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Best Local
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Data Library, November 1996
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                                                     15-Oct-1999 #text_change 15-Oct-1999
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A/Cross-references: GB:AE008917; PIDN:AAL53049.1; PID:g17983909; GSPDB:GN00190 A/Experimental source: strain 16M C/Genetics:
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C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AF3485
C;Accession: AF3485
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, F, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letese Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
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A;Molecule type: DNA
A;Residues: 1-92 <WIL>
A;Cross-references: EMBL:281454; PIDN:CAB03802.1; GSPDB:GN00023; CESP:B0391.10
A;Experimental source: clone B0391
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A; Residues: 1-94 < AAA>
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A; Accession: T46349
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A; Residues: 1-93 < KUR>
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tive 0; Mismatches
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0; Mismatches
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hypothetical protein APE1485 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: E72628
                                                                                                                    RESULT
S69741
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Reference number: A72450; MUID:99310339; PMID:10382966
                                          C;Species: Saccharomyces cerevisiae
C;Date: 22-Aug-1996 #sequence_revision
C;Accession: S69741
                                                                                 hypothetical protein YDR455c - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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A; Residues: 1-100 < KAW>
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C;Accession: 50.
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       August 1995
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i, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
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R, anonymous, The European wature 402, 769-777, 1999
Nature 402, 769-777, 1999
A, Title: Sequence and analysis of chromosome A, Title: Sequence A85001; MUID: 20083488; PN
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A;Reference number: S69555
A;Accession: S69741
A;Molecule type: DNA
A;Moseldues: 1-102 <DIB>
A;Cross-references: EMBL:U33007; NID:g927685; PID:g2194171; GSPDB:GN00004; MIPS:YDR455c
C;Genetics:
                                                                                                                                                                                                                                                                              glycine-rich protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: B83356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Microbiol. 22, 175-191, 1996
A; Title: Organizational characteristics and information content of
A; Reference number: 873076; MUID:97055432; PMID:8899719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Sulfolobus solfataricus
C;Date: 11-Oct-1997 #sequence_revision
C;Accession: 875401
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A;Experimental source: strain P2
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C; Superfamily: Saccharomyces
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A; Status: nucleic ac
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A;Map position: 4R
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A; Residues: 1-107 < STO
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A;Description: color change hormone and local neuromodulator (;Superfamily: adipokinetic hormone (;Superfamily: adipokinetic hormone (;Superfamily: adipokinetic hormone (;Superfamily: adipokinetic hormone) reuropeptide; pyroglutamic acid F;1-25/Domain: signal sequence #status predicted <SIG> F;26-33/Product: red pigment concentrating hormone #status predicted <PEP> F;26-33/Product: red pigment concentrating hormone-precursor-related peptide #status predicted F;36/Modified site: pyrrolidone carboxylic acid (GIn) (in mature form) #status predicted F;36/Modified site: amidated carboxyl end (Trp) (amide in mature form from following gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Immunol. 149, 3927-3936, 1992
A;Title: L chain isotype regulation in horse. I. Characterization of A;Reference number: A46516; MUID:93094587; PMID:1460283
A;Accession: D46516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig lambda chain V region - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
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C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 18-Jun-1999
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A;Title: Molecular cloning of crustacean red pigment concentrating hormone precursor. A;Reference number: JN0761; MUID:93384606; PMID:8373416
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nuclear receptor NHR-15 - Caenorh
C;Species: Caenorhabditis elegans
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A; Residues: 1-110 <LIN>
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C;Date: 26-Aug-1994 #sequence revision 09-Sep-1994 C;Accession: 845909; 849506; $55850 R;Aljinovic, G; Pohl, F.M.; Pohl, T.M. submitted to the Protein Sequence Database, August
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kawarabayasi, Y.; Sawada, M.; Ohfuku, Y.; Funahashi, DNA Res. 5, 55-76, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: The nuclear receptor superfamily has undergone extensive A; Reference number: Z22443; MUID:99148134; PMID:10022975 A; Accession: T43354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change
C;Accession: T43354
                                                                       A;Molecule type: DNA
A;Residues: 1-116 <ALJS
A;Cross-references: EMBL:Z35919; NID:g536281; PID:g536283; MIPS:YBR051w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: PH0880
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 14-Aug-1998
C;Accession: H71076
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                                            R;Aljinovic,
                                                                                                                                                   A;Reference number: S45906
A;Accession: S45909
                                                                                                                                                                                                                                                                                                probable membrane protein YBR051w - yeast (Saccharomyces cerevisiae)
N;Alternate_names: hypothetical protein YBR0504A
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submitted to the EMBL Data Library, October 1994
A;Description: Sequence and analysis of 24 kb on
                                                                A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                     RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA29974.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Complete sequence and gene organization of the A;Reference number: A71000; MUID:98344137; PMID:9679194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                ;Species: Saccharomyces cerevisiae
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llarity 100.0%;
Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus horikoshii
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Pred. No. 2.3e+02;
); Mismatches 0;
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Pred. No.
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chromosome II of Saccharomyces cerevisi

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C;Accession: D90510
C;Accession: D90510
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.;
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redcarrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
submitted to GenBank, April 2001
spinorition: Sulfolobus solfataricus complete genome.
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A; Accession: S49506
A; Molecule type: Name
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C;Superfamily: Saccharomyces probable membrane prote:
C;Keywords: transmembrane protein
F;1-21/Domain: transmembrane #status predicted <TMI>
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A;Title: Sequence and analysis of 24 kb on
A;Reference number: S55846; MUID:95321020;
A;Accession: S55850
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A;Experimental source: strain S288C
R;Aljinovic, G.; Pohl, T.M.
R;Kawarabayasi, Y., Hino, Y.; Horikawa, H.; Y. awa, H.; Takamiya, M.; Masuda, S.; Funahashi, DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerob:
                                                                                 hypothetical protein APE0638 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: A72651
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A; Residues: 1-117 < KUR>
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A; Residues: 1-116 < ALW >
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A; Accession: D90510
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Best Local :
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Best Local
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5; Conserv
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transmembrane #status predicted <TM3>
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100.0%; Pred. No. 2.3e+02;
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Pred. No.
an aerobic hyper-thermophilic Crenarchaeon,
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PMID:7597852
                                         Yamazaki, S.; Haikawa, Y.; Jin-no, K.;
i, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
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A;Accession.
A;Molecule type: DNA
A;Residues: 1-124 <BEV>
A;Residues: 1-124 <BEV>
Control of the control of the
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Aug-1987 #sequence_revision 08-Aug-1987 #text_C;
C;Date: 08-Aug-1987 #sequence_revision 08-Aug-1987 #text_C;
C;Accession: A23063
R;Soma, G.I.; Kitahara, N.; Andoh, T.
Biochem. Biophys. Res. Commun. 124, 164-171, 1984
A;Title: Molecular cloning and characterization of a cDNA A;Reference number: A23063; MUID:85046489; PMID:6208900
A;Accession: A23063
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A;Residues: 1-119 «KAW»
A;Cross-references: DDBJ.AP000060; NID:g5104188; PIDN:BAA79609.1; PID:g5104294
A;Experimental source: strain K1
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A;Accession: A72651
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-119 <SOM>
A;Cresidues: 1-119 <SOM>
A;Cross-references: GB:K02816; NID:g205853; PIDN:AAA41758.1; PID:g205854
C;Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: APE0638
C;Superfamily: Aeropyrum pernix hypothetical protein APE0638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T04505
R;Bevan, M.; Brandt, P.; Dose, S.;
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A; Accession: T04505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F8F16.200 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                             A; Map position:
                                                                                                                                                                                                                                                                                                                                             A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Date: 30-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T04505
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                                                                                                                                                                                                                                                                                                                Genetics:
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les 5; Conserv
                                                                                                                                                             Local
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                                                            1 SSSSG
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Pred. No. 2.3e+02;
0; Mismatches 0;
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Pred. No. 2.3e+02;
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Pred.
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DNA-binding protein p9 - mouse (;Species: Mus musculus (house mouse) C;Date: 30-Jun-1989 #sequence_revision C;Accession: AL8084 R;Ballard, D.W.; Philbrick, W.M.; Bothw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 28
A54670
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A;Description: Barly jasmonate-inducible genes of tobacco cells.
A;Reference number: Z14629
A;Accession: T02225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Nicotiana tabacum (common tobacco)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 18-Jul-2001
C;Accession: T02225
                                                                                                                                                                                                                                                                                                                                                                                         C; Keywords: DNA L
F; 2-127/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:X79805; NID:g619160; PIDN:CAA56200.1; PID:g619161 R;Ge, H.; Roeder, R.G. Cell 78, 513-523; 1994 Cell 78, 513-523; 1994 A;Title: Purification, cloning, and characterization of a human coactiva. A;Reference number: A54669; MUID:94340740; PMID:8062391 A;Accession: A54669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell 78, 525-534, 1994
A;Title: A novel mediator of class II gene transcription with homology to viral immediat A;Reference number: A54670; MUID:94340741; PMID:8062392
A;Accession: A54670...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: A54670;A54669
                                                                                                                    RESULT
A28084
                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:453302
C;Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2
C;Keywords: DNA binding; nucleus; phosphoprotein
F;2-127/Product: RNA polymerase II transcription cofactor p15 #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-127 <GEA>
A;Cross-references: GB:U12979; NID:g531394; PIDN:AAA20980,1; PID:g531395
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A; Residues: 1-127 < KRE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-126 < KOJ>
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Best Local
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                                                                                                                                             29
                                                                                                                                                                                                                                                                                                                                   Local Similarity
D.W.; Philbrick, W.M.; Bothwell, A.L.M
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5; Conserv
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                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                            Score 22; DB 2;
Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                              30-Jun-1989
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                                         #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 31
T01487
                                                                                                                                                                                                                                                                                                                                             hypothetical protein F1707.11 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
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                                                                    A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                  R;Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; O; rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome 1 BAC F1707 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                           A; Gene: ATSP: F1707.11
  A;Map position:
A;Introns: 60/2
                                                                                                                A;Residues:
                                                                                                                  A;Molecule type: DNA
A;Residues: 1-131 <VYS>
                                                                                                                                                                                      A; Accession: T01487
                                                                                                                                                                                                          A;Reference number: Z14334
                                                                                                                                                                                                                                                                                                                               C; Accession: T01487
                                                                                                                                                         A;Status: translated from
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EMBL:AC003671; NID:g2833627; PID:g3176681; GSPDB:GN00059; ATSP:F1707

GB/EMBL/DDBJ

A.; Oji,

o ;

ji, O.; Liu, S.; L J.R.; Federspiel,

. Li.

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C;Accession: H86156
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, A;Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T14P4.4 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_chang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 263, 8450-8457, 1988
A;Title: Identification of a novel 9-kDa polypeptide from nuclear extracts. DNA binding
A;Reference number: A28084; MUID:88228080; PMID:3372536
A;Accession: A28084
                                                                                                                                                                                                                 A;Cross-references:
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-129 <STO>
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A; Residues: 1-127 <BAL>
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Pred. No. 2.5e+02;
Mismatches 0;
                                                                                          Score 22; DB 2;
Pred. No. 2.5e+02;
; Mismatches 0;
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Maiti, R.; Marziali,
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A;Cross-references: GB:M31776; NID:g179514; PIDN:AAA35603.1; R;Sudoh, T.; Maekawa, K.; Kojima, M.; Minamino, N.; Kangawa, Biochem. Biophys. Res. Commun. 159. 1427-1434, 1989 A;Title: Cloning and sequence analysis of cDNA encoding a pre A;Reference number: A30163; MUID:89193743; PMID:2522777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 07-Sep-1990 #sequence_revision 02-Dec-1994 #text_change 08-Dec-2000 C;Accession: A36736; A30163; A34461; B34661; B34661; B34661 R;Seilhamer, J.J.; Arfsten, A.; Miller, J.A.; Lundquist, P.; Scarborough, R.M.; Biochem. Biophys. Res. Commun. 165, 650-658, 1989 A;Title: Human and canine gene homologs of porcine brain natriuretic peptide. A;Reference number: A36736; MUID:90088474; PMID:2597152 A;Accession: A36736
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A;Title: Genomic analysis reveals chromosomal variation in natur A;Reference number: Z20994; MUID:98422450; PMID:9748430
A;Accession: T31324
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                               A; Molecule type: protein
A; Residues: 103-134 (KAM)
A; Residues: 103-134 (KAM)
R; Hino, J.; Tateyama, H.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 167, 693-700, 1990
A; Title: Isolation and identification of human brain natriuretic peptides in cardiac
                                                                                                                                                                                    A,Title: Isolation and sequence determination of human brain A;Reference number: A34143; MUID:90092577; PMID:2136732 A;Accession: A34143
                                                                                                                                                                                                                                                      A;Cross-references: GB:M31776; NID:g179514; PIDN:AAA35603.1; R;Kambayashi, Y.; Nakao, K.; Mukoyama, M.; Saito, Y.; Ogawa, FEBS Lett. 259, 341-345, 1990
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                     A; Reference number: A90161; MUID: 90211249; PMID: 2138890 A; Accession: A34661
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A; Residues: 1-134 < SUD>
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A; Residues: 1-134 <SEI>
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Matches 5
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Alternate names: brain natriuretic factor-32 (BNF-32);
Contains: brain alpha natriuretic peptide; brain gamma
Species: Homo sapiens (man)
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5; Conserv
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Pred. No. 2.6
0; Mismatches
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Pred. No. 2.6e+02;
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K.; Matsuo,
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Y.; Shiono,
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                     A; Experimental source: C; Genetics:
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999
C;Accession: F81457; T02810
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A;Molecule type: protein
A;Residues: 103-134 <HI2>
C;Genetics:
                                                                                                                                                                                    R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Meroc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution A;Reference number: A81455; MUID:99178987; PMID:10077609
                                                                                                                                                                                                                                                                                                                                  probable membrane protein L2759.2 [imported] - Leishmania major (strain Friedlin)
C;Species: Leishmania maior
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A; Residues: 1-134 < NYA>
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submitted to the Protein
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                                              A;Cross-references: GB:AE001274; NID:g3264850; PIDN:AAC24633.1; PID:g2995586; GSPDB:GN00A;Experimental source: strain MHOM/IL/81/Friedlin
                                                                                          A; Molecule type: DNA
A; Residues: 1-138 < PYL>
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A; Introns: 58/3
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A; Cross-references: GDB:127884; OMIM:600295
A; Map position: 1936-1936
A; Introns: 44/3; 130/1
A; Introns: 14/3; 130/1
C; Superfamily: natriuretic peptide A precursor
C; Keywords: brain; diuretic; hormone; natriuretic; osmoregulation
F;1-26/pomain: signal sequence #status predicted <SIG>
F;1-26/pomain: brain gamma natriuretic factor #status experimental
F;27-134/Product: brain alpha natriuretic peptide #status experimental
F;103-134/Product: brain alpha natriuretic peptide #status experimental
F;112-128/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T27B3.70 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
C;Accession: T46114
                                                                                             A, Note: T27B3.70
C, Superfamily: Arabidopsis thaliana hypothetical
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Fartmann, b.,
Sequence I
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Conservative
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                        100.0%; Score 22;
100.0%; Pred. No.
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Pred. No. 2.6e+02;
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    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Sterr, W.; Holland,
                                                                                                                                                                                                                                                                                                                                                                                      January 2000
                        2.6e+02;
                                                   DB 2;
                                                                                                                                                                                                                      clone T27B3
                                                                                             protein T21C14.30
                                              Length 134;
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experimental <ANF>
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    <u>,,</u>
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#text_change 19-May-2000

P.; Lemley, C.; Magness,

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of protein-c

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RESULT 38
H72610
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hypothetical protein APE1058 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: C72705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: F82953
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, F. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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C; Superfamily: Leishmania major hypothetical protein L2759.2
                                                                                                                                                         A; Nolecule type: DNA
A;Residues: 1-140 < KAW>
A;Cross-references: DDBJ:AP000060;
A;Cross-references: DDBJ:AP000060;
                                                                                                                                                                                                                                         A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A;Reference number: A72450; MUID:99310339; PMID:10382966 A;Accession: C72705
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A;Residues: 1-138 <STO>
A;Cross-references: GB:AE004966; GB:AE004091; NID:g9951872; PIDN:AAG08922.1; GSPDB:GN00:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: PA5537
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                                                                                                                                            A; Experimental C; Genetics:
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A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PA5537 [imported] - Pseudomonas aeruginosa (strain PAO1)
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                                                            Query Match
Best Local S
Matches 5
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Best Local :
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Res. 6, 83-101, 1999
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les 5; Conserv
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                                                                            100.0%; Score 22;
100.0%; Pred. No.
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Pred. No.
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s 0;
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K.R.; Kas,
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A.; Larbig,
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K.; Lim,
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J.; K
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If Virus
C;Species: Orf virus
C;Species: Orf virus
C;Species: Orf virus
C;Species: Orf virus
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: D49530
C;Accession: D49530
R;Lyttle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
J. Virol. 68, 84-92, 1994
A;Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus
A;Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus
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B45637
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Moseidues: 1-148 < LYT'>
A;Cross-references: GB:S67522; NID:g456900; PIDN:AAB29223.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:141422,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: Ī-148 <SNE>
A;Experimental source: isolate COL8
A;Experimental source: isolate COL8
A;Note: sequence extracted from NCBI backbone (NCBIN:78806, NCBIP:78808)
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A;Title: Polymorphism of the alleles of the merozoite surface antigens MSA1 and A;Reference number: A45637; MUID:92131063; PMID:1775170
A;Accession: B45637
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C;Date: 20-Aug-1999 #sequence_revision
C;Accession: H72610
                                                                                                                     A;Reference number: A49530;
A;Contents: NZ7
A;Accession: D49530
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 40
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Best Local S
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H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh,
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Pred. No. 2.9
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Pred. No. 2.8e+02;
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h, Y.; Yamazaki,
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Maximum Match 100%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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SARA STRGC
YFX1 RHILE
ULL1 VZUD
IM13 ORYSA
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MIH PENVA
RPCH CARMA
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P15 RAT
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RNBR SHEEP
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p11031 mus musculu
p16860 homo sapien
Q29543 ovis aries
Q91012 gallus gall
P52585 orf virus
Q60154 schizosacch
P87350 axis porcin
P79351 capreolus c
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Q9cqe5
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Q8a521
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RESULT 2
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"Characterization and nucleotide sequence of the fixABC operon in Rhizobium"
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01-APR-1993
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PIR; JQ0311; JQ0311.
Hypothetical protein.
SEQUENCE 71 AA; 7939 M
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PIR; E
                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentities requires a license agreement (See http://www.isb-sib.ch/ar send an email to license@isb-sib.ch).
                                                                                                                                                  Davison A.J., Scott J.E.;
"The complete DNA sequence of varicella-zoster virus.";
J. Gen. Virol. 67:1759-1816(1986).
-i- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1
EHV-1 51, HSV-6 ORF17R, EBV BBLF1, HVS 38, AND VZV 49.
                                                                                                                                                                                                                                                                   Varicella-zoster virus (strain Dumas)
Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Varicellovirus.
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01-MAR-1989
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Mol. Gen. Genet. 218:536-544(1989).
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13, Last sequence update)
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RESULT 5
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Q9XGY5;
16-OCT-2001
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Mitochondrial import inner membrane translocase
(Deafness dystonia protein 1 homolog).
TIMMBA OR TIMBA OR DDP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bauer M.F., Brunner M., Hofmann S.;

"Cloning and mapping of the Tim10/DDP gene family encodin finger proteins involved in mitochondrial carrier import. Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Likely to be involved in the import and inshydrophobic membrane proteins into the mitochondrial membrane (By similarity)
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Ehrhartoideae;
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Eukaryota; Viridiplantae;
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15-SEP-2003
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PF02953; zf-Tim10_DDP; 1.
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al import inner membrane translocase
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Pred. No. 69;
D; Mismatches
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RESULT 6
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bauer M.F., Brunner M., Hofmann S., "Cloning and mapping of the Tim10/DDP gene family encodi finger proteins involved in mitochondrial carrier import Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                       This SWISS-PROT entry 15 Logistope the Swiss Institute of Bioinfo the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                        Penaeus vannamei (Penoeid shrimp) (European white shrimp).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Pena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Mammalia; Eutheria;
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MEDLINE=94332243; PubMed=8055060;
                                                                                                                                                                                                                                                                                              NCBI_TaxID=6689;
                                                                                                                                                                                                  inhibiting
                                                                                                                                                                                                                "Molecular
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by non-profit institutions as long as its content
ified and this statement is not removed. Usage by an
                                                                                                                               FUNCTION: Inhibits Y-organs where molting is secreted. A molting cycle is initiated diminishes or stops (By similarity).
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een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                    SWISS-PROT entry is copyright. It is produ
een the Swiss Institute of Bioinformatics
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PF02953; zf-Tim10_DDP; 1.
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hormone-like neuropeptide from the white shrimp Penaeus
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(See http://www.isb-sib
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Linck B., Klein J.M., Mangerich S., I
"Molecular cloning of crustacean red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
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Eukaryota; Metazoa. Arthuro
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                                                                                         Signal; Pyrrolidone
SIGNAL 1
                                                                                                                                                                                                                                                                               modified and this statement is not
                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                           CHROMATOPHORES
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R 1 10
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concentrating hormone precursor (
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HIS HORMONE ADAPTS THE ANIMAL TO
CONCENTRATION OF THE PIGMENT OF
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Query Match

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Alzawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,
Ala Alzawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,
Ala Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ala Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ala Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ala Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ala Kuehl P., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Ala Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Alake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Ala Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Ala Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Ala Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Alayons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Ala Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Ala Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Alayashizaki Y., Soshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Alayashizaki Y., Soshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AK012037; BAB27988.1; -.
EMBL; AK012327; BAB28164.1; -.
MGD; MGI:1913746; 2700038C09R1k.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AK003282; BAB22687.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection."; Nature 409\!:\!685\!-\!690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K.,
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Mammalia; Eutheria; Rodentia;
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ч. Adachi
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Q63396;
Q1-NOV-1997 (Rel. 35, Crea;
01-NOV-1997 (Rel. 35, Last
28-FEB-2003 (Rel. 41, Last
Activated RNA polymerase I
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01-OCT-1994 (Rel. 35,
01-NOV-1997 (Rel. 35,
Hypothetical 13.4 kDa
YBR051W OR YBR0504A,
                                      MEDIINE=85046489; PubMed=6208900; Soma G.-I., Kitahara N., Andoh T.; Soma G.-I., Kitahara N., Andoh T.; "Molecular cloning and characterization of a cDNA clone for a prote: specifically expressed in embryo as well as in a chemically induced pancreatic B cell tumor of rat."; Biochem. Biophys. Res. Commun. 124:164-171 (1984).

-I-FUNCTION: GENERAL COACTIVATOR THAT FUNCTIONS COOPERATIVELY WITH TARS AND MEDIATES FUNCTIONAL INTERACTIONS BETWEEN UPSTREAM ACTIVATORS AND THE GENERAL TRANSCRIPTIONAL MACHINERY. BINDS SINGLE-STRANDED DNA (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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TRANSMEM 24 44
TRANSMEM 70 90
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                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
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"Sequence and analysis
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S0000255; YBR051W.
S0000255; YBR051W.
POTENTIAL.
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Rodentia;
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100.0%; Pred. No.
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CONTROLLED
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YΒ
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  PROTEIN KINASES THAT TARGET
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TISSUE-Bone marrow, Cervix, and Lung;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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01-NOV-1997 (Rel. 35, Last sequence update)
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Activated RNA polymerase II transcriptional c
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FAC; T02139; -.
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Ra Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Vallalon D.K., Madan A., Rodrigues S., Sanchez A., Rahey J., Helton E., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M., Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Usuminal domain of transcription cofactor PC4 reveals dimeric SDNA binding site.";

Nat. Struct. Biol. 4:900-903(1997).

-i- FUNCTION: GENERAL COACTIVATOR THAT FUNCTIONS COOPERATIVELY WITH TAFS AND MEDIATES FUNCTIONAL INTERACTIONS BETWEEN UPSTREAM ACTIVATORS AND THE GENERAL TRANSCRIPTIONAL MACHINERY. BINDS SINGLE-STRANDED DNA.

-i- SUBCELLULAR LOCATION: Nuclear.
-i- PTM: ACTIVITY OF P15 IS CONTROLLED BY PROTEIN FUNCTION

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EMBL; BC018189; AAH18189.1;
EMBL; BC022339; AAH22339.1;
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MEDLINE-88228080; PubMed=337zb36;
Ballard D.W., Philbrick W.M., Bothwell A.L.M.;
Ballard D.W., Philbrick W.M., Bothwell A.L.M.;
"Identification of a novel 9-kDa polypeptide from nrimary structure, and in
                                                                              DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PC4) (p14) (S
RPO2TC1 OR PC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Activated RNA
                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                PIR; A28084; A28084.
                                                                                                                        DOMAIN
                                                                                                                                                 CHAIN
                                                                                                                                                                                               Pfam; PF02229; PC4; 1.
Transcription; Transcription regulation; Activator; Nuclear protein;
                                                                                                                                                                                                                                                       TRANSFAC; T02138; -
                                                                                                                                                                                                                                                                     HSSP; P53999;
                                                                                                                                                                                                                           IGD; MGI:104811; Rpo2tc1.
nterPro; IPR003173; PC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding properties, primary structure, and in vitro expression. Biol. Chem. 263:8450-8457(1988).
FUNCTION: GENERAL COACTIVATOR THAT FUNCTIONS COOPERATIVELY WITH TARS AND MEDIATES FUNCTIONAL INTERACTIONS BETWEEN UPSTREAM ACTIVATORS AND THE GENERAL TRANSCRIPTIONAL MACHINERY. BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO YEAST SUB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: PROTEOLYSIS IS REQUIRED FOR PS
PTM: ACTIVITY OF P15 IS CONTROLLED
THE REGULATORY DOMAIN. PHOSPHORYLAT
FUNCTION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SINGLE-STRANDED DNA.
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                          Similarity
5; Conserv
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(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
NA polymerase II transcriptional coactivator p15
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                           Conservative
                                                                                                                                                                                      Phosphorylation
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                                                                             TRANSCRIPTIONAL COACTIVATO
SER-RICH.
LYS-RICH.
SER-RICH.
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7425871692FFCOEC CRC64;
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Pred. No.
                                        Score 22;
Pred. No.
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                                                                                                                                   RNA POLYMERASE II
TIONAL COACTIVATOR P15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 DNA-BINDING ACTIVITY.
BY PROTEIN KINASES THAT
TION INACTIVATES COFACTOR
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01-AUG-1990
15-SEP-2003
  "Isolation
peptide in
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange CC,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Bishards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villaln D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                 Blakesiey R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-lenging human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89193743; PubMed=2522777;
Sudoh T., Maekawa K., Kojima M., Minamino N., Kangawa K., Mc
"Cloning and sequence analysis of cDNA encoding a precursor
brain natriuretic peptide.";
Biochem. Biophys. Res. Commun. 159:1427-1434(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANFB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sealhamer J.J., Arfsten A., Miller J.A., Scarborough R.M., Lewicki J.A., Porter J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                 Hino J., Tateyaa H., Minamino "Isolation and identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Pancreas, and Spleen;
MEDLINE=22388257; PubMed=124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide.";
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                                               Inouye
                                                                       Kambayashi
                                                                                                                                                                               Biochem. Biophys.
                                                                                                                                                                                                                                                                                                               SEQUENCE OF 27-58 AND 103-134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                             MEDLINE=90092577; Pub
Kambayashi Y., Nakao
                                                                                                                                                                                                                                                                                 MEDLINE=90211249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                       atrium.";
               Y., Nakao K., Muko
Yoshida N., Imura
and sequence deter
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                                                                                                                                                                                                                                                                                 PubMed=2138890;
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                                                                                                     PubMed=2136732;
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                                                                                                                                                                                  Commun.
                             determination
                                                                               Mukoyama
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                                                     Η.
                                                                                                                                                                                                                                    N., Kangawa K., Matsuo of human brain natriure
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                             of human brain natriuretic
                                                                             Saito Y., Ogawa Y., Shiono
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                                                                                                                                                                                                                                                                                                                                                                                                                    full-length
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Matches 5
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15-JUL-1998
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EMBL; BC025785; AAH25785.1; -.
PIR; A36736; AWHUB.
Genew; HGNC: 7940; NPPB.
                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartiod
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00710; NATPEPTIDES ProDom; PD006651; Br natrius SMART; SM00183; NAT_PEP; 1.
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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SIGNAL
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InterPro; IPR000663; Natr_peptide.
Pfam; PF00212; ANP; 1._____
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SEQUENCE FROM N.A.
                      NCBI_TaxID=9940;
                                                                         Ovis aries
                                                                                                Ribonuclease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibition of renin and aldosterone secretion. It is thought to play a key role in cardiovascular homeostasis. Helps restore the body's salt and water balance. Improves heart function. SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: BRAIN AND ALSO IN ATRIA, BUT AT MUCH LOWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for the treatement of heart failure.
SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHARMACEUTICAL: Available under the for the treatement of heart failure.
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                                                                                                                                                             SHEEP
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                                                                       (Sheep).
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                                                                                               (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
s, brain (EC 3.1.27.-) (BRB).
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    27
103
112
25
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                                                                                                                                                                                                                                                                                                                            A,
                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal;
                                              Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                            14726
                                                                                                                                                                                                                                                                                                                                                    93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphism.
                                                                                                                                                                                                                                                                           ۰,
                                                                                                                                                                                                                                                                                                                                       /FTId=VAR_014581.
M -> L (in dbSNP:5230).
/FTId=VAR_014582.
                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR_014580.
R -> H (in dbSNP:5229).
                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                             GAMMA-BRAIN NATRIURETIC PEPTIDE.
BRAIN NATRIURETIC PEPTIDE (BNP-3
                                                                                                                                                                                                                                                                                     Score 22;
Pred. No. 1
                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                    -> L (in dbSNP:5227).
                                                                                                                                                                                                                                                                                                                            DC884D9408462146 CRC64;
                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                             143 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               name
                                                                                                                                                                                                                                                                                   1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no restrictions
                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nesiritide (Scios). Used
                                                                                                                                                                                                                                                                                                 Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                              (BNP-32).
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                                                Bovoidea;
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TS22CLT 15
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AC Q9101
AC Q9101
DT 01-NC
DT 01-NC
DT 01-NC
DT 02-NC
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _CHICK
TS22_CH
Q91012;
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ACT SITE
DISULFID
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DISULFID
                                      MEDILINE=96437509; PubMed=8840185; Sawada K., Agata K., Eguchi G.; "Characterization of terminally differentiated cell state by "Characterization of terminally differentiated cell state by categorizing cDNA clones derived from chicken lens fibers."; Int. J. Dev. Biol. 40:531-535 (1996).
-i- FUNCTION: MAY SERVE AS A TRANSCRIPTIONAL REPRESSOR.
-i- SUBUNIT: FORMS HOMODIMER OR HETERODIMER. CAN FORM AN HETERODIME WITH TILZ2/THG-1 (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001427; RNaseA. Pfam; PF00074; rnaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S81745; AAB36139.1; -. HSSP; P00656; 2RNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Mol. Evol. 41:850-858(1995).
-- SUBCELLULAR LOCATION: Secreted.
-- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Confalone E., bc...
                                                                                                                                                                                                                                                                                                                                                                                                                                           Regulatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00794; RIBONUCLEASE. ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vento M.T., Furia A.; "Molecular evolution of
                                                                                                                                                                                                                                                                                                                                                         Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00127; RNASE_PANCREATIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96139017; PubMed=8587129;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         CBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHICK
  SWISS-PROT entry is copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00092; RNAse
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(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;

J. Created)
Last sequence update)
Last annotation update)
TSC-22 (TGFB stimulated clone 22 homolog)

                                                                                                                                                                                                                                                                                                                                                      Neognathae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .0%; Score 22; DB 1; .0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₩;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICLEASE; Glycoprotein.
BY SIMILARITY.
O-LINKED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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                                                                                                                                                                                                                                                                                                                                                         Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E3C3F6AFFC3B341A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
    Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 AA
  is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carsana A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                               HETERODIMER
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RESULT 16
VEGH_ORFN7
Query Match
Best Local
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01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=94076465; PubMed=8254780;
Lyttle D.J., Fraser K.M., Fleming
"Homologs of vascular endothelial
poxvirus orf virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the E
the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD007152; TSC-22_Dip_Bun; 1. PROSITE; PS01289; TSC22; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D49740; BAA08574.1; -. HSSP; P80220; 1DIP.
                                                                                 InterPro; IPR002400; GF_cysknot.
InterPro; IPR000072; PD_growth_factor.
Pfam; PP00341; PDGF; 1.
PRINTS; PR00438; GFCYSKNOT.
ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                  modified and this statement
entities requires a license
or send an email to licenses
                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.
-!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
-!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                  J. Virol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vascular
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                                      PROSITE; PS00249; PDGF 1; FALSE NEG.
PROSITE; PS50278; PDGF 2; 1.
Mitogen; Growth factor; Glycoprotein; Signal.
                                                                                                                                                                           EMBL; S67522; AAB29
PIR; D49530; D49530
HSSP; P15692; 2VPF.
                                                                                                                                                                                                                                                                                             the European
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virus (strain NZ7) (OV uses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORFN7
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                                                                                                                                                                                                        S67522; AAB29223.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               996 (Rel. 34, Created)
996 (Rel. 34, Last sequence update)
9001 (Rel. 40, Last annotation update)
endothelial growth factor homolog precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                    68:84-92 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 AA;
                                                                                                                                                                                                                                     email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                 Bioinformatics Institute. There are no rest-
profit institutions as long as its content
this statement is not removed. Usage by an
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                                                                                                                                                                                        D49530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulation; Repressor; Nuclear protein.
77 98 LEUCINE-ZIPPER.
4 AA; 15384 MW; 937FD74E14F2973D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NZ-7).
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                                                                                                                                                                                                                                                   agreement
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Pred. No. 1.2
); Mismatches
             VASCULAR ENDOTHELIAL
                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                               S.B., Mercer A.A., Robinson A.J.; growth factor are encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148
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                                                                                                                                                                                                                                                   (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                              There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.2e+02;
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               GROWTH FACTOR
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RA MEDILINE-21849401; PubMed=11859360;
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gotlins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gotlins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gotlins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seger K., Sharp S.,
RA Rylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Galblert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RI Nature 415:871-880(2002).
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                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the Buropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein SPBC19C7.05.
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28-FEB-2003
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Fungi; Ascomycota; Schizosacch
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ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse_Pc; 1.
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                                                                                                                                                                                                                                                                      use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                          "Secretory ribonuclease genes
Gene 212:259-268(1998).
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98278842; PubMed=9611269; Breukelman H.J., van der Munnik N., Kleineidam
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DOMAIN 5 10
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Cervidae;
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                                                                                                                                                                                PROSITE;
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SIMILARITY: Belongs to the pancreatic ribonuclease family.
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Cervinae; Axis.
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            sukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI TaxID=4932;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
Cervidae, Odocoileinae, Capreolus.
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37, Last sequence update)
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Pred. No. 1.3e+02;
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Sasanuma S.-I., Sasanuma M., Tsuchiya Y
Yamazaki M., Tashiro H., Eki T.,
"Analysis of the nucleotide sequence of
Saccharomyces cerevisiae.",
Nat. Genet. 10:261-268(1959).
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STRAIN=S288c / AB972;
MEDLINE=95400292; PubMed=7670463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                        Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K. Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sec-independent protein translocase TATB OR SCO5150 OR SCP8.13.
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28-FEB-2003
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DOMAIN 93 10
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                                                                                                                                               Nature 417:141-147(2002).

-I- FUNCTION: Required for correct localization of precursor protein bearing signal peptides with the twin arginine conserved motif S/T-R-R-X-F-L-K. This sec-independent pathway is termed TAT for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
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                       (By similarity).
SUBCELLULAR LOCATION: Membrane bound
SIMILARITY: Belongs to the tatB famil
                                                                                               twin-arginine translocation system. This system mainly transports proteins with bound cofactors that require folding prior to expor
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$0001899; YFR003C.
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P03292;
21-JUL-1986
21-JUL-1986
01-APR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL939122; CAC01351.1; -. HAMAP; MF_00237; -; 1. InterPro; IPR003998; TatB.
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                Alestroem P., Akusjaervi G., Pettersson M., Pettersson U., "DNA sequence analysis of the region encoding the terminal and the hypothetical N-gene product of adenovirus type 2.", Biol. Chem. 257:13492-13498(1982).
                                                                                                                                                                                                                                                                                                                                                                 Gingeras T.R., Sciaky D., Gelinas R.E., Bing-Dong Kelly M.M., Bullock P.A., Parsons B.L., O'Neill K. "Nucleotide sequences from the adenovirus-2 genome J. Biol. Chem. 257:13475-13491(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human adenovirus type 2 Viruses; dsDNA viruses,
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21-JUL-1986 (Rel. 01, Last sequence up
01-APR-1990 (Rel. 14, Last annotation
Hypothetical protein C-168.
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TRANSMEM 2
                                                                                    PIR; F92351; A03864.
Hypothetical protein.
SEQUENCE 168 AA; 1
                                                                                                                          EMBL; J01917; -; NOT_ANNOTATED
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                                                                                                                                                                    entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10515;
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Pred. No.
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Neill K.E.,
2 genome.";
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RESULT 23
P25B_HUMAN
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XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Altachul S.F. Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

XX Altachul S.F. Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

XX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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XX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Hopkins R.F., Jordan H., Moore T., Rubin G.M., Hong L.,

XX Hopkins R.F., Jordan H., Moore T., Rubin G.M., Hong L.,

XX Hopkins R.F., Jordan H., Moore T., Rubin G.M., Hong L.,

XX Hopkins R.F., Jordan H., Moore T., Rubin G.M., Hong L.,

XX Hopkins R.F., Jordan H., Moore T., Jordan G.C.,

XX Hopkins R.F., Jordan H., Moore T., Malek J.A., Gunaratne P.H.,

XX Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Hillalon D.K., Muzny D.M., Green E.D., Dickeon M.C.,

XX Hopkins R.F., Jordan J.W., Green E.D., Dickeon M.C.,

XX Hopkins R.F., Jordan R., Schmutz J., Myers R.M.,

XX Hopkins R.F., Jordan R., Schein J.E., Jones S.J.M., Marra M.A.,

XX "Generation and initial analysis of more than 15,000 full-length

XX "Generation and initial analysis of more than 15,000 full-length

XX "Generation and initial analysis of more than 15,000 full-length

XX "Generation and initial analysis of more than 15,000 full-length

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28-FEB-2003
28-FEB-2003
15-SEP-2003
                      009049;
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY072034; AAL62338.1; -.
EMBL; BC038970; AAH38970.1; -.
SEQUENCE 170 AA; 18460 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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 Wang S., Mao Y.;
 Mac Y.;</li
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EMBL; D63362;
HSSP; P05451;
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Y172_
Treponema pallidum.
Bacteria; Spirochaetes;
NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                          CHAIN
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                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003990; Pancreatis Pfam; PF00059; lectin c; 1. PRINTS; PR01504; PNCREATITSAP.
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between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED BACTERIAL PROLIFERATION.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED INTESTINE, MODERATELY IN COLON AND AT AN EXTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUB-Liver, an
MEDLINE-97208868; PubMed-9055810;
Narushima Y., Unno M., Nakagawara
Suzuki Y., Noguchi N., Takasawa S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                     Signal, Lectin;
SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding type III Reg,
Gene 185:159-168(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okamoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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rPro; IPR001304; Lectin_C.
                                                                                                   TREPA
                                                                                                                                                           138
                                                                                                                                                                                1 SSSSG
                                                                                                                                                                                                      Similarity 5; Conserv
                                                                                                                                                           SSSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit institutions as long
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                                           (Rel. 40,
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(Rel. 40,
1 protein T
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27
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                                                                                                   STANDARD;
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174
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                    19307
                                            , Last sequence up, Last annotation TP0172.
                                                                                                                                                                                                                100.0%;
                                                                              Created)
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            Spirochaetales;
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                                                                                                                                                                                                                                                           PANCREATITIS-ASSOCIATED E
C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                     response; Acute phase; Multigene family. POTENTIAL.
                                                                                                                                                                                                     Score 22; DE
Pred. No. 1.5
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                   PRT;
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                                                                    update)
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                                                                                                   175
                                                        update)
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                                                                                                                                                                                                                1.5e+02;
            Spirochaetaceae;
                                                                                                   Ā
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gai T., Yonekura
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                                                                                                                                                                                                                                                                                               FORM)
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                                                                                                                                                                                                       Indels
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                          PROTEIN
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I gamma.";
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RESULT
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            RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cosavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stabbli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bilt C., Fletcher C., Fujita M., Gariboldi M.,
RA Bustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98332770; PubMed=9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayron R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Regulator of G-protein signaling 10 (RGS10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9CQE5; Q9D3L2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE001201; AAC65162.1; -. PIR; A71358; A71358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spirochete.";
Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=Nichols;
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Head, and MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter J.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ypothetical protein; EQUENCE 175 AA; 1
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19544 MW;
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Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteome.
05BB08483DBFA0F4 CRC64;
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RESULT 27

K2C3_BOVIN STANDARD; PRT; 182 AA.

ID — K2C3_BOVIN STANDARD; PRT; 182 AA.

AC P04561;

DT 20-MAR-1987 (Rel. 04, Created)

DT 20-MAR-1987 (Rel. 04, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa; C
Mammalia; Eutheria; C
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=85128114; PubMed=6084625;
JORCANO J.L., Franz J.K., Franke W.W.;
JORCANO J.L., Franz J.K., Eranke bovine
"Amino acid sequence diversity between bovine
polypeptides of the basic (type II) subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50132; RGS; 1.
Signal transduction inhib
DOMAIN 41 156
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ProDom; PD001580; Regl_Gprotein;
SMART; SM00315; RGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AK009686; BAB26440.1; -.
EMBL; AK009283; BAB26193.1; -.
EMBL; AK017214; BAB30688.1; -.
HSSP; P49799; 1AGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a celebrate the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO THEIR INACTIVE GDP-BOUND FORM. ASSOCIATES SPECIFICALLY WITH THE ACTIVATED FORMS OF THE G PROTEIN SUBUNITS G(I)-ALPHA AND G(Z)-ALPHA BUT FAILS TO INTERACT WITH THE STRUCTURALLY AND FUNCTIONALLY DISTINCT G(S)-ALPHA SUBUNIT. ACTIVITY ON G(Z)-ALPHA IS INHIBITED BY PALMITOYLATION OF THE G-PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1915115; Rgs10.
InterPro; IPR000342; Regl_Gprotein.
Pfam; PF00615; RGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                         Differentiation
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keratin, type II cytoskeletal 60 kDa, component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse
This SWISS-PROT entry is copyright.
                                               -i- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIPID
                                                                         ferentiation 28:155-163(1984).
SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE
MISCELLANGOUS: THERE ARE TWO TYPES OF CYTOSKELETAL
MICROFIERILLAR KERATIN, I (ACIDIC) AND II (NEUTRAL
(40-55 AND 56-70 KILODALTONS, RESPECTIVELY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ຫ
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21151 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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A -> E (IN REF. 1; BAB306.
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Pred. No. 1.6
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9897860505962286 CRC64;
  It is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.6e+02;
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produced through
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                                                                                                                                                                                                                                               epidermal cytokeratin as determined from cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                          TO AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovoidea;
                                                                                                                                                                   KERATINS
                                                                                                             BASIC)
     a collaboration
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K2CA_BOVIN
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                 NON TER
                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jorcano J.L., Franz J.K., Franke W.W.; "Amino acid sequence diversity between bovine epidermal cytokeratin polypeptides of the basic (type II) subfamily as determined from cD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=85128114; PubMed=6084625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Keratin, type II cytoskeletal 68 kDa, component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin.
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                                                                                           PROSITE;
                                                                                                                                  PIR; A02949; KRBOZA.
InterPro; IPR001664; IF.
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SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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COIL 2.
STUTTER.
; C263102147632F66 CRC64;
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND II (NEUTRAL
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RESULT 29
ATKC_BACTN
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ATKC BACTN

C Q8A521;
C Q8A521;
T 15-SEP-2003 (Rel. 42, Created)
T 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Potassium-transporting ATPase C chain (EC 3.6.3.12) (Potassium-transporting ATPase C chain) (ATP phosphohydrolase [pc transporting] C chain) (Potassium binding and transloc;
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STRAIN=VPI-5482 / ATCC 29148;
MEDLINE=22550858; PubMed=12663928;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
                                                                                                                                HAMAP; MF_00276; -;
Hydrolase; Transport
                                                                                                                                                         EMBL; AE016936; AA077530.1; -.
                                                                                                                                                                                 or send an
                                                                                                                                                                                                                   the European Bioinformatics Institute. Thuse by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                            Science 299:2074-2076(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=818;
                                                                                                                                                                                entities requires a license agreement (S
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                        modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                            TRANSMEM
                                                                                                           inner membrane;
                                                                                                                                                                                                                                                                                                                            potassium transport (or KDP) system, which catalyzes the hydrolysis of ATP coupled with the exchange of hydrogen and potassium ions. The C subunit may be involved in assembly of t KDP complex (By similarity).

CATALYTIC ACTIVITY: ATP + H(2)O + K(+) (Out) = ADP + phosphate
                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the kdpC family.
                                                                                                                                                                                                                                                                                                        K(+)(In).
SUBCELLULAR LOCATION: Membrane-associated.
                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: One of the components of the high-affinity ATP-driven
                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through
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79
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                                                                                                                                                                                                                                             the Swiss Institute
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aceae; Bacteroides.
                                                                                                                                Transport; Potassium transport;
                                                                                              189 AA;
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H2 SUBDOMAIN.
V2 SUBDOMAIN.
E2 SUBDOMAIN.
                                             Score 22; DE Pred. No. 1.6); Mismatches
                                                                                                         Potential
                                                                                                                                                                                                                                            of Bioinformatics
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Pred. No. 1.6e+02
; Mismatches 0
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                                                         1.6e+02;
                                                                       DB
                                                                                                                                Transmembrane
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01-NOV-1997
01-NOV-1997
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                                SNXA HUI
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J. Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            related in sequence to the cystatin inhibitors.";
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PIR; 146051;
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                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                            Phosphorylation; SIGNAL 1
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MEDLINE=95113864; PubMed=7814406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                  PTM: MULTIPLY PHOSPHORYLATED AT SERINE RESIDUES IN SER-X-GLU/SER(P) SEQUENCES, A RECOGNITION MOTIF FOR PHOSPHORYLATION SECRETORY PATHWAY PROTEIN KINASE.
SIMILARITY: SOME, TO CATHELICIDIN AND CYSTATINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       FIGURE CHEM. 270:10359-10359(1995).

FUNCTION: Could coordinate an aspect of bone turnover.

SUBCELLULAR LOCATION: Secreted.

TISSUE SPECIFICITY: IN LIVER AND BONE BUT NOT IN HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                 KIDNEY,
                                            HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOVIN
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                                                                                                                                                                                                                                                                           U03872; AAA63582.1;
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L. Chem. 270:10359-10359(1995).
                                                                                                                                                                                                                                                                                                s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphoprotein
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(Rel. 41, Last annotation
)sphoprotein 24 precursor (
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BY SIMILAI
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                                                                                                                                                      Score 22; DB 1;
Pred. No. 1.7e+02;
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cora; Bovoidea;
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CYPM_HU
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Matches 5
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P30405;
                                                 Bergsma D.J., Eder C., Gross M., Kersten H., Sylvester Appelbaum E., Cusimano D., Livi G.P., McLauglin M.M., K Porter T.G., Silverman C., Dunnington D., Hand A., Pric Bossard M.J., Brandt M., Levy M.A.; "The cyclophilin multigene family of peptidyl-prolyl is Characterization of three separate human isoforms."; J. Biol. Chem. 266:23204-23214(1991).
                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin F).
PPIF OR CYP3.
                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transport; Protein transport.
DOMAIN 10 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF121860; AAD27833.1; -. Genew; HGNC:14974; SNX10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             trafficking (By similarity).
-!- SIMILARITY: BELONGS TO THE SORTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21378165; PubMed=11485546; Teasdale R.D., Loci D., Houghton F., I harge family of endosome-localized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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            SEQUENCE FROM TISSUE=Ovary;
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                               MEDLINE=92078192; PubMed=1744118;
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PS50195; PX; 1.
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Primates;
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Pred. No.
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d proteins related to
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RA Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Schapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rosards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Warra M.A.;
"Generation and initial analysis of more than 15,000 full-length
ruman and mouse cDNA sequences."
"Generations isomerization of proteins. It catalyzes
cthe cis-trans isomerization of proline imidic peptide bonds in
CC oliopeptides
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Matches 5
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Q11071;
Q1-NOV-1997
Q1-NOV-1997
28-FEB-2003
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                  Hypothetical B0416.3.
                                                                                                                                           CAEEL
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPRO02130; CSA_PPIAse.
Pfam; PF00160; pro isomerrase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA PPIASE 1; 1.
PROSITE; PS500772; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M80254; AAA58434.1; -.
EMBL; BC005020; AAH05020.1; -.
PIR; A41581; A41581; A41581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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 Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                              Cyclosporin; Isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC: 9259; PPIF.
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                                                                                                                                                                                                                                                                                                                                                                                            Transit peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Mitochondrial matrix. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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5; Conserv
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                               (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
L protein B0416.3 in chromosome X.
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                                                                                                                                                                                                                                                                                                   Score 22; DB 1;
Pred. No. 1.8e+02;
                                                                                                                          PRT;
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                                                                                                                          210 AA
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RESULT 34
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                                                                                                                                           linked to abparage... 1 1:27-34 (1986).

Glycoconj. J. 3:27-34 (1986).

-!- CATALYTIC ACTIVITY: Broad specificity for cleavage of proteins.

hur strong preference for Z-Arg-Arg-|-NHMec amongst small molecular strong preference for Z-Arg-Arg-|-NHMec among
                                                                                                                                                                                                                                                                                      van Kuik J.A., Hoffmann R.A., Mutsaers J.H.G.M., van Halbeek I Kamerling J.P., Vliegenthart J.F.G.;
"A 500-MHz 1H-NMR strudy on the N-linked carbohydrate chain of bromelain. 1H-NMR structural-reporter-groups of fucose alpha() linked to asparagine-bound N-acetylglucosamine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P14518;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Bromelain, stem (EC 3.4.22.32)
           SUBSTRATES.

-!- MISCELLANEOUS: THE GEOMETRY & THE REACTIVITY OF THE CATALYTIC SITE ARE DIFFERENT FROM THOSE OF OTHER CYSTEINE PROTEINASES.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ritonja A., R
Barrett A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Commelinidae incertae sedis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WormPep; B0416.3; CE02433.

Hypothetical protein; Transmembrane.
TRANSMEM 61 81
TRANSMEM 85 105
TRANSMEM 115 135
TRANSMEM 115 135
TRANSMEM 171 191
POTENTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding of cystatin."; FEBS Lett. 247:419-424(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bromeliaceae; Ananas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ananas comosus (Pineapple)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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ARE DIFFERENT FROM 'SIMILARITY: BELONGS; S03964; S03964.
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5; Conserv
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POTENTIAL.
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DFAC15D9933CB5FE CRC64;
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Pred. No. 1.8e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rawlings N.D.,
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                                                                                                                                                                                                                                                                                                                                    fucose alpha(1-3)-
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MEROPS; C01.005; -. GlycoSuiteDB; P14518; HSSP; P14080;

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LB29
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WEDLINE-21016720; Pubmed=11130713;

XX MEDLINE-21016720; Pubmed=11130713;

X3 Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

X4 Salanoubat M., Lemcke K., Rieger M., Mache R., Puigdomenech P.,

X4 A Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

X5 A Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

X6 A Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

X7 A Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

X8 A Mincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

X8 A Chaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,

X8 A Wirmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,

X8 Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

X8 A Wezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

X8 A Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

X8 A Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

X8 A Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati D.,

X8 Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,

X9 Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

X9 Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

X9 Reichelt J., Scharfe M., Berger-Llauro C., Purnelle B., Masuy D.,

X9 Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,

X9 Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,

X9 Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
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Best Local S
Matches 5
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Q9M2J7;
15-SEP-2003
15-SEP-2003
15-SEP-2003
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
16-SEP-2003 (Rel. 42, Created)
17-SEP-2003 (Rel. 42, Created)
18-SEP-2003 (Rel. 42, Created)
19-SEP-2003 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22063719; PubMed=12068116;
Shuai B., Reynaga-Pena C.G., Sprin
"The LATERAL ORGAN BOUNDARIES gene
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene family.";
Plant Physiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
STRAIN=cv. Columbia;
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e family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _TaxID=3702;
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S gene defines
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIFICITY
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            Mewes H.-W.,
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RESULT 36
RB3D_HUMAN
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                                            RAPARCO REPORTED TO THE REPORT OF THE REPORT
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Creasy T.H., Haas B., Malti R., Wu D., Peterson J., Van Aken S.,
Pai G., Militecher J., Sellers P., Gill J.E., Felbblyum T.V.,
Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter
Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.
Sasamoto S., Kimura T., Idesawa K., Kasashima K., Kishida Y.,
Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
Watanabe A., Yamada M., Yasuda M., Tabata S.;
"Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana.";
TISSUE=Cvary;
TISSUE=Cvary;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.
Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999
15-JUL-1999
15-SEP-2003
Ras-related
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095716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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-!- TISSUE SPECIFICITY: Expressed in r
-!- SIMILARITY: Contains 1 LOB domain.
                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Hematopoietic;
MEDLINE=99147844; PubMed=10023084;
Mishio H., Suda T., Sawada K.-I., Miyamoto T., Koike T., Yamaguch
"Molecular cloning of cDNA encoding human Rab3D whose expression
upregulated with myeloid differentiation.";
Biochim. Biophys. Acta 1444:283-290(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR;
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EMBL; AL137081; CAB68157.1;
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PROSITE; PS50891; LOB; 1.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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(Rel. 38, Last sequence update)
(Rel. 42, Last annotation updat
protein Rab-3D.
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Primates;
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, OAA96378B50B8B1F CRC64;
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Pred. No. 1.9e+02
; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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, Shea T.P.,
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RESULT
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     BARRAR
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

1. FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN REGULATED C. EXCLYPTOSIG (BY SITILABITY)
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 5
                                                                          TREPA
Y733 TREPA
O83715;
16-OCT-2001
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MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0003928; F:RAB small monomeric GT
GO; GO:0007516; P:hemocyte development;
InterPro; IPR003579; GTPase Rab.
InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR001806; Small GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
     Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND
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                           16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prenylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exocytosis;
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INDUCTION: ACTIVATED IN MYELOID DIFFERENTIATION.
SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXOCYTOSIS (BY SIMILARITY).
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN
BLOOD. CONSTITUTIVELY EXPRESSED AT LOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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5; Conserv
                                                                                                                                                                                                                                                                                                  SSSSG
                                                                                                                                                                                                                                                                 SSSSG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
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217
219
219
                     (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
(Rel. 40, Last a protein TP0733.
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                                                                                                                                   STANDARD;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
METHYLATION (BY SIMILARITY).
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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3. 1.9e+02;
0;
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3., Carninci P., Prange C.,
3., Abramson R.D., Mullahy S.,
Abramson R.D., Mullahy S.
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W LEVELS IN ALL
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 219;
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                           P20934;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
EVIZA protein precursor (Ecotropic viral integration EVIZA OR EVI-2A OR EVI-2.
                                                      Buchberg A.M., Bedigian H.G., Jenkins N.A., Copeland N.G.;
Buchberg A.M., Bedigian H.G., Jenkins N.A., Copeland N.G.;

"Evi-2, a common integration site involved in murine myeloid
leukemogenesis.";

Mol. Cell. Biol. 10:4658-4666(1990).

-I- FUNCTION: MAY COMPLEX WITH ITSELF OR/AND OTHER PROTEINS WITHIN THE
MEMBRANE, TO FUNCTION AS PART OF A CELL-SURFACE RECEPTOR.

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- DISEASE: EXPRESSION OF THIS GENE IS ALTERED BY VIRAL INTEGRATION
AND THIS ALTERED EXPRESSION MAY PREDISPOSE CELLS TO MYELOID
                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                             -
                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Brain;
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Petterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Spiro
NCBI_TaxID=160;
                                                                                                                                                                                                                                                       NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                           EV2A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome. SEQUENCE 219 AA; 23327 MW; E52AD7CB975E9ADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                            MEDLINE=90355981;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Treponema pallidum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98332770; PubMed=9665876;
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                            SIMILARITY: HIGH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B71
SWISS-PROT entry
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371288; B71288.
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TISSUE-Peripheral blood;

Velten F.W., Rogel-Gaillard C., Renard C., Pontarotti P.

Tazi-Ahnini R., Vaiman M., Chardon P.;

Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

Submitted (JUN-1997) to the EMBL/GenBank/DDBJ CORNEODESMO-!- SUBCELLULAR LOCATION: SECRETED; FOUND IN CORNEODESMO-!- SUBCELLULAR STRUCTURES THAT ARE INVOLVED IN DESQUA
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                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long. The second and this statement is not removed. Usage by and modified and this statement is not removed.
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P:cell proliferation; NAS
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Shuai B., Reynaga-Pena C.G., Sprin
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BOUNDARIES gene defines a novel, plant-specific
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Sheet P., Cordes M., Abu-Threideh J.,
J., Graves T., Harmon G., Edwards J.,
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RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
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RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C.,
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RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McComble W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:769-777(1999).
CC -!- SIMILARITY: Contains 1 LOB domain.
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Q8ty47 lotus corni
Q8t2b4 dictyosteli
Q8q1e8 mamestra co
Q9c716 arabidopsis
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Q87072 pseudorabie
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NML; Y1580 NMTER ONFLICT ON TER EQUENCE EQUENCE Y Match Local Sim hes 5;	[2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUB-Kidney; MEDLINE-96312514; PubMed=8700860; Brown D.D., Wang Z., Furlow J.D., Remo B.F., Pinder A., "The thyroid hormone-induced tail laevis metamorphosis."; Droc. Natl. Acad. Sci. U.S.A. 93:	Xenopodinae; Xenopus. NCBI_TAXID=8355; [1] SEQUENCE FROM N.A. TISSUE=Kidney; Spindler B., Mastroberardino L., Verrey F.; "Effect of aldosterone on proto-oncogenes in Xenopus cells."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ database	157384; 157384; 1-JUN-1998 1-JUN-1998 1-OCT-2002 1-OCT-2002 008-related concrust led ukaryota; l
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Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

Parkhill J., Wren B.W., Mungall K., Feltwell T., Holroyd S.,

A Dayles K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

A Whitehead S., Barrell B.G.;

"The genome sequence of the food-borne pathogen Campylobacter jejun

"Treveals hypervariable sequences.";

Nature 403:655-668(2000).

REMBL, AL139079; CAB73644.1; -.

RHPDOTHETICAL protein; Complete proteome.

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Calcium channel alpha 13 subunit (Fragment).
CA-ALPHA-1T OR CAALPHAIT OR CG4222 OR CG15899.
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Hypothetical protein Cj1656c.
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Bukaryota; Metazoa; Arthropoda; Haraboda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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Seki M., Iida K., Satou M., Sakurai T., Akiyama F.
Nakajima M., Enju A., Kamiya A., Narusaka M., Cai
Hayashizaki Y., Shinozaki K.;
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length cDNA.";
"Arabidopsis thaliana full-length cDNA.";
"Arabidopsis thaliana full-length cDNA.";
"Bumitred (NOV-2002) to the EMBL/GenBank/DDBJ dat
EMBL, AKI18607; BAC43206.1; -.
Hypothetical protein.
SEQUENCE 61 AA; 6632 MW; 891504108E726D75 CR/
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Q8GWV7;
01-MAR-2003
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Rhizobiaceae;
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Rhizobium leguminosarum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conditioned medium factor (CMF).
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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Bacteria; Proteobacteria;
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Pred. No. 2.2e+02
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MEDLINE=22247741; Pubmed=12271122;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
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                                                                                     Li Q., Donly C., Li L., Wil
Submitted (JAN-2002) to the
EMEL; U59461; AAM09194.1;
DNA-binding.
SEQUENCE 76 AA; 9034 MW;
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Q8T2B4;
01-JUN-2002
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SETOBO
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Li S., Erlandson M., Moody D., Gillott C.;
"A physical map of the Mamestra configurata nuc
genome and sequence analysis of the polyhedrin
J. Gen. Virol. 78:265-271(1997).
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01-UIN-2002 (TrEMBLrel. 21, Lat
01-CCT-2002 (TrEMBLrel. 22, Lat
Basic DNA-binding protein P6.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical 6.8 kDa protein.
Dictyostelium discoideum (Slime mold)
Eukaryota; Mycetozoa; Dictyosteliida;
                                                                                                                                                                                                                                                                   MEDLINE=21884635; PubMed=11886270;
Li Q., Donly C., Li L., Willis L.G., Theilm
"Sequence and Organization of the Mamestra
Nucleopolyhedrovirus Genome.";
Virology 294:106-121(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mamestra configurata nucleopolyhedrovirus.
Viruses, dsDNA viruses, no RNA stage, Bacu
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  Score 22; DB Pred. No. 2.6 ; Mismatches
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mestra configurata
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
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RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Kim C.J., Jed A.D., Lansen N.F., Hughes B., Huizar L.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzerg S.L., Schwattz J.R., Shinn P., Southwick A.M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (Tremblrel. 17, Last annotation update)
 SEQUENCE FROM N.A. MEDLINE=22080411; Li L., Donly C., L
                                                                              Mamestra configurata nucleopolyhedrovirus Viruses; dsDNA viruses, no RNA stage; Bacu Nucleopolyhedrovirus.
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01-MAR-2003
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01-OCT-2002
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EMBL; AC074025; AAG51155.1;
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MEDLINE=21016719; PubMed=11130712;
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                                                              NCBI_TaxID=204440;
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PubMed=12083822;
Li Q., Willis L.G.,
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22, Last sequence update)
23, Last annotation updat
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Q8VAY2;
01-MAR-2002
01-MAR-2002
01-JUN-2002
                        STRAIN=Taiwan;

Lo C.-F., Kou G.-H.;

Lo C.-F., Kou G.-H.;

Lo C.-F., Kou G.-H.;

Lo C.-F., Kou G.-H.;

Submitted (OCT-2001) to the

EMBL; AF332093; AAL33240.1;

EMBL; AF440570; AAL89160.1;
                                                                                                                                                                                                           Lo C.F., Kou G.H.; "Identification of a nucleocapsid protein (VP35) gene of shrimp spot syndrome virus and characterization of the motif important targeting VP35 to the nuclei of transfected insect cells."; Virology 293:44-53(2002).
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Virology 277:100-110(2000).
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                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN=16M / ATCC 23456 / Biotype 1;

MEDLINE=20020109; PubMed=11756688;

MEDLINE=20020109; PubMed=11756688;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Rez Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson Haselkorn R., Kyrpides N., Overbeek R.;

"The genome sequence of the facultative intracellular path Brucella melitensis.";

Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein BMEI0255.
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EMBL; U27486; AAB26948.1; -.
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STRAIN-TNL;
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Hypothetical protein; Complete proteome.
SEQUENCE 79 AA; 9255 MW; 107F207BE17CA1D7 CRC64;
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Yamasaki
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Stx2 converting bacteriophage I.
Viruses; dsDNA viruses, no RNA s
Lambda-like viruses.
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                     Waterston R.;
"Direct Submission.";
Submitted (AUG-2001) to t
EMBL; U40798; AAA81475.1;
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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                                                                                                                                                                     "The sequence of C. Submitted (NOV-1995)
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01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                     the RIKEN Genome Exploration Research Group Phase I & "Analysis of the mouse transcriptome based on function 60,770 full-length CDNAs.";
Nature 420:553-573(2002).

EMBL; AK080491; BAC37932.1; -.

SEQUENCE 85 AA; 9426 MW; 449DC44B917C96B2 CRC64;
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                                                                       MEDLINE=96357035; PubMed=8764019; Pallister J., Wright P.J., Sheppard M.; Raingle gene encoding the fiber is restricted in the fowl adenoviruses."; Virol. 70:5115-5122(1996).
EMBL; U40588; AAC55305.1; SEQUENCE 86 AA; 9456 MW; 32FD3DC6D8:
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STRAIN-C57BL/6J; TISSUE=Cerebellum;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Viruses; dsDNA viruses,
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Rodentia;
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Q9DUC3;
01-MAR-2001
                                                                                                                                                                                                                               Genome Biol.
                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                       "Full-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
EMBL; AY088610; AAM66933.1; -.
Hypothetical protein.
SEQUENCE 87 AA; 9530 MW; 8B4C449C621B4B7F
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Haas B.J., Volfovsky N.,
Feldmann K.A., Flavell R.
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Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.;
"Species-specific TT viruses in humans and nonhu
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Feldmann K.;
                                                                                                                                                                                                                                                                  "Full-length messenger RNA sequences greatly annotation.";
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Virology 277:368-378(2000).
EMBL; AB041959; BAB19314.1;
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Score 22; DB
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01-OCT-2000
                                                                                                                                                                                                         Newbigin E., Brewer P.;
"Statistical analysis of a gene tightly linked incompatibility locus of Nicotiana alata.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ d EMBL, AY159325, AAN78179.1; -.
Hypothetical protein.
SEQUENCE 87 AA; 10025 MW; AC0D753D05AEID5C
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Nicotiana alata (Winged tobacco) (Persian tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core endicots;

Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical pollen protein.
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Hypothetical protein.

SEQUENCE 87 AA; 9961 MW;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
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Newbigin E.;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical pollen protein.
Nicotiana alata (Winged tobacco) (Persian tobacco).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
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"Statistical analysis of a g
incompatibility locus of Nic
Submitted (OCT-2002) to the
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Ricotiana alata (Winged tobacco) (Persian tobacco).

Ricotiana (Winged tobacco) (Persian tobacco).

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
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Hypothetical pollen protein
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                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 87 AA; 9917 MW;
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SEQUENCE 87
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical pollen protein.
Nicotiana alata (Winged tobacco) (Persian tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
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"Statistical analysis of a gene tightly linked to the se incompatibility locus of Nicotiana alata.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY159328; AAN78182.1; -.
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Micotlana alata (Winged tobacco) (Persian tobacco).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Solanales; Solanaceae; Nicotlana.
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"Statistical analysis of a gene tightly linked to the self-
"Statistical analysis of a gene tightly linked to the self-
incompatibility locus of Nicotiana alata.";
Submitted (CCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY159329; AAN78183.1; -.
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                                SEQUENCE FROM N.A. STRAIN=Mf-TTV3;
                                                                                                         Viruses; ssDNA vi
NCBI_TaxID=68887;
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87 AA; 9975 MW;
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RESULT 32
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Q9SF26;
Q1-MAY-2000 (TrEMBLrel. 1:
01-MAY-2000 (TrEMBLrel. 1:
01-DEC-2001 (TrEMBLrel. 1:
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phylogenetic relatedness.";
Virology 277:368-378(2000).
EMBL; AB041958; BAB19311.1; -
EMBL; AB041958; BAB19311.1; -
SECUENCE 87 AA; 9896 MW; 036B13AF4E0F9322 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-Mf-TTV3;
STRAIN-ef-TV3;
MEDLINE-20534983; PubMed=11080484;
MEDLINE-20534983; PubMed=12080484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Putative type III effector HolProZ (Fragment).
Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                Pathogen Pseudomonas syringae.
Science 295:1722-1726(2002).
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21862332; PubMed=11872842;
Guttman D.S., Vinatzer B.A., Sarka
Greenberg J.T.;
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SEQUENCE FROM N.A. STRAIN=cv. Columbia;
                                                                                         F11F8_40.
                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Species-specific TT viruses in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okamoto H., Nishizawa T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-2000)
                                NCBI_TaxID=3702;
                                                                              Arabidopsis thaliana
                                                                                                     Putative dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonadaceae;
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                                                                                                                                                                                                                                                                 Local Similarity
nes 5; Conserv
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Bevan M., Lamar B., St

Mayer K.F.X., Lemcke I

Submitted (AUG-1999) t
                Q9JII8
Q9JII8;
01-OCT-2000
01-OCT-2000
01-OCT-2000
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EMBL, ACO16661; AAF23309.1; -...
EMBL, BC016661; AAF23309.1; -...
InterPro; IPR001804; Isodh.
Pfam; PP00180, isodh; 1...
                                                                                                                                                                                                                                                                                                                                                                                                      EU Arabidopsis sequencing project;
submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL109787; CAB52447.1; -.
EMBL; AL161577; CAB79792.1; -.
Hypothetical protein.
SEQUENCE 91 AA; 10077 MW; D3930098D29E4EC:
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Roside
eurosids II; Brassicales; Brassicaceae. Arabidomorio
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01-MAY-2000 (TrEMBLrel. 23, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 10.1 kDa protein.
T10C21.90 OR AT4G30740.
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91 AA; 9576 MW;
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01-AUG-1998
01-MAR-2003
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Q983E1;
01-OCT-2001
01-OCT-2001
01-MAR-2002
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01-MAR-2002 (TrEMBLrel 20, L
Hypothetical protein mll8367.
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EMBL; AP003013; BAB53940.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 91 AA; 9393 MW; AFB66BFB34D86C81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaneko T., Nakamura Y., Sato S., Asamizu E., K
Watanabe A., Idesawa K., Ishikawa A., Kawashin
Kishida Y., Kiyokawa C., Kohara M., Matsumoto
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo
Takeuchi C., Yamada M., Tabata S.;
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CURT. BIOL. 10:873-876(2000).

EMBL; AF223952; AAF87329.1; -.
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Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Phyllobacteriaceae; Mesorhizobium.
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STRAIN=129/Sv;
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Matsumoto M., Matsuno A.
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core ereurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Science 282:2012-2018(1998).
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MEDLINE=99069613; PubMed=9851916;
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NCE 92 AA; 10330
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udicots; Rosidae;
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Q9BRT7 PRELIMINARY;
Q9BRT7;
01-JUN-2001 (TrEMBLrel. 17,
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HSSP; P00949; 3PMG
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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EMBL; AE009620; AAL53049.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 93 AA; 9464 MW; 6C088B163FB233E5 CRC64;
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MEDILINE=20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
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                                                                                                                                                                                                     IPR005843; PG_PMM_C.
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                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                Boecher M.,
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                                                                                                                                                                                                                              CAB70880.1;
                                                                                                                                                                      10387 MW;
                                                                                                                                                                                                                                                                                                                         Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                               Brandt P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
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                                                                                                                          Score 22; DB 4;
Pred. No. 3.3e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                      90219A5DE18527C6 CRC64;
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                        94
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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Endaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1] - SEQUENCE FROM N.A.
RC SITSUE-Bladder;
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
Strausberg R.;
STRAUSS97; AAH05997.1; -
SQ SEQUENCE 94 AA; 10958 MW; 35012833158BBA7F CRC64;
SQ SEQUENCE 94 AA; 10958 MW; 35012833158BBA7F CRC64;
Query Match
Best Local Similarity 100.0%; Score 22; DB 4; Length 94;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSSG 5
Best Local Similarity 0; Mismatches 0; Indels 0; Gaps 0;
SSSG 61

Search completed: December 11, 2003, 09:57:59
Job time: 22 secs
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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seq length: 2000000000
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1. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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t	2	28	28	28	28	28	28	28	28	Score
	100	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match
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1	၁ ၁	20	20	20	18	18	17	16	14	
7671 0616	22V02127	AAY25357	AAY33597	AAY43496	AAW19543	AAW17094	AAR95062	AAR72707	AAR34034	ID
בפלינות דיוויינו מפפ	Dentide linker use	IFNAR2/IFN-beta co	VH-VL domain linke	Linker for dual av	Chimeric protein p	Gly(4)-Ser linker	scFv spacer peptid	Linker for apo A-I		Description

45	44	. 43	42	41	40	39	38	37	36	ပ	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	H	10
28	28	20	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28
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ABG31102	22	ABP52872	မ္	ABG31505	ABG31035	8	AAE25959	8	ABB79971	ABB79970	AAE28173	AAE28934	ABP56192	AAB57784	AAB57374	AAB55527	AAB50848	AAB68571	AAB74580	AAB81033	AAG62613	AAG62343	AAE06269	AAG63011	AAU05173	AAU05172	AAE08730	AAE11873	ABB56480		AAY43750	21	22	AAB14535	AAB00156
Linker peptide for	inger pro	, ii	peptide us	FLexible peptide l	Binding domain-imm	VH and VL antibody	peptic	Synthetic linker p	Linker peptide use		Linker peptide #5	c	ptic	Flexible polylinke	flod	፳	nt prote	eptide #1	xt-depende	r peptide us	•	peptide SE	ine linker	linker u	Ħ	Lieving	Peptide linker #9	peptide	singl	from II	used	Peptide linker use	xpression vect	×	2

ALIGNMENTS

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RESULT 1
AAR34034
09-OCT-1991;
18-JUN-1992;
08-OCT-1992;
                                                                                                                                                                                 Linking sequence whose encoding DNA can be ligated between apo A-I- and a B-100-encoding DNA sequence.
                        Curtiss LK, Koduri KR,
                                                                                             09-OCT-1992;
                                                                                                              15-APR-1993.
                                                                                                                                                Synthetic.
                                                                                                                                                               Lipoprotein; apoprotein; B-100; A-I; LDL; HDL; assay.
                                                                                                                                                                                                          25-MAR-2003 (updated)
13-AUG-1993 (first entry)
                                                                                                                                                                                                                                     AAR34034;
                                                                                                                                                                                                                                                      AAR34034 standard; Protein;
        WPI; 1993-134378/16
                                                                                                                              WO9307165-A1
                                         (SCRI ) SCRIPPS RES INST.
                                                          91US-0774633.
92US-0901706.
92US-0959946.
                                                                                             92WO-US08634.
                        Smith RS,
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                        Witztum JL,
                        Young SG;
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RESULT 2
AAR72707
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Matches 5
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18-JUN-1992;
08-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 having ATCC Accession No. 8746. Polypeptides specifically claimed, include residues 217-297, 216-310, 216-312, 216-352, 216-377, 1-377, 295-297, 117-297, 140-297. DNA sequences encoding the polypeptides are also claimed. Also claimed are a fusion polypolypeptide that contains: (a) a first amino acid residue sequence up to 250 residues in length that includes residues 120-135 of apo A-I, (b) a second amino acid residue sequence up to 375 residues in length that includes 120-135 of apo A-I, (b) a second includes residues 217-297 of apo B-100 and DNA encoding it. (Updated on 25-MAR-2003 to correct PN field.)
                      A dispersible apo A-I/B-100 fusion polypeptide is claimed which contains a first AA sequence of apo A-I (Bee AAR72605) and that includes at least AA sequence positions 120-135 (see AAR72606). The two sequences are operatively linked. An exemplary linking sequence is AAR72707 whose encoding DNA can be ligated between an apo A-I and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide mimic of native apo B-100 and native apo A-I - useful in assays for LDL and HDL in plasma samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The inventors claim a portion of the polypeptide contg. apo B-100 that immunoreacts with antibodies secreted by the hybridoma MB47
                                                                                                                                           New apo:lipoprotein B-100 peptide(s) in assay systems for detecting LDL ar
                                                                                                                                                                                     WPI; 1995-161146/21
                                                                                                                                                                                                              Curtiss LK,
                                                                                                                                                                                                                                                                                                                     09-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                18-APR-1995
                                                                                                                                                                                                                                                                                                                                                                          US5408038-A
                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                            Apo A-I; LDL cholesterol; low density lipoprotein; fusion polypeptide; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linker for apo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR72707 standard; Peptide; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
            B-100
                                                                                                      Disclosure; Column 18; 41pp; English.
                                                                                                                                                                                                                                        (SCRI)
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mes 5; Conserv
                                                                                                                               ssay systems
fluids.
           encoding
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92US-0901706.
92US-0959946.
            DNA
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           sequence
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                                                                                                                                                                                                               Smith RS,
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Pred. No.
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                                                                                                                                                                                                               Witztum
                                                                                                                                             s) and fusion peptide(s)
and HDL cholesterol lev
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AAW17094;

AAW17094 standard; peptide; 5

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RESULT 3
AAR95062
ID AAR9
RESULT 4
AAW17094
ID AAW1
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AC AAW1
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                                                                                                                                                                                       A flexible spacer peptide (AAR95062) is used to link the light chain variable domain to the heavy chain variable domain of a single chain recombinant antibody (scFv). The scFv may be derived from a monoclonal antibody, e.g. MAb FRP5, and forms the ligand domain of a multidomain protein (see also AAR95053 and AAR95056-59) that is used with an effector nucleic acid in a novel nucleic acid transfer system suitable for gene therapy. The ligand domain has a target cel recognition function and allows cellular internalization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid transfer system; gene transfer; gene therapy; cell_targeting; multidomain protein; vector; cancer; scFv;
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                      Nucleic acid transfer system for gene therapy, e.g. against of includes toxin translocation domain to target nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  scrv spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR95062;
                                                                                                                                                                                                                                                                                      Disclosure; Page 8; 106pp; English.
                                                                                                                                                                                                                                                                                                            specific cell
                                                                                                                                                                                                                                                                                                                                                                       Fominaya J, Wels W;
                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9613599-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR95062 standard;
                                                                                                                                                                              multidomain protein/nucleic acid complex.
                                                                                                                                                                                                                                                                                                                                                                                              (WELS/) WELS
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ilarity 100.0%;
Conservative (
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                                                                                                                             Score 28;
Pred. No.
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Pred. No. 9.3e+05;
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                                                                                                                   Mismatches
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                                                                                                                            DB 17;
9.3e+05;
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                           (II) a modified human interleukin-3 (hII-3) AA sequence; (III) a modified human c-mpl ligand; and a colony stimulating factor (CSF); and L1 = a linker capable of linking R1 to R2. This sequence represents an example of a linker used to construct the proteins of the invention. Vectors comprising the nucleic acid molecules are useful for the recombinant production of HP. The nucleic acid molecules are useful in gene therapy. The HP's are useful for stimulating the production of haematopoietic cells in patients, selective ex vivo expansion of stem cells and for treatment of haematopoietic disorders. Disorders that can be treated include leukopaenia, neutropaenia, aplastic anaemia and thrombocytopaenia. In vitro uses include the ability to stimulate bone marrow and blood cell activation and growth before infusion into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel haematopoietic protein (HP) comprising an amino acid (AA) sequence of formula: R1-L1-R2; R2-L1-R1; R1-R2; or R2-R1; where R1 and R2 are independently selected from: (I) a modified human granulocyte-colony stimulating factor (hG-CSF) AA sequence; (II) a modified human interleukin-3 (hIL-3) AA sequence; (III) a modified human interleukin-3 (hIL-3) AA sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bauer SC,
Klein BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haematopoietic protein; human; granulocyte-colony stimulating factor; G-CSF; interleukin; c-mpl ligand; linker; gene therapy; aplastic anaemia; stem cell expansion; leukopaenia; neutropaenia; vector; bone marrow; thrombocytopaenia; blood cell activation; growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multi-functional haematopoietic receptor agonists - stimulate the production of haematopoietic cells in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9712985-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 33; 616pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-APR-1997
Pseudomonas exotoxin; myelin basic protein; chimeric protein; autoimmune disease; multiple sclerosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-226228/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-1996;
                                              Chimeric protein pentapeptide linker for the MBP moiety and PE moiety.
                                                                                                                                               AAW19543 standard; peptide; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SEAR ) SEARLE & CO G D.
                                                                                                                                                                                                                                                                                               l Similarity
5; Conserv
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Lee SC, M
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                                                                                                                                                                                                                                                                                               100.0%; ilarity 100.0%; Conservative 0,
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                                                                                (first entry)
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McKearn JP,
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                                                                                                                                                                                                                                                                                               Score 28; DB
Pred. No. 9.3
0; Mismatches
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McWherter CA,
                                                                                                                                                                                                                                                                                               ; DB 18;
. 9.3e+05;
ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beraud E,
Yarkoni S;
                                                                                                  metastasis-associated receptor ligand; angiogenesis; cell anti-angiogenic protein; avb3-integrin; cemarthy; arthritis; mattlar degeneration; diabetic retinopathy; hemangioma; ps osteoporosis; thrombosis; angina; atheroscierosis; antivir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Pseudomonas exotoxin-myelin basic protein chimeric proteins used for the treatment of auto:immune diseases, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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17-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                           Linker for dual avb3 receptor/metastasis-associated receptor ligands.
                                                                                                                                                                                                                          26-JAN-2000
                                                                                                                                                                                                                                                                                    AAY43496 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               while having no effect on non-target cells.
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                                                                                                                                                             Interferon-alpha-2b; IFN-alpha; avb3 antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YISS ) YISSUM
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5; Conserv
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95IL-0116044
                                                                                         antifungal
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                                                                                                                                                                                                                                                                                    Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No.
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hes 0;
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                                                                                                                                                                 avb3
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basic protein (I
                                                                                                                                              cell proliferation;
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14-OCT-1999 WO9951638-A1

07-APR-1999;

08-APR-1998;

98US-0081074 99WO-US04295

(SEAR) SEARLE & CO G D.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical compounds of the invention. These compounds are dual avb3 receptor/metastasis-associated receptor ligands, and inhibit angiogenesis and thus proliferation of (cancer) cells. One component binds to the avb3 receptor and the other to a metastasis-associated receptor. The avb3 antagonists may also be conjugated to anti-angiogenic proteins, such as IFN-alpha and its derivatives. The compounds are used to treat angiogenesis-related disorders (mediated by the avb3-integrin), specifically cancer (of lung, breast, ovary, prostate, stomach, colon, kidney or bladder, also melanoma, hepatoma, sarcoma and lymphoma), arthritis and macular degeneration, and also diabetic retinopathy, hemangioma, psoriasis, osteoporosis, thrombosis, angina, atherosclerosis etc. The compounds may also be useful as antiviral, antibacterial and
                                                                                                                                                                                                                Antigen binding; single chain; variable domain; VH domain; light chain; heavy immunoglobulin chain; VL domain; anticancer; antivital; tumor; antibacterial; antimalarial; antiinflammatory; treatment; prevention; diagnosis; vaccine; autoimmune disease; inflammation; blood disorder;
                                                          09-APR-1998;
                                                                                      09-APR-1998;
                                                                                                                  14-OCT-1999
                                                                                                                                               DE19816141-A1
                                                                                                                                                                                                     transplant
                                                                                                                                                                                                                                                                                        VH-VL domain linker peptide #9
                                                                                                                                                                                                                                                                                                                                                  AAY33597;
                                                                                                                                                                                                                                                                                                                                                                             AAY33597 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antifungal agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antagonist and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 86; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases, e.g. cancer
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  Kontermann R,
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                             (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.
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                                                                                                                                                                                                        rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quence represents a linker used to join the avb3 the metastasis-associated receptor ligand, in the
 Sedlacek H,
                                                          98DE-1016141.
                                                                                     98DE-1016141
                                                                                                                                                                                                                                                                                                                                                                             Protein; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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  Mueller R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 20;
Pred. No. 9.3e+05;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for treating angiogenesis-related
                                                                                                                                                                                                      nervous system disorder; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
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RESULT 8
AAY25357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a novel single-chain molecule (I) that binds multiple antigens and comprises two variable domains of heavy immunoglobulin chains (VH), having specificities A and B and two cariable domains of light chains (VL), also with specificities A and B.

The domains are provided as two VH-VL constructs which are attached via a peptide (P). Any VH and VL may be replaced by their functional crayments. The products of the invention have anticancer, antiviral, antibacterial, antimalarial and antiinflammatory activity. (I) are used to treat, prevent or diagnose tumors (e.g. as tumor vaccines), autoimmune diseases and inflammation (e.g. transplant rejection and arthitis), compared the diseases and inflammation (e.g. transplant rejection and arthitis), compared the diseases and inflammation (e.g. transplant rejection and arthitis), compared the disorders (e.g. of the coagulation and/or circulatory systems, such as anemia, leucopenia, thrombocytopenia and hypertension), nervous system considered and modern and arthitis (e.g. transplant rejection), nervous system including, when (I) include a fusogenic peptide, use for gene transfer. (I) are produced simply and in predominantly homogeneous form, in a wide sequence represents a VH-VL domain linker peptide which is used to cillustrate the method of the invention.
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Matches 5
                                                                                                                                                                                                                                                                                                                      IFNAR2; IFN-beta; type I interferon; IFNAR/IFN complex; IFN; antivir; human interferon alpha/beta receptor; anticancer; immunomodulatory; anti-arthritic; antidiabetic; treatment; hepatitis; viral infection; hairy cell leukemia; Kapost's sarcoma; multiple myeloma; cancer; lupi diabetes; multiple sclerosis; rheumatoid arthritis; myasthenia gravii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polyspecific binding agents containing variable heavy and light constructs connected via peptide linker, used for treatment, preven
                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                        acquired immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY25357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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WPI; 1999-405115/34.
                                                 Cunningham
                                                                                                                                     19-DEC-1997;
                                                                                                                                                                      18-DEC-1998;
                                                                                                                                                                                                                                        WO9932141-A1
                                                                                                                                                                                                                                                                                                                                                                                                                               IFNAR2/IFN-beta complex peptide fragment 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY25357 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-581511/50
                                                                                   (ISTF ) ARS APPLIED RES SYSTEMS (MCIN/) MCINNIS P G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Page 17; 20pp;
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                                                   McKenna
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Pred. No. 9.3
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                                                                                                                                                                                                                                                                                                                                                                                                antiviral;
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                                                                                                                                                                                                                                                                                                                                                                                          anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration.
              The specification describes multifunctional proteins which comprise combinations of angiostatin, endostatin, interferon, thrombospondin, interferon inducible protein and platelet factor 4, and have anti-angiogenic and/or anti-tumor activity. The multifunctional prot
                                                                                                                      New multifunctional proteins useful for treating angiogenic-mediated
                                                                                                                                                                              Bolanowski MA, Car
Klein BK, McKearn
                                                                                                                                                                                                                                                  01-OCT-1997;
                                                                                                                                                                                                                                                                          30-SEP-1998;
                                                                                                                                                                                                                                                                                                       08-APR-1999
                                                                                                                                                                                                                                                                                                                                 WO9916889-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiostatin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide linker used to make multifunctional proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY02127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY02127 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention describes a novel method for /pe I interferon (IFN) by administering
                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                      cell production;
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                                                                               Page 111; 121pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                          endostatin; interferon; thrombospondin;
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                                                                                 English.
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Pred. No.
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having similar
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target protein, a second binding domain capable of forming neutralising complex with an induced epitope of the target protein and a linker connecting the binding domains. SCD4-SCFV(17b) comprises a soluble CD4 fragment (containing domains D1 and D2) fused to a single chain Fv portion of antibody 17b via a linker. sCD4-SCFv(17b), its variant, analogue or mimetic is used for inactivating gp120 protein of HIV, and for neutralising HIV. It is also used for blocking and preventing the binding of the viral or recombinant gp120 protein to soluble CD4 or lymphocyte CD4 and for inhibiting HIV replication. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. ANY02125-32 represent peptide linkers used to make the
                                                                                                                                                         sCD4-SCFv(17b) is a neutralising bispecific fusion protein capable binding to two sites of its target protein. The protein comprises a first binding domain capable of binding to an inducing site on the
                                                                                                                                                                                                                                Claim 30; Page 45; 55pp; English.
                                                                                                                                                                                                                                                                                Novel neutralizing bispecific fusion proteins effective in viral such as HIV neutralization, comprises two different binding domains, inducing-binding domain and induced-binding domain functionally linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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domain; single chain antibody; chimera;
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domain functionally linked
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The invention relates to raising a neutralising antibody response to a broad spectrum of HIV (human immunodeficiency virus) strains and isolates, comprising the administration of a peptide which corresponds to or mimics highly conserved portions of the gp41 envelope glycoprotein which are important in mediating the process of viral entry into host cells. Such peptides can correspond to or mimic the coiled coil solution structure of the N-helical domain (the heptad repeat region), or can correspond or mimic the C-helical domain (the
                                                                                                                                                                                                                                                                                                                                 Raising neutralizing antibody response to human immunodeficiency virus, comprises administering a polypeptide capable of forming a stable coiled-coil solution structure -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV-1; gp41; N-helical domain; heptad repeat region; C-helical gp41 transmembrane-proximal amphipathic alpha-helical segment; core 6-helix bundle; viral entry inhibition; immunogenic; antibdy; humoral response; broad spectrum vaccine; anti-HIV;
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07-JAN-2000; 2000US-0480336.
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                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-465959/40
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WEISS C D.
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le linker.
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC transmembrane-proximal amphipathic alpha-helical segment), or the CC gp41 core 6-helix bundle, which is formed by the interaction of CC the N- and C-helical domains of three gp41 proteins. The peptides CC can be administered either singly or as a combination (particularly CC a combination of N-helical and C-helical peptides), and can be CC multimerised. For example, N- and C-helical peptides), and can be CC alternately linked together to form a peptide which mimics the core CC einvolved in viral entry. As these portions of gp41 are well conserved, CC such antibodies may be effective against a broad range of HIV strains CC and isolates. The peptide compositions of gp41 are well conserved, CC such antibodies may be effective against a broad range of HIV strains CC prophylactic or therapeutic vaccine to generate antibodies which reduce CC or inhibit the ability of HIV to infect uninfected cells. A composition CC reduce HIV infection of uninfected cells. Antibodies raised against centry-relevant gp41 structures may also be used therapeutically and as tools to further elucidate the mechanism of HIV cell entry. The presents a peptide linker which may be used to CC present sequence represents a peptide linker which may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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                                                                                                                              N-terminally modified cancerous endothelial
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                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                          Modified RNase; eosinophil derived neurotoxin protein; EDN; cancer; Kaposi's sarcoma; neoplastic endothellal cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expression vector CANTAB5E inserted peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB06226 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                            non-neoplastic
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nilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                             endothelial cell; expression
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cells
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                                                                                                                              A targeted to and are cytotoxic used to treat especially Kaposi'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB
Pred. No. 9.3
0; Mismatches
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The present sequence is a peptide which was inserted into expression vector pCANTAB5E to enable more flexible folding of the human eosinon derived neurotoxin protein (EDN), which was expressed by the vector. The protein can be directed to cancerous cells using additional N-terminal peptides, where it exerts a cytotoxic effect. The protein can, therefore

eosinophil

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Example 9;

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psoriasis and smooth muscle cell migration. Interferon alpha is a family of proteins which possess complex antiviral, antineoplastic and immunomodulating activities. Interferon alpha is effective against a variety of cancers including hairy cell leukaemia, chronic myelogenous leukaemia, malignant melanoma and Karposi's sarcoma. Multi-functional bioconjugates comprising both a vb 3 antagonists and interferon alpha 2b can exhibit greater biological activity when compared to a single factor or having improved half-life or decreased adverse side effects, or a combination of
                                                                                                                                             Bioconjugates comprising one or more a vb 3 antagonist moieties coupled to a peptide or polypeptide having anti-angiogenic properties can be used for treating a human patient with an angiogenesis mediated disease, e.g. cancer, arthritis, or macular degeneration. The a vb 3 integrin is normally associated with endothelial cells but can promote the formation of blood vessels (angiogenesis) in tumours. The a vb 3 integrin is also known to play a role in tumour metastasis, neoplasia, osteoporosis, Paget's disease, retinopathy, arthritis, periodontal disease, retinopathy, arthritis, periodontal disease.
                                                                                                                                                                                                                                                                                                                                                                  New bioconjugates comprising an avb3 antagonist and a metastatic-associated receptor ligand, useful for treating cancer and other angiogenic diseases, or as antiviral, antifungal or antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biconjugate; a_vb_3 integrin; interferon alpha; angiogenesis; cancer; tumour; osteoporosis; Paget's disease; Karposi's sarcoma; periodontal disease; metastasis; peoplasia; retinopathy; arthritis; psoriasis; leukaemia; malignant melanoma; atherosclerosis; smooth muscle cell migration; inhibition; treatment; antagonist; angina; thrombosis; restenosis; antiviral; antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY83210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide linker used in construction of a_vb_3 integrin/IFN alpha.
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                                                                                                                                                                                                                                                                                                                        Claim 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SEAR ) SEARLE & CO
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                                                                                                                                                                                                                                                                                                                      Page 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer, particularly Kaposi's sarcoma, and to neoplastic and non-neoplastic endothelial cel
                                                                                                                                                                                                                                                                                                                      123pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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Pred. No.
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                                                                    The present sequence represents a linker used in the construction of bispecific single-chain polypeptides of the invention. These polypeptides comprise domains providing binding-site of inmunoglobu chains or antibodies specifically recognizing CD19 and CD3 antigen. The polypeptide destroys CD19-positive target cells without any need of T-cell pre and/or co-stimulation, by recruiting cytotoxic T-lymphocytes and so specific lysis by T-cells rather than a direct effect by an antibody is achieved. The bispecific single-chain content of the present of the pres
polypeptides, or nucleotides encoding them, are used for the of B-cell malignancies, B-cell mediated autoimmune diseases myasthenia gravis, Morbus Basedow, Hashimoto thyroiditis o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DOER/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Linker used to construct a bispecific single-chain antibody.
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                                                                                                                                                                                                                                                                                                               Claim 10; Page 49;
                                                                                                                                                                                                                                                                                                                                                                   Novel multifunctional polypeptide especially non-Hodgkin lymphoma .
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-013241/01
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RIETHMUELLER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loeffler
                                                                                                                                                                                                                                                                                                                                                                                            treating B-cell malignancies
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fusion protein. The invention relates to an isolated nucleic acid construct (I) comprising a region encoding an interleukin-12 (II-12) fusion protein (comprising an II-12 p35 subunit, an II-12 p40 subunit and I inker peptide (joining the subunits) and a region encoding a B7 protein. (I) may be used to produce II-12 fusion proteins according to standard recombinant DNA methodologies. The fusion proteins may be reduced either in vitro in a fermentation culture or in vivo as part of a gene therapy protocol (in this case (I) is used to transform a patients cells, which then secrete the functional polypeptide to supplement the CC patients own production of II-12 or to rectify mutations which lead to this way may be used to treat any disease which responds to II-12 such as tumours (both solid and dispersed of the kidney, breast, colon, ovarian and cervical tumours and melanomas) and in particular, tumours of the blood such as leukaemia. Alternatively, the polypeptides may be used as an antagonists of its activity. The antibodies and antagonists of company to the production of first bodies to II-12 and to assay for the used to inhibit the activity of II-12. (I) may also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid constructs encoding interleukin-12 fusion proteins useful for treating leukemia and other cancers -
                                                                                                                                                                                                                                                                                                         This sequence represents a linker that can be used in an interleukin-12 fusion protein. The invention relates to an isolated nucleic acid construct (I) comprising a region encoding an interleukin-12 (IL-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
IL-12 p40 subunit; gene therapy; tumour; leukaemia; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linker
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                                                                                                                                                                                                                                                                                                                                                                                                                    treating
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Pred. No.
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                                                                                            The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alphal domain and a betal domain linked through an amino acid linker and a multimerisation domain. The first and the second molecule are linked through the multimerisation domain to form a multimeric complex. The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostically as a probe which hybridizes to sequences encoding IL-12 and the antibodies may be used to detect the presence of IL-12 polypeptides in samples. They may be used diagnostically to quantitate the expression of the polypeptide by patients and hence which subjects may be in need of restorative therapy.
                                          multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus erythematosus. The present sequence is a linker used to connect the
                                                                                                                                                                                                                                                                                                       Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alphal and betal domain linked through amino acid linker and multimerization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-2000; 2000US-191274P.
15-MAY-2000; 2000US-204249P.
23-JAN-2001; 2001US-264003P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single chain; immunosuppressive; antidiabetic; antiinflammatory; antiranemic; antirheumatoid; antirharthritic; neuroprotective; vaccine antianaemic; antirheumatoid; antipae sclerosis; autoimmune disease; insulin dependent diabetes; multiple sclerosis; myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis; rheumatoid arthritis; systemic lupus erythematosus; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; MHC; major histocompatibility complex; MHC class II; mult single chain; immunosuppressive; antidiabetic; antiinflammatory;
                                                                                                                                                                                                                                                         Claim
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Pred. No. 9.3
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                               single chain
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04-MAR-1996;
17-FEB-1994;
                                                                                                                             The present invention relates to a method for evolving a polynucleotide coward a desired functional property. The method comprising providing polynucleotides comprising two or more species variants, shuffling the polynucleotides to form a population of recombinant polynucleotides, selecting or screening for recombinant polynucleotides that have evolved toward the desired functional property, and repeating the steps to obtain the polynucleotide. The methods are useful for evolving a polynucleotide coward a desired functional property and for obtaining a recombinant polynucleotide having a desired functional property. The methods are also useful for generating and selecting nucleic acid fragments encoding mutant proteins. The methods are also useful in molecular backcross to eliminate unnecessary or silent mutations, in the study of repetitive DNA sequences and to mutate ribozymes and aptamers. The present sequence is spacer peptide used in the antibody display and screening methods.
                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 12; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Evolving polynucleotides with desired functional property, involves shuffling polynucleotides comprising species variants to form a population of recombinant polynucleotides, and selecting/screening the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-610489/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shuffling; recombinant polynucleotide; selecting; screening; IL-1beta; functional property; molecular backcross; spacer peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-1998;
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95WO-US02126.
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                                         Score 28; DB 22; I
Pred. No. 9.3e+05;
Pred. No. 9.3e+05;
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Pred. No. 9.3e+05;
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                                                                                                                                                                                                                                                                                                           protein (ZFP) that modulates the expression of the molecular target, or isolating membranes from cell comprising ZFP. The methods allow for high throughput screening of candidate compound and reduces the incidence of false positives. The methods are useful for screening a compound for interaction with a molecular target or for screening a compound for its effect on a cellular process. The method is useful for testing a compound for its capacity to transduce a signal to the molecular target or its capacity to block transduction of a signal through the molecular target, and for performing biochemical drug-screening assays. The present sequence is a peptide linker used for linking ZFPs.
                                               AAU05172;
                                                                            AAU05172 standard; peptide; 5
                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of screening a compound for interaction with a molecular target. The method involves contacting first and second cells with the compound and determining the values of properties of the compound. The second cell comprises an exogenous zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening compound for interaction with molecular target by contacting compound with cells, comprising exogenous zinc finger protein that modulates expression of target, and determining values of properties of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE08730 standard; peptide; 5 AA.
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nilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
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Pred. No. 9.3e+05;
Mismatches 0;
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                                                                                                                                                                                                                                                  Length 5;
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                                                                                                                                                                                                                      Gaps
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24-OCT-2001

(first entry)

Pain-relieving target construct, linker moiety

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RESULT 20
AAU05173
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Best Local Similarity
Warches 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents the amino acid sequence of linker moiety #1 used to make a pain-relieving target construct. The construct comprises a pain-relieving agent linked to a ligand motety that selectively binds to or is taken up by the tissue associated with the painful interior disease site. The construct is used for treating pain associated with an interior disease site. Since the pain-relieving agent is delivered by the ligand to the disease site intractable pain situated in the interior of the body such as caused by various tumours, such as breast cancer, lung cancer, Hodgkin's and non-Hodgkin's lymphoma, and neuroblastoma, and ischaemic and diseased tissues can be managed using a lower level of the pain relieving agent than is required when the pain-relieving agent is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treatment of pain associated with an interior disease site, involves administering a pain-relieving target construct to the patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200147512-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hodgkin's lymphoma; neuroblastoma; ischaemic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2001
                                     06-DEC-2000; 2000WO-US42661
                                                                                                                     Synthetic
                                                                                                                                           Pain relief; tumour; therapeutic; breast cancer; lung Hodgkin's lymphoma; neuroblastoma; ischaemic.
                                                                                                                                                                                                                                                                     AAU05173 standard; peptide; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pain relieving agent injected in the free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 32; Page 20; 31pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Luiken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FLUO-) FLUORO PROBE INC
            08-DEC-1999;
                                                                05-JUL-2001
                                                                                                                                                                                     Pain-relieving target construct, linker moiety #2.
                                                                                                                                                                                                                 24-OCT-2001
                                                                                          WO200147512-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  relief; tumour; therapeutic; breast cancer; lung cancer;
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                                                                                                                                                                                                                                                                                                                                                                1 GGGGS 5
                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AA;
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                 (first entry)
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            99US-0457498
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                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB
Pred. No. 9.3
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
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RESULT 21
AAG63011
ID AAG63
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Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents the amino acid sequence of linker moiety #2 used to make a pain-relieving target construct. The construct comprises a pain-relieving agent linked to a ligand moiety that selectively binds to or is taken up by the tissue associated with the painful interior disease site. The construct is used for treating pain associated with an interior disease site. Since the pain-relieving agent is delivered by the ligand to the disease site intractable pain situated in the interior of the body such as caused by various tumours, such as breast cancer, lung cancer, Hodgkin's and non-Hodgkin's lymphoma, and neuroblastoma, and ischaemic and diseased tissues can be managed using a lower level of the pain relieving agent than is required when the pain-relieving agent is injected in the free state.
                                                                                                                                                                                                                                                                                                                                           Neurotrophin-1; NNT-1; ciliary neurotrophic factor receptor alpha-chain; CNTFRalpha; fusion protein; gp130 receptor; LIFRbeta receptor; neurodegenerative disorder; nervous tissue; skelettal muscle; muscle mass; amylotrophic lateral sclerosis; Parkinson's disease; Huntington's disease; obesity; cancer; fertility; endometriosis; blastocyst transplantation; haematopoiesis; thrombocytopaenia; retinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 32; Page 20; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treatment of pain associated with an interior disease site, in administering a pain-relieving target construct to the patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG63011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG63011 standard; peptide; 5
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                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide linker used to link NNT-1 and sCNTFRalpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FLUO-) FLUORO PROBE INC
                                                                         27-JAN-2000;
12-OCT-2000;
                                                                                                                        26-JAN-2001; 2001WO-FR00254
                                                                                                                                                         02-AUG-2001
                                                                                                                                                                                        WO200155219-A2
                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                 retinitis
                                            (FABR ) FABRE MEDICAMENT SA PIERRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 100.0%;
Similarity 100.0%;
5; Conservative (
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                                                                                                                                                                                                                                                                                                                                 pigmentosa.
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                                                                           2000FR-0001035.
2000FR-0013090.
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                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                    /note= "this sequence is repeated 1-10 times,
preferably 2-4 times"
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Pred. No. 9.3
0; Mismatches
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. 9.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG63011-14 represent peptide linkers used to produce a fusion protein, comprising neurotrophin-1 (NNY-1) and a soluble ciliary neurotrophic factor receptor alpha-chain (sCNTFRalpha) protein. The fusion protein is cused to prepare a medicament for the modulation of the activity of the CC used to prepare a medicament for the modulation of the activity of the CC immune, haematopoietic, nervous, or reproductive system, liver, bone CC or skeletal muscle cells. It is also used to make a medicament to C facilitate the proliferation or inhibit the differentiation of cloned CC cells, preferably embryonic stem cell clones. The fusion protein is CC also used as a medication for preventing or treating neurodegenerative CC disorders, for the repair or regeneration of nervous tissue or skeletal correct amylotrophic lateral sclerosis, Parkinson's and Huntington's CC disease, obesity and its related disorders, and cancer. The fusion CC prevent amylotrophic lateral sclerosis, Parkinson's and Huntington's CC disease, obesity and its related disorders, and cancer. The fusion CC protein may also be used to improve fertility, especially to prevent CC haematopoiesis, especially in treating thrombocytopaenia, and for the treatment of retinitis, especially rétinitis pigmentosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enzymatic inactivation; target DNA; nuclease; DNA binding domain; human immunodeficiency virus; HIV; hepatitis B; herpes virus; polyoma virus; papilloma virus; FokI nuclease; FN; hybrid enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine linker
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                       Enzymatically inactivating target DNAs such as Human Immunodeficiency Virus, Hepatitis B, herpesvirus, Polyoma virus and/or Papilloma Virus nucleic acids, and human, animal, viral and bacterial genes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6265196-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1999;
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                                                                                                                                                                                                                       Chandrasegaran
                                                                                                                                                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS
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5; Conser
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Pred. No.
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thes 0;
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Best Local
The present invention relates to a chimeric protein which consists of at least two functional protein units where each protein unit comprises the dimerisation domain of a member of the steroid/thyroid hormone nuclear receptor superfamily. The protein units are linked by a linker peptide, and the two protein units form a functional entity. The invention includes a method for modulating the expression of an exogenous gene in an organism or cell containing the chimeric protein. The cell or organism also contains a DNA construct comprising the exogenous gene under the control of a response element with which the chimeric protein interacts. The response element controls the expression of the exogenous gene. The method also involves administering to the subject or cell an effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for enzymatically inactivating a target DNA using nucleases. The method comprises preparing a protein containing a nuclease domain, delivering the protein to human, animal, or plant, and enzymatically inactivating the target DNA. The nuclease related to the invention comprises a DNA binding domain that specifically binds to the target DNA. The method is used for enzymatically inactivating target DNAs such as human immunodeficiency virus (HIV), hepatitis B, herpes virus, polyoma virus and/or papilloma virus nucleic acids, and human, animal, viral and bacterial genes. The present sequence is a glycine linker which is used for the construction of clones producing the hybrid enzymes, e.g., ZF-Foki nuclease (FN) enzyme, used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steroid hormone; thyroid hormone; receptor; DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                          Disclosure; Page 13;
                                                                                                                                                                                                                                                                            Novel chimeric protein useful for modulating exogenous gene expression in subjects, comprises two functional protein units, each containing dimerization domain of steroid/thyroid hormone nuclear receptor
                                                                                                                                                                                                                                                                                                                                                                                          Gage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2000; 2000WO-US41224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200136447-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Linker peptide SEQ ID 2 used in chimeric protein construction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG62343 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
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Pred. No. 9.3e+05;
Mismatches 0;
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RESULT 24
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                                                                                                                                       The present invention relates to a method of identifying a bioactivity or biomolecule of interest, involving introducing a labeled substrate and a recombinant clone into a capillary tube of a capillary array, culturing the tube to allow the substrate and clone to interact and provide a detectable signal and detecting the signal to identify the capillaries containing the activity or molecule of interest. This can be used to identify enzymes for use in the biotechnology and chemical industries, and in drug discovery, particularly of antibacterial compounds. The present sequence is a linker peptide described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a
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12-OCT-2000; 2000US-0687219
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                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 79; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant clone in a capillary tube of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-367710/38.
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                                                                                                                            invention.
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Similarity
5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                             a bioactivity or biomolecule of interest, involve
substrate labeled with a detectable molecule and
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Pred. No. 9.3e+05;
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                                         Length 5;
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                                                                                                                                                                                      Sequence
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linker; glucose.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Page 2; 7pp; Japanese
         1 GGGGS
                                                                  Similarity
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                                                                     Conservative
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                                                                  Score 28; DB
Pred. No. 9.3
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RESULT 26
AAB74580
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 AAB74580 standard;
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peptide;
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05-JUN-2001 AAB74580; (first entry)

Context-dependent functional entity spacer peptide

Context-dependent functional entity; efficacy enhancement; selective recognition domain; thrombogenic potential; cance arthritis; atherosclerosis; burn. arthritis; potential; cancer; inflammation;

Synthetic.

WO200125413-A1

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                                   Producing cell with
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Disclosure; Page 11; 42pp; English
                                                                                                                                              19-JUL-1999; 99US-0144513.
07-JUL-2000; 2000US-0611736.
                                                                                                                                                                                                           25-JAN-2001
                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                  Transgenic plant; expression cassette.
                                                                                                                                                                                                                                                                                                          Linker peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enhancing the efficacy of active and diagnostic agents and treating pathological conditions in a subject by administering the agent with a context-dependent functional entity, useful for treating e.g. malignant
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                     population of transgenic plants involves transforming plant minimal transgene expression cassette by direct DNA transfer and regenerating transgenic plants from transformed cells -
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Pred. No. 9.3e+05;
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RESULT 28
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Best Local S
Matches 5
                                                                                                            a fluorescent protein indicator. The indicator comprises a sensor polypeptide that is responsive to a chemical, biological, electrical or physiological parameter, and a fluorescence protein functional group. The sensor polypeptide is operatively inserted into the fluorescent moiety. The fluorescent indicator is useful for detecting the presence of a response inducing member in a sample. The method involves contacting the sample with the indicator and detecting a change in fluorescence, in which a change is indicative of the effect of the parameter on the sensor polypeptide. The novel fluorescent proteins are advantageous due to their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for producing a population of transgenic plants, comprising transforming intact plant cells with minimal transgene expression cassettes by direct DNA transfer techniques, and regenerating a population of transgenic plants from transformed plant cells. The present sequence is a linker peptide, which can be used in the expression cassette of the present invention.
      Sequence
                                                                                       polypeptide. The reduced size as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel fluorescent proteins comprising a sensor protein inserted into them, useful for measuring the response of a sensor biological, chemical, electrical or physiological parameter in vivo or in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                               transfer)-based
                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a linker moiety used in the construction
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-032017/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-2001
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99US-0316920.
                                                               sensors.
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-++ve 0;
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                                                                                    fluorescent proteins are advantageous ed to the FRET (fluorescence resonance
                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
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Pred. No. 9.3e+05;
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RESULT 29
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29-OCT-1999; 99US-0170453.
13-DEC-1999; 99US-0170453.
14-JAN-2000; 2000US-0176195.
14-FEB-2000; 2000US-0182296.
11-APR-2000; 2000US-0196527.
                                                                                                             The present invention relates to a new method for modulating a biological function of an endothelial cell or hematopoletic cell. The method involves introducing into a cell, an antagonist that inhibits binding between a PDZ protein and a PL protein. The inhibitor is used to treat a disease mediated by hematopoletic cells, e.g. autoimmune disease. It may also be used to prevent transplantation rejection of a solid organ transplant. The method may also be used in the treatment of inflammation, allergy, inflammatory bowel diseases, ulcerative colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, insulin-dependent disease, Hashimoto thyroiditis, osteoarthritis, graft rejection, transplantation rejection), atherosclerosis, cancers, infectious diseases, ischemia, vasulitis and Crohn's disease.
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14-MAY-1999;
21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                Modulating a biological function of an endothelial cell or hematopoietic cell, useful for treating autoimmune diseases and infectious diseases, by administering an antagonist that inhibits binding between a PDZ protein and a PL protein -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation; allergy; asthma; multiple sclerosis; cancer; infection.
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                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                      Disclosure;
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                            Similarity
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                            Conservative
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99US-0134118.
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Pred. No. 9.3e+05;
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CC prototypical proteins: PSD95, Drosophila large disc protein and Zonnla CC Occludin I protein. PDZ domain proteins are involved in synapse formation by organising transmembrane neurotransmitter receptors through contracted lular interactions. The inhibitors identified by the present invention can be used to treat a disease mediated by haematopoietic convention can be used to treat a disease mediated by haematopoietic convention can be used to treat a disease mediated by haematopoietic configuration and the present structure of the present convention of allergies), inflammatory bowel diseases, ulcerative colitis, lieitis, conventions, autoimmune diseases (e.g. asthma), atopic conventitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple conventitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple conventitis, autoimmune diseases, Hashimoto thyroiditis, conventitis, atherosclerosis, cancers, infectious disease. The conventition of a solid organ transplant. The present sequence is a flexible polylinker cused in the construction of fusion polypeptides of the PDZ-PL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-1999;
14-MAY-1999;
21-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New inhibitors of binding of a PDZ protein and PL protein for inhibiting T cell-mediated response by hematopoietic cells, or for treating diseases characterized by inflammatory and humoral immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endothelial cell; haematopoietic cell; PDZ domain protein; PL domain protein; leukocyte activation; synapse formation; transmembrane neurotransmitter receptor; autoimmune disease; transplantation rejection; inflammation; allergy; inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis; asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
                                                                                                                                                                                                                                                                                                    introducing into a cell an antagonist that inhibits binding between a PDZ domain protein and a PL domain protein to result in inhibition of leukocyte activation. PDZ domains of proteins are named after three
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                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for modulating a biological function of an endothelial cell or haematopoletic cell, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 86; 139pp; English
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99US-0162498
99US-0170453
2000US-0176195
2000US-0182296
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99US-0134117
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RESULT 31
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         The present invention relates to a method for modulating a biological function of an endothelial cell or haematopoietic cell, comprises introducing into a cell an antagonist that inhibits binding between a PDZ domain protein and a PL domain protein to result in inhibition of leukocyte activation. PDZ domains of proteins are named after three prototypical proteins: PSD95, Drosophila large disc protein and Zonula Occludin 1 protein. PDZ domain proteins are involved in synapse formation by organising transmembrane neurotransmitter receptors through intracellular interactions. The inhibitors identified by the present
                                                                                                                                                                 comprises inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PL domain protein; leukocyte activation; synapse formation; transmembrane neurotransmitter receptor; autoimmune disease; transplantation rejection; inflammation; allergy; inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis; asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antagonists.
                                                                                                                                                                          Modulating a biological function of a hematopoietic cell for treating an allergic response, or diseases mediated by immune system cells, comprises introducing into the cell a PDZ-PL interaction enhancer or
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14-MAY-1999;
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                                                                                                                                         Disclosure;
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99US-0162498
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2000US-0196426
2000US-0196527
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                        The present invention describes a chimeric bifunctional molecule (I) comprising at least a first functional molecule covalently linked to a second functional molecule, which is able to modulate the activity of the permeability transition pore complex (PTPC) of the mitochondria.

(I) has the function of specifically targeting and entering a tissue cell population. The second functional molecule has the function of specifically targeting and inducing or preventing the death of the cells by apoptosis by regulating the opening or the closing of the PTPC of the mitochondria or its fragment. (I) has virucide, neuroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          allergies), inflammatory bowel diseases, ulcerative colitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopi dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, m sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
                                                                                                                                                                                                                                                                                                                                                                                                          New chimeric bifunctional molecules that target specific cells regulate the apoptosis function of the permeability transition complex of the mitochondria, useful for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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Pred. No. 9.3e+05;
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                                                                                                                                to display one or more heterologous peptides or proteins. The baculovirn is useful for the delivery of a peptide or protein into the nucleus. It is also useful in libraries (genomic or CDNA) and peptide displays, particularly in selecting target genes, in the functional analysis of genes and their products, or screening these libraries. The present sequence is a linker peptide used in the invention.
                                                                                                                                                                                                                                                                      New engineered baculoviruses, useful for the delivery of proteins into the nucleus, libraries or peptide displays, e.g. in selecting target genes, comprises capsids modified to display heterologous proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                         Sequence
                                                                                                                                                                                                                    The invention relates to a baculovirus, whose capsid has been modified
                                                                                                                                                                                                                                             Disclosure; Page 6; 17pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-2001; 2001GB-0006063.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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Pred. No.
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9.3e+05;
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RESULT

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Linker peptide useful in fluorescent targetting construct.

19-DEC-2002

(first entry)

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                                                                                                                        RESULT 35
                                                                                                                                                                                                                                                                                                                     The present invention relates to methods and compositions for identifying CC a gene. The method involves contacting a cell comprising a putative gene CC sequence (PGS) with an exogenous molecule that binds to and modulates the expression of the PGS, and assaying the cell for at least one selected phenotype, where if one or more of the selected phenotypes are observed. CC the PGS is identified as a gene. The methods include the use of exogenous molecules such as zinc finger proteins (ZFPS) which are capable of CC binding to and modulating expression of gene transcription, targetted to CPGS, followed by assay of one or more selected phenotypes. The ZFPS are CC useful for determining the phenotypic consequences and function of gene expression. The method is useful to explore biological processes such as cransformation, tumour progression, inflammatory response, neurological components, etc. The method can very rapidly identify genes that are up or CC down-regulated in different tissues or in response to specific stimuli.

CC The present sequence is a linker peptide used to link two zinc finger proteins. This peptide is used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                Sequence
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                                                                                          ABB79970 standard;
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100.0%; Pred. No. 9.
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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28-JUL-1999;
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Tumour; cancer; infection; heart attack; stroke; necrosis; ischaemia; diagnosis; fluorescence; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                    claimed).
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                                                  Linker peptide useful in fluorescent targetting construct.
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99US-0362805.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of a flexible spacer peptide linker that can be used to link a fluorescent moiety to a ligand moiety fluorescent targetting constructs of the invention. A claimed method for in vivo diagnosis of diseased tissue involves: irradiating a body part with light having at least one excitation wavelength of 401-500 nm; directly viewing fluorescence emitted i response to light from a fluorescent targeting construct administered to the subject and which has specifically bound to and/or been taken up by the diseased tissue; and determining the location and/or surface area of the diseased tissue from the fluorescence provided by the targetting construct. The ligand
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Misc-difference 1..5
                            Synthetic linker peptide
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                                                                                              ABG80672;
                                                                                                                           ABG80672 standard;
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28-JUL-1999;
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99US-0362805.
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Molecular antigen array; vaccine; antigen; antimicrobial;

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The invention relates to a composition comprising: (a) a non-natural CC molecular scaffold comprising: (i) a core particle effected from: (CC (1)) a core particle of a non-natural origin; and (2) a core particle of trattal origin; and (1) an organiser comprising at least one first CC attachment site, where the organiser is connected to the core particle by at least one second attachment site, where the antigen or antigenic determinant with CC attachment is amyloid beta peptide (Abeta 1-42) or its fragment, and CC where the second attachment site is selected from: (i) an attachment site on the second attachment site is selected from: (i) an attachment site on the second attachment site is selected from: (i) an attachment site of association through at least one non-peptide bond to the first attachment site; and where the antigen or antigenic determinant; and cocurring with the antigen or antigen or antigen or antigen or antigen or antigen or antigen or antigen array. Its composition is used interact through the association to form an ordered and repetitive cocurring ordered and repetitive antigen array. The composition is used in immunisation and as a vaccine for diseases such as influenza, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's casthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's casthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's casthma, acute lymphablastic leukaemia, non-Hodgkin's lymphoma, Grave's casthma, acute lymphablastic leukaemia, non-Hodgkin's lymphoma, Grave's casthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's casthma, acute lymphoblastic leukaemia, hon-Hodgkin's 
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04-MAY-2001;
05-OCT-2001;
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LUEOEND R.
STAUFENBIEL M.
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LECHNER F.
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; 2001US-288549P.
; 2001US-326998P.
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Piossek C;
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                                                                                                                                    The present invention relates to novel immunoglobulin molecules that bind to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing tumour growth and for inhibiting angiogenesis. The present sequence is a linker peptide used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used in the molecular antigen array.
                                                                                                                        angiogenesis. The present sequence single chain (scFv) antibodies.
                                                                                                                                                                                                                                                                            Novel immunoglobulin molecule for reducing tumor growth, binds to kinase insert domain-containing receptor with an affinity comparable human vascular endothelial growth factor, and neutralizes activation
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                                                                                                                                                                                                                                                                                                                                                                                          (ZHUZ/) ZHU Z.
(WITT/) WITTE L.
                                                                                                                                                                                                                                                                                                                                            2002-589175/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             scFv antibody.
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Pred. No. 9.3e+05;
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Pred. No. 9.3
D; Mismatches
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                                                                                                                                                                                                                                                                                                                                        The invention relates to methods and reagents for determining the apparent affinity (Kd) of binding between a PDZ domain and a ligand. The invention also relates to methods and reagents for determining the Ki of an inhibitor of binding between a PDZ domain and a ligand, identifying an agent that enhances binding of a PDZ domain and a ligand, and determining the potency (K-enhancer) of binding between a PDZ domain and a ligand, by determining the ligand bound with an immobilised polypeptide comprising a PDZ domain and an on-PDZ domain on a surface. The modulator (preferably, an inhibitor) of interaction between PDZ and PL is useful for treating a disease characterised by leukocyte activation, e.g., an autoimmune disease that is characterised by inflammatory or humoral immune response, and for reducing inflammation in a subject. This sequence represents a peptide linker of a VH and VI antibody relating to the PDZ domain peptides and ligands of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assays for determining the affinity of binding between a PDZ domain a ligand, and determining the Ki of an inhibitor of the binding, comprises using a polypeptide comprising a PDZ domain and a non-PDZ
         Binding domain-immunoglobulin fusion protein associated linker
                                          05-NOV-2002
                                                                                                       ABG31035 standard; Peptide; 5
                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory; humoral immune response; inflammation; peptide linker.
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ligand; Ki; inhibitor; K-enhancer;
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Conservative 0
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                                       (first entry)
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ror: K-enhancer: leukocyte; autoimmune disease;
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Search completed: December 11, Job time : 29.2 secs

2003, 09:55:23

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a binding domain-immunoglobulin fusion protein that is capable of at least one immunological activity, comprising a binding domain polypeptide fused to an immunoglobulin hinge region polypeptide capable of specifically binding to an antigen, or an immunoglobulin heavy chain CH2 or CH3 constant region polypeptide fused to the hinge region polypeptide or to the CH2 constant region polypeptide. The fusion protein is useful for treating a subject having or suspected of having a B-cell disorder or malignant condition e.g. rheumatoid arthritis, myasthenia gravis, Grave's disease, Hashimoto's thyroiditis, type I diabetes mellitus, multiple sclerosis, systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroprotective; gene therapy; single chain antibody; variable fragment; scFv; binding domain-immunoglobulin fusion protein; B-cell disorder; malignant condition; rheumatoid arthritis; myasthenia gravis; psoriasis; Grave's disease; Hashimoto's thyroiditis; type I diabetes mellitus; multiple sclerosis; systemic lupus erythematosus; Sjograns syndrome; multiple sclerosis; systemic lupus erythematosus; Sjograns syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human binding domain-immunoglobulin fusion protein useful for treating a subject having or suspected of having a B-cell disorder malignant condition e.g. rheumatoid arthritis
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                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 79; 136pp; English.
                                                                                                                                                                                                                   in the creation of binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ledbetter JA,
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                                                                                      Conservative
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                                                                                 Score 28; DB 23;
Pred. No. 9.3e+05;
Mismatches 0;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued Patents AA:*
1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
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28
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
      GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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  US-07-959-946-6
US-08-176-500-140
US-08-471-052A-140
US-08-25-224-54
US-08-236-918A-18
US-08-236-918A-18
US-08-264-800A-58
US-08-244-469-5
US-08-133-577-6
US-08-133-577-6
US-08-528-523-13
US-08-528-523-13
US-08-528-523-13
US-08-471-800-140
US-08-471-939-140
US-08-471-939-140
US-08-92-523-75
US-08-917-668-140
US-08-917-668-12
US-08-655-202-25
US-08-655-202-25
US-08-792-553-15
US-08-792-553-15
US-08-792-553-15
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Sequence 6, Appli
Sequence 140, App
Sequence 140, App
Sequence 140, App
Sequence 140, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
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Sequence 140, App
Sequence 13, Appl
Sequence 140, App
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Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 110, Appl
Sequence 110, Appl
Sequence 112, Appl
Sequence 12, Appl
Sequence 15, Appl
Sequence 24, Appl
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100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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US-09-133-508A-62	US-09-367-953B-26	US-09-362-805-2	US-09-362-805-1	US-09-232-863-62	US-09-281-792B-26	US-09-091-814-1	US-08-818-252-40	US-09-099-015-64	US-09-075-511-64	US-09-215-035-3	US-09-046-992-5	US-09-100-856A-62	US-08-621-859-64	US-08-776-271-3	US-09-397-951-12	US-08-722-258-54	US-08-818-253-40
•	Sequence 26, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 62, Appl	Sequence 26, Appl	Sequence 1, Appli	•	•	Sequence 64, Appl	Sequence 3, Appli	Sequence 5, Appli	Sequence 62, Appl	Sequence 64, Appl	Sequence 3, Appli	Sequence 12, Appl	Sequence 54, Appl	Sequence 40, Appl

ALIGNMENTS

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US-07-959-946-6
US-07-959-946-6
Sequence 6, Application US/07959946
Patent No. 5408038
GENERAL INFORMATION:
APPLICANT: Moduri, Raju G.
APPLICANT: Wouldry, Rephen G.
APPLICANT: Voung, Stephen G.
APPLICANT: Wottiss, Linda K.
ITILE OF INVENTION:
APPLICANT: Outtiss, Linda K.
APPLICANT: Outtiss, Linda K.
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COMPUTER ENGLANCE FORM:
APPLICATION INFORMATION:
APPLICATION NUMBER: US/07/959,946
FILLING DATE: 19921008
FILING DATE: 19921008
FILING DATE: 19921008
FILING DATE: 18-UN-1992
ATTORNATION FOR SEQ ID NO: 6:
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
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REFERENCE/DOCKET N
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Query Match Best Local Similarity

100.0%;

Score 28; DB 1; Pred. No. 2.5e+05;

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Matches

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Query Match
Best Local Similarity
Matches 5; Conserv:
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US-08-176-500-140
                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-176-500-140
                                                                                                                                                                                       US-08-471-052A-140
                                                                                                                            Patent No. 5625033
GENERAL INFORMATION:
                                                                                                                                                                   Sequence 140, Application US/08471052A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 140
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 11(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEPHONE: 212 790-9090
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LENGTH: 5 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/013,416
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APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                   CORRESPONDENCE ADDRESS:
                                                                          APPLICANT: Kay, B. K. APPLICANT: Fowlkes, D. TITLE OF INVENTION: T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino a STRANDEDNESS: TOPOLOGY: unk
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COUNTRY: U.S.A.
ZIP: 10036-2711
                                                            MBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08176500
: Pennie & Edmonds
1155 Avenue of the Americas
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                                                                            Totally Synthetic Affinity Reagents
                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 28; DB 1; 100.0%; Pred. No. 2.5e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-999
TELEPAX: 212 869-8864/9741
TELEPX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
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Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 54, Application US/08225224
Patent No. 5635599
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                  ZIP: 94105-1493

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/225,224

FILING DATE: 8-APR-1994

CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                             STREET: Steuar CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PASTAN, ITA
APPLICANT: KREITMAN, ROBERT J.
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 100.0%; Score 28; DB 1;
Local Similarity 100.0%; Pred. No. 2.5e+05
nes 5; Conservative 0; Mismatches 0
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Y: U.S.A.
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Steuart Street Tower, One Market Plaza
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RESULT 3

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RESULT 6
US-08-463-163-1
                                                                                                                                                                                                                                                                                                     NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                    Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDEER: US 08/060,843
FILING DATE: 07-May-1993
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                 Similarity
5; Conserve
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51 University Street
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                                                                                                                                                  100.0%; Score 28; DB 1; 100.0%; Pred. No. 2.5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 28; DB 1; 100.0%; Pred. No. 2.5e+05;
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RESULT 7
US-08-566-800A-58
; Sequence 58, Application US/08566800A
; Patent No. 5736364
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Best Local Similarity
Thes 5; Conserve
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GENERAL INFORMATION:
APPLICANT: Kelley, Robert F.
APPLICANT: Lazarus, Robert A.
APPLICANT: Lee, Geoffrey F.
TITLE OF INVENTION: NO. 5736364el Factor VIIa Inhibitors
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/227,227
FILLING DATE: 22-JAN-1981
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/911,227
FILLING DATE: 24-SEP-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,361
FILING DATE: 21-APR.1989
PRIOR APPLICATION NUMBER: US 07/865,722
FILING DATE: 08-APR.192
APPLICATION NUMBER: US 07/865,722
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
PRIOR TEATTON MIMMER: 32.762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,163
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FitzGerald, David J
APPLICANT: Chaudhary, Vijay K.
APPLICANT: Pastan, Ira H.
APPLICANT: Waldmann, Thomas A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Queen, Cary L.
TITLE OF INVENTION: Recombinant Antibody-Toxin Fusion Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 2.5
0; Mismatches
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CORRESPONDENCE ADDRESS:

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Query Match
Best Local Similarity
Marches 5; Conserve
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; GENERAL INFORMATION:
; APPLICANT: Paul, Ralph W.
; APPLICANT: Overell, Robert
; TITLE OF INVENTION: ENVELO
; TITLE OF INVENTION: DELIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-244-469-5
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                                                                                                     ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,469
FILING DATE: 01-UNC-1994
CLASSIFICATION: 514
AUTORNEY/AGENT INFORMATION:
NAME: DY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5,
NAME: Dylan, Tyler M.
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 2262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
CLASSIFICATION: 514
ATTORNEY / ACCUSATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: KUDINEC, Jeffrey S.
REGISTRATION UMBER: 36,575
REFERENCE/DOCKET NUMBER: P0958B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                          STREET: 755 PAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08244469
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755 PAGE MILL ROAD
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415/952-9881
                                                                                                                                                                                                                                                                                                                         USA
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                                                        22627-20007.20
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; MOLECULE TYPE:
US-08-189-331-140
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Matches
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PATENT NO. 5747334
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                               Matches
                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                            TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 140
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: Concur
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                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
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1155 Avenue of the Americas
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                                                                 Conservative
                                                                                                                                            unknown
E: peptide
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                                                                                                                                                                               single
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                                                               100.0%; Score 28; DB 1; 100.0%; Pred. No. 2.5e+05; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                 1101-155
                                                                                              Length 5;
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                                                                 Indels
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                                                                 Gaps
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US-08-333-577-6 ; Sequence 6, Application US/08333577 ; Patent No. 5786206

RESULT 10

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SENERAL INFORMATION:

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Best Local Similarity
Matches 5; Conserva
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-333-577-6
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/08575361A
                                                                                                                                                                                                                                                                                                                                           Patent No. 5792640
GENERAL INFORMATION:
APPLICANT: Chandri
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APPLICANT: Koduri, Raju
APPLICANT: Koduri, Raju
APPLICANT: Witztum, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotei
TITLE OF INVENTION: Pan Native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (312)616-5
TELEFAX: (312)616-546
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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LENGTH: 5 amino acids
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REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                    ADDRESSEE: Cushman Darby & Cushman L.L.P.
STREET: 1100 New York Avenue, NW, Ninth Floor, East
STREET: Tower
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                                                                                                                                                                               CITY: Washington
                                                                                                                                             COUNTRY:
                                                                                                                        20005-3918
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                                                                                                                                                                                                                                                                                               Chandrasegaran, Srinivasan
NVENTION: A GENERAL METHOD TO CLONE HYBRID
NVENTION: RESTRICTION ENDONUCLEASES USING 11g
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                                                                                                                                             USA
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(312)616-5460
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RESULT 12
US-08-564-955-64
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                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION UMMBER: US/08/564,955
FILING DATE: 30-NOV-1995
CLASSIFICATION NUMBER: US 08/198,431
APPLICATION NUMBER: US 08/198,431
APPLICATION NUMBER: US 08/198,431
APPLICATION NUMBER: US 08/198,431
APPLICATION NUMBER: US 08/537,874
PILING DATE: 17-FEB-1994
PRIOR APPLICATION NUMBER: US 08/537,874
APPLICATION NUMBER: US 08/537,874
FILING DATE: 30-OCT-1995
PRIOR APPLICATION NUMBER: PCT/US95/02126
APPLICATION NUMBER: PCT/US95/02126
FILING DATE: 17-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: DUNN, TRACY J.
REFERENCE/DOCKET NUMBER: 16528J-014611US
TELECHONE: (415) 326-2400
TELEFRAY: (415) 326-2400
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Patent No. 5
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INFORMATION FOR SEQ ID NO:
TELEFAX: (415) 576-03
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LENGTH: 5 amino acids
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REFERENCE/DOCKET NUMBER: PN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: STEMMER, APPLICANT: CRAMERI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Kokulis, Paul N.
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         TELEPHONE: (415)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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IT: TWO EMBARCADERO CENTER, 8TH FLOOR
SAN FRANCISCO
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5811238
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)GY: linear
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ilarity 100.0%;
Conservative (
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             576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANDREAS M.
METHODS FOR GENERATING POLYNUCLEOTIDES
HAVING DESIRED CHARACTERISTICS BY ITERATIVE SELECTION AND
RECOMBINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WILLEM P.C.
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Pred. No. 2.5e+05;
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MOLECULE TYPE:
HYPOTHETICAL: I
FRAGMENT TYPE:
US-08-528-523-13
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US-08-528-523-13
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Best Local (
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                                                                                Query Match
                                                     Matches
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APPLICANT: Hoelze
                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94114572.4
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 703-243-6333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Arlington
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                    Local
                                                                                                                                                                                                                                                                                                           NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: Merck 1717
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/528,523 FILING DATE: 06-NOV-1992 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                              STRANDEDNESS:
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                                                   l Similarity
5; Conserv
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5824782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T: Strittmatter, Wolfgang
T: Matzku, Siegfried
INVENTION: Immunoconjuga
                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                        64191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Millen, White, Zelano & Branigan, P.C. 2200 Clarendon Boulevard, Suite 1400
                                                                                                                                                                                                            5 amino acids
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ilarity 100.0%;
Conservative (
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Pred. No.
                                                   Score 28; DB 2; I
Pred. No. 2.5e+05;
; Mismatches 0;
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RESULT 14

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US-08-537-874-62
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Best Local Similarity
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                                                                                                                                                                                                                                                     Sequence 86, Application US/08448418 Patent No. 5837242
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                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Hollig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                  APPLICANT:
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LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: EP PCT/US95/02126
FILING DATE: 17-FEB-1995
APPLICATION UNMBER: US 08/198,431
FILING DATE: 17-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                    APPLICANT:
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                                              TITLE OF INVENTION: Multivaler TITLE OF INVENTION: Proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: not
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Prospero, Terence D
Winter, Gregory P
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                                                                                                                                  Marks, James D
McGuinness, Brian T
                                                                                                                                                                   Hoogenboom, Hendricus RJM
Malmqvist, Magnus
                                                                                                                                                                                                       Holliger, Kaspar-Philipp
Griffiths, Andrew D
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Marshall O'Toole Gerstein Murray and Borun
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                                                Multivalent and Multispecific Binding Proteins, Their Manufacture and Use
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Pred. No.
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6300 Sears Tower 233 South Wacker Drive

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Best Local S
Matches 5
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MOLECULE TYPE: peptide linker
-08-448-418-86
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CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: C12N 15/62, 15/70, C
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02492
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9225453.1
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9300816.7
FILING DATE: 16-JAN-1993
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INFORMATION FOR SEQ ID NO: 86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: EP 93303614.
FILING DATE: 10-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9319969.3
FILING DATE: 22-SEP-1993
                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                    APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 141
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                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                CITY: New York
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                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                        10036-2711
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Y: U.S.A.
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US/08/471,939
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US-08-471-800-140
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TELECOMMUNICATION INFORMATION:
TELEPHONES 212 790-9090
TELEFAX: 212 869-8864/9741
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 140, Ap
Patent No. 58521
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Best Local Similarity
                                                                                        APPLICATION NUMBER: 08/013,416
PILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-999
TELEPAX: 212 869-8864/9741
TELEX: 66141 PENNIE
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APPLICANT: Kayles, D. M.

APPLICANT: Fowlkes, D. M.

APPLICANT: Fowlkes, D. M.

TITLE OF INVENTION: Totally Synthetic Affinity Reagents
                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 01-FEB-1
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0: FILING DATE: 06-JUN-1995 CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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STRANDEDNESS: sin
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STRANDEDNESS:
                   TYPE: amino acid
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                                       LENGTH:
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                                       5 amino acids
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; MOLECULE TYPE: peptide US-08-471-800-140
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Best Local Similarity
Watches 5; Conserva
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US-08-932-589-58
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US-08-647-449-26
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Best Local Similarity 100.
Thes 5; Conservative
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                                                                                     Sequence 26, Application US/08647449 Patent No. 5916794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,589
FILING DATE: 17-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/566800
FILING DATE: 12/04/95
FILING DATE: 12/04/95
ATTORNEY/AGENT INFORMATION:
NAME: KUDINEC, Jeffrey S.
REGISTRATION NUMBER: 36,575
REGISTRATION ONUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0958BD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                    GENERAL INFORMATION:
APPLICANT: Chandre
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 650/225-82:
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
SOFTWARE: WINPATION DATA:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lazarus, Robert A.
APPLICANT: Lee, Geoffrey F.
TITLE OF INVENTION: No. 5874407el Factor VIIa Inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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               Chandrasegaran, Srinivasan
VENTION: METHODS FOR INACTIVATING TARGET DNA
VENTION: FOR DETECTING CONFORMATIONAL CHANGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kelley, Robert F.
                                                                                                                                                                                                                                                                            Conservative
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100.0%; Pred. No. 2.5e+05;
ative 0; Mismatches 0;
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100.0%; Pred. No. 2.5e+05;
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                                                                                                                                                                                                                                                                                                          Length 5;
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                 IN A NUCLEIC ACID
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COUNTRY: USA
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,840
PTILING DATE: 21-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      맑
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US-08-821-840-1
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REFERENCE/DOCKET NUMBER: PNK/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEFX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5919456
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08821840 Patent No. 5919456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local &
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Puri, Raj K.
APPLICANT: Debinski, Waldemar
APPLICANT: Pastan, Ira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Kokulis, Paul N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,449
FILING DATE: 07-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: IL-13 Rec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W., NINTH FLOOR, STREET: TOWER CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 2005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
APPLICATION NUMBER:
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5; Conserva
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Obiri, Nicholas
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US 08/404,685
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: MATTHEAKIS, LARRY C.
APPLICANT: DOWER, WILLIAM J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
REFERENCE/DOCKET NUMBER: 16528X-003230US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
                                                                                                                                FILING LALL.
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US94/12206
APPLICATION NUMBER: PCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: DUNN, TRACY J.
NAME: DUNN, TRACY J.
NAME: DUNN, TRACY J.
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NAME: DUNN, TRACY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 17-JAN-1996
APPLICATION NUMBER: US 0:
                                                                                                                                                                                                                                                                                                           FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP STREET: TWO EMBARCADERO CENTER, 8TH FLOOR CITY: SAN FRANCISCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94111-3834
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                                                                                                                                                                                                                                                                   NUMBER: US 08/144,775
US 29-OCT-1993
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V: IN VITRO PEPTIDE AND ANTIBODY DISPLAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                            US 08/300,262
                                                                                                                                                                                                                                                                                                                                                                                                         US 08/586,176
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Pred. No. 2.5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5;
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US-08-471-068-140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-902-623-75
                                                                                                                              ; MOLECULE TYPE: US-08-471-068-140
                                                              Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                              TELEPHONE: 212 790-9090
TELEPAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 140
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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STATE: N.
COUNTRY: U.S...
COUNTRY: U.S...
TP: 10036-2711
TP: PRADABLE F
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/471, FILING DATE: CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/189,331
                                                                                                                                                                                                                                                                                                NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KAY, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                            LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1155 Avenue of the Americas
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                                                              100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                unknown
                                                                                                                                              peptide
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Pred. No. 2.5e+05;
); Mismatches 0;
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RESULT 23 US-08-308-494A-1

Sequence 1, Application US/08308494A Patent No. 5959083

SENERAL INFORMATION:

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Query Match
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                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/08665202
                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
"""" "YOUNGED. INC/08/108 4944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: DE P4118120.4
FILING DATE: 03-UN-1991
ATTORNEY_AGENT INFORMATION:
NAME: Kullk, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 05552-1186-02000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/308,494A FILING DATE: 21-SEP-1994 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/891,739 FILING DATE: 01-JUN-1992 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                       COUNTRY:
                                                                                              CITY: San Francisco
                                                                                                               STREET:
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                                                                                                                                     DDRESSEE:
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                                                                                                                                                                                                                                                                                     5977322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: peptide
                                                                           California
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E: Dunner
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seeman, Gerhard
                                                                                                               E: Townsend and Townsend and Crew LLP 
Two Embarcadero Center, Eighth Floor
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                                                           USA
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100.0%; Pred. No. 2.5e+05;
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Matches
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER: 38,498
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) $76-0200
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pastan, Ira
APPLICANT: Kuan, Chien-Tsun
APPLICANT: Kuan, Chien-Tsun
TITLE OF INVENTION: Immunotox:
TITLE OF INVENTION: Disulfide
TITLE OF INVENTION: Pseudomon
TITLE OF INVENTION: Activatio
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 25:
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SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,668
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FILING DATE: 13-OCT-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                              FILING DATE: 21-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94111-3834
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                                            13-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunotoxin Containing a
Disulfide-Stabilized Antibody Fragment Joined to a
Pseudomonas Exotoxin that Does No. 5980895 Require Proteolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 28; DB 2; 100.0%; Pred. No. 2.5e+05;
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    WO PCT/US96/16327
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US-08-792-553-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 38,347
REPERENCS/DOCKET NUMBER: 072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D
REGISTRATION NUMBER: 38,3
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tsien, Roger
APPLICANT: Heim, Roger
                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Tandem Fluorescent Protein Constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 4225 EX
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
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STRANDEDNESS:
                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hunter, Tom
                                                                                                                                                TOPOLOGY:
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                                                          Conservative
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                                                                                                                                                  linear
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                                                                                                                               peptide
                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 28; 100.0%; Pred. No.
                                                                       100.0%; Score 28; DB 2; 100.0%; Pred. No. 2.5e+05;
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                                                         Mismatches
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                                                                                    Length 5;
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                                                         Indels
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US-08-751-767A-24
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                                                                                                                                                                                                                                                         RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-751-767A-24
                                                                                                        Sequence 40, Application US/08818253
Patent No. 5998204
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: MIYAWAKI, Atsushi
TITLE OF INVENTION: FUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/08751767A Patent No. 5994104 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-BOSE #1.0, Version
CURRENT APPLICATION DATA: 08/751,767A
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: SADOFF, B.J.
REJETRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22201
COMPUTER READABLE FORM:
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APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                      NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..5
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide LOCATION: 1..5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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Pred. No. 2.5e+05;
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COUNTRY:

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US-08-722-258-54
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                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,258
FILING DATE: 08-JAN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/04468
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 54,
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OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,253
FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 619/678-5070
TELEPAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: linker moiety; sequence repeated indefinitely
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Circularly Permuted Ligands and TITLE OF INVENTION: Circularly Permuted Chimeric Mo. NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
NAME: Halle, NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kreitman, Robert J. APPLICANT: Puri, Raj K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                  APPLICATION NUMBER: US 08/225,224 FILING DATE: 08-APR-1994
                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
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; MOLECULE TYPE: peptide
US-08-722-258-54
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-09-397-951-12
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Patent No.
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Best Local Similarity
Matches 5; Conserv
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 54:
                                                                                                              TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO:
                                                                                                                                  APPLICANT: KUAN, Chi-
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397,951
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REFERENCE/DOCKET NUMBER: 011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                            APPLICATION NUMBER: 08/809,668
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16327
FILING DATE: 11-OCT-1996
ATTORNEY/AGENT IMPORMATION:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,70
                                              STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
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ilarity 100.0%;
Conservative C
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Kuan, Chien-Tsun
               peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunotoxin Containing a Disulfide-Stabilized Antibody Fragment Joined to a Pseudomonas Exotoxin that Does No. 6074644 Require Proteolytic Activation
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Pred. No. 2.5e+05;
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Best Local Similarity
Marches 5; Conserv
                                          RESULT 32
US-08-621-859-64
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US-08-776-271-3
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                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-776-271-3
             Sequence 64, Application US/08621859 Patent No. 6117679
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conser
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/
FILING DATE: 05-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: FILING DATE: 05-JAN-1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pastan, Ira
APPLICANT: Chang, Kai
TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 01-DEC
                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                            GGGGS
                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                    100.0%; Score 28; DB 3; 100.0%; Pred. No. 2.5e+05;
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Pred. No. 2.5e+05;
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US-09-100-856A-62
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                                                                                                                                                                      Sequence 62, Application US/09100856A Patent No. 6132970 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 64:
                                                                        APPLICANT: Stemmer, Willem P.C.
APPLICANT: Crameri, Andreas
TITLE OP INVENTION: DNA Mutagenesis by Random Fragmentation
TITLE OP INVENTION: and Reassembly
NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/621,859 FILING DATE: 25-MAR-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Libbeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/02126
FILING DATE: 17-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,431
FILING DATE: 17-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 30-CCT-1995
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APPLICATION NUMBER:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                    ADDRESSEE:
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SEE: Townsend and Townsend and Crew LLP : Two Embarcadero Center, 8th Floor San Francisco
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Two Embarcadero Center, Eighth Floor
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Crameri, Andreas M.
VENTION: Methods for Generating Polynucleotides
VENTION: Having Desired Characteristics by Iterative Selection
VENTION: Recombination
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Pred. No. 2.5e+05;
); Mismatches 0;
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                                                COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOPTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/09/046,992
FILING DATE: 24-MAR-1998
CLASSIFICATION: 435
CRASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018097-014610
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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APPLICATION NUMBER: US 08
FILING DATE: 17-FEB-1994
ATTORNEY/AGENT INFORMATION:
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APPLICANT: Yarkoni,
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ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M
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nes 5; Conserv
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STATE: NY
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                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2811
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US-09-215-035-3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 05-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
                                                                                                                                                                                   TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: I
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 700 TELECOMMUNICATION INFORMATION: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 01-DEC-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PAPPLICATION NUMBER: WO PAPP
                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
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APPLICANT: Chang, Kai
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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STRANDEDNESS: sin
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CITY: San Francisco
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                                                                        STRANDEDNESS
                                                                                                              TYPE: amino acid
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                                                                                                                                                        5 amino acids
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Present on Mesothelium, Mesotheliomas and Ovarian Cancers
and Methods and Kits for Targeting the Antigen
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Query Match
Best Local Similarity
Matches 5; Conserva
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                                                                                                            US-09-075-511-64
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                                          Matches
                                                          Query Match
Best Local (
                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 0180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/621,859
FILING DATE: 25-MAR-1996
APPLICATION NUMBER: US 08/564,955
FILING DATE: 30-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/537,874
FILING DATE: 30-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/02126
FILING DATE: 17-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 17-FEB-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                         Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                                                                 NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                              STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
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6165793
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Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                              5 amino acids
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                                                                                                                           peptide
                                                          100.0%;
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Methods for Generating Polynucleotides
Methods for Generating Polynucleotides
Having Desired Characteristics by Iterative Selection and
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                                                                                                                                                                                                                                                                                                                                                                                      US 08/198,431
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                                                       Score 28; DB 3;
Pred. No. 2.5e+05;
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                                          Mismatches
                                                                         Length 5;
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RESULT 38
US-08-818-252-40
; Sequence 40, Application US/08818252B
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Query Match
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US/08/621,859
FILING DATE: 25-MAR-1996
APPLICATION NIMBER: US 08/564,955
FILING DATE: 30-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NIMBER: US 08/537,874
FILING DATE: 30-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NIMBER: WO PCT/US95/021
PRIOR APPLICATION UNMBER: WO PCT/US95/021
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 17-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,431
FILING DATE: 17-FEB-1994
ATTORNEY/AGENT INFORMATION:
NUMBER: 15-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIE: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: PATENTIA Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stemmer, Willem P.C. APPLICANT: Crameri, Andreas M.
                                                                                                                                                                                                                                                                                                                                                            NAME: Liebeschuetz, Joe REGISTRATION NUMBER: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/099,015 FILING DATE:
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CITY: San Francisco
                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
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Two Embarcadero Center, Eighth Floor
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                                       Conservative
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                                                        100.0%;
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Methods for Generating Polynucleotides
Having Desired Characteristics by Iterative Selection and
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                                     Score 28; DB 3;
Pred. No. 2.5e+05;
Mismatches 0;
                                                                          Length 5;
                                       Indels
                                       0,
                                       Gaps
                                       0
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APPLICANT: Anthony Cahill, Spencer J.
APPLICANT: Epp, Janet K
APPLICANT: Epp, Janet K
APPLICANT: Kerwin, Bruce A.
APPLICANT: Mathews J., Antony
TITLE OF INVENTION: GLOSINS CONTAINING BINDING DOMAINS
FILE REFERENCE: EXTB2005
CURRENT APPLICATION NUMBER: US/09/091,814
CURRENT FILING DAYE: 1998-06-22
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: TSien, Roger Y.
APPLICANT: Hydwaki, Atsushi
ITITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
ITITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/08/818,2528
CURRENT FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 40
                                                                                                                                                                                  RESULT 40
US-09-281-792B-26
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Tatches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence:Amino Acid; OTHER INFORMATION: Linker US-09-091-814-1
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US-09-091-814-1
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US-08-818-252-40
                                                               Sequence 26, Application US/09281792B
Patent NO. 6265196
GENERAL INFORMATION:
APPLICANT: Chandrasegaran, Srinivasan
APPLICANT: Chandrasegaran, Srinivasan
TITLE OF INVENTION: METHODS FOR INACTIVATION TARGET DNA AND
FOR DETECTING CONFORMATIONAL CHANGE IN A NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application Patent No. 6218513
GENERAL INFORMATION:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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les 5; Conservative
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: VENABLE, BAETJER, HOWARD & CIVILETTI, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGGGS 5
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Pred. No. 2.5e+05;
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Pred. No.
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Search completed: December 11, 2003, 09:59:52 Job time : 9.4 secs

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Query Match
Best Local Similarity
Tatches 5; Conserv:
                                                                                                                  US-09-281-792B-26
                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/281,792B
FILING DATE: 31-Mar-1999
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORWATION:
NAME: Hobbs, Ann S.
REGISTRATION NUMBER: 36,830
REFERENCE,DOCKET NUMBER: 36595160594
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4800
TELEPAX: 202-962-4800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                MOLECULE TYPE: peptide SEQ ID NO: 26:
1 66668
                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                               LENGTH: 5 amino acids
                                      Conservative
                                                        100.0%;
                                      0; Mismatches
                                                      Score 28; DB 3; 1
Pred. No. 2.5e+05;
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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 2000000000
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Match Length
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                      1000.
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/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOME.pep:*
/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOME.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOME.pep:*
/cgn2_6/ptodata/1/pubpaa/US10E_PUBCOME.pep:*
/cgn2_6/ptodata/1/pubpaa/US10E_PUBCOME.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOME.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCT_N
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-6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
-6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
-6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
-6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
-6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
6/ptodata/1/pubpaa/US09A PUBCOMB.pep:
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                                US-09-287-849-44
US-09-147-142-31
US-09-144-645-1
US-09-858-616-2
US-09-989-789-3
US-09-976-787-2
US-09-976-787-2
US-09-976-787-2
US-09-976-787-3
US-09-976-787-180
US-09-976-962-36
US-09-333-527-5
US-09-333-527-5
US-09-333-527-6
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                                                Sequence 44, Appl
Sequence 31, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 45, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 51, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 5, Appl
Sequence 6, Appl
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Sequence 346, App	e 42,	44,	e 19,	e 81,	e 32,	e 47,	e 84,	e 84, App	e 23		œ	ω	e 21	e 2,	e 1,	e 40	æ	е 8,		4	14	Sequence 3, Appli	12:	е 6,	e 1	e 22	e ω,	equence 10, App	Sequence 25, Appl

ALIGNMENTS

RESULT 1 US-09-287-849-44

Sequence 44, Application US/09287849 Patent No. US20020009459A1

GENERAL INFORMATION:
APPLICANT: Reed, S
APPLICANT: Skeiky,

Reed, Steven G.

APPLICANT:
APPLICANT:

Skeiky, Yasır Dillon, Davin

Yasir A.W. Davin C.

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APPLICANT: COTIXA Corporation
ITILE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
ITILE OF INVENTION: and Their Uses
ITILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 199-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1

LENGTH: 6
                                                        US-09-287-849-44
Query Match
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                                                                                   OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                              FEATURE:
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                                                                                Description of Artificial Sequence:flexible polylinker
  100.0%; Score 28;
  DВ
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Length 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-147-142-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-214-645-1
                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: linker peptide
US-09-214-645-1
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 1999-09-27;
PRIOR APPLICATION NUMBER: PCT/US97/12239
PRIOR FILING DATE: 1997-07-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 5
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Best Local Similarity
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APPLICANT: ATWELL, John Leslie
TITLE OF INVENTION: HIGH AVIDITY POLYVALENT AND POLYSPECIFIC REAGENTS
FILE REFERENCE: 016786/0212
CURRENT APPLICATION NUMBER: US/09/147,142
CURRENT FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: PCT/AU98/00212
EARLIER APPLICATION NUMBER: PCT/AU98/00212
EARLIER FILING DATE: 1998-03-26
EARLIER FILING DATE: 1998-03-27
ROBERT APPLICATION NUMBER: AU PO 5917
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TITLE OF INVENTION: METHOD OF DNA SHUEPLING WITH
TITLE OF INVENTION: POLYNUCLECTIDES PRODUCED BY BLOCKING OR INTERRUPTING A
TITLE OF INVENTION: SYNTHESIS OR AMPLIFICATION PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HUDSON, Peter John APPLICANT: KORTT, Alex Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/214,645
CURRENT FILING DATE: 1999-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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                                                      Score 28; DB y; L
Pred. No. 6.2e+05;
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; Mismatches
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ches 0;
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; Sequence 45, Application U
; Patent No. US20020045158A1
; GENERAL INFORMATION:
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                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: linker US-09-779-233-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/858,616
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US 09/571,499
PRIOR FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: US 09/557,276
PRIOR FILING DATE: 2000-04-24
PRIOR APPLICATION NUMBER: US 08/692,002
PRIOR FILING DATE: 1996-08-02
PRIOR FILING DATE: 1996-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09858616
Patent No. US20020031771A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
TITLE OF INVENTION: SEQUENCE BASED SCREENING
FILE REFERENCE: DIVER1210-6
                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45
LENGTH: 5
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Best Local Similarity
                                     Matches
                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Case, Casey
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFERENCE: 8325-0010
                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
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PRIOR FILING DATE: 1995-12-07
PRIOR APPLICATION NUMBER: US 08/944,795
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TYPE: PRT
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                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                           TYPE: PRT
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                                                     100.0%; Score 28; DB 9; 100.0%; Pred. No. 6.2e+05;
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Pred. No. 6.2e+05;
); Mismatches 0;
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US-09-192-854-180
; Sequence 180, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVESTION: Methods for Select
; FILE REFERENCE: 3789/72916
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                                                                                                                                                     RESULT 8
                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: peptide linker US-09-976-787-21
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Patent No. US20020063379A1

GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect 8.0 for Windows SEQ ID NO 21
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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LENGTH: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR PILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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nes 5; Conserv
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                   for Selecting Functional Peptides
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Pred. No.
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RESULT 10
US-09-333-527-5
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US-09-761-962-36
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CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/743,872
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin version 3.0
SEQ ID NO 36
LENGTH: 5
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APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: Identification and Characterization
TITLE OF INVENTION: Variants of Mu-
TITLE OF INVENTION: opioid Receptor (MOR-1) Gene
FILE REFERENCE: 830002-2000.1
                                                                                                                                                                                                                                        Sequence 5, Application US/09333527 Patent No. US20020078472A1
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CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 180
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APPLICANT: Paul C
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: basic unit of a linking peptide
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                                                                                                                                    NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                              APPLICANT: Paul CHRISTOU; Eva STROGER; Rainer FISCHER; Carmen MARTIN-VAQUERO; Stef
TITLE OF INVENTION: METHODS AND MEANS FOR EXPRESSION OF MAMMALIAN POLYPEPTIDES
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 100.0%; Score 28; DB 9; Local Similarity 100.0%; Pred. No. 6.2e+05;
                                                                        ADDRESSEE: Fulbright & Jaworski L.L.P
STREET: 666 Fifth Avenue
CITY: New York City
                                  COUNTRY: USA
                                                           STATE:
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                                                         New York
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MEDIUM TYPE:

Diskette, 3.25 inch, 1.44mb

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Query Match
Best Local Similarity
Watches 5; Conserv:
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RESULT 12
US-09-815-837-116
US-09-815-837-116
; Sequence 116, Application US/09815837
; Patent No. US20020082411A1
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Patent No. US20020081614A1
GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 8
                                                                                                                                                                                       Matches
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APPLICANT: Zhang, Lei
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Functional Genomics Using Zinc Finger Proteins
FILE REFERENCE: 019496-002000US
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: US/09/925,796
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/395,448
PRIOR PILING DATE: 1999-09-14
PRIOR APPLICATION NUMBER: 09/229,037
PRIOR APPLICATION NUMBER: 09/229,037
PRIOR FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 23
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                  LENGTH: 5
TYPE: PRT
TYPE: PRT
ORGANISM: Artificial Sequence
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REFERENCE/DOCKET NUMBER: KL/JIC 202.1 -
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/089
FILING DATE: June 15, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
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5; Conserv
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Pred. No. 6.2e+05;
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Pred. No. 6.2e+05;
); Mismatches 0;
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APPLICANT: COTIXA COrporation
TITLE OF INVENTION: Immune Medators and Related Methods
FILE REFERENCE: 014058-005670US
CURRENT APPLICATION NUMBER: US/09/815,837
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 60/191,274
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: US 60/204,249
PRIOR APPLICATION NUMBER: US 60/204,049
PRIOR APPLICATION NUMBER: US 60/204,003
PRIOR FILING DATE: 2000-05-15
PRIOR FILING DATE: 2001-01-23
NUMBER: OF 60/264,003
PRIOR FILING DATE: 2001-01-23
NUMBER: OF SEQ ID NOS: 129
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US-09-815-837-116
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                                                                                                                                                             OTHER INFORMATION: Flexible polylinker US-09-033-525-5
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                                                                              Best Loc
Matches
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                                                                                                                       Query Match
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Best Local Similarity
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APPLICANT: Belotstotaky, Ruth
APPLICANT: Lorberboum-Galski, Haya
APPLICANT: Lorberboum-Galski, Haya
TITLE OF INVENTION: CHIMERIC PROTEINS WITH CELL-TARGETING
TITLE OF INVENTION: SPECIFICITY AND APOPTOSIS-INDUCING ACT
TILE REFERENCE: 9457-009-999
CURRENT FALLING DATE: 1998-03-02
CURRENT FILLING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 10
SOFTMARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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  GGGGS 5
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Arimilli, Subhashini
Wang, Aijun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Azar, Yehudith
                                                                        100.0%; Score 28; DB 9; ilarity 100.0%; Pred. No. 6.2e+05; Conservative 0; Mismatches n.
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RESULT 14 US-09-779-451-7

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APPLICANT: Case, Casey C.

APPLICANT: Urnov, Fyodor

TITLE OF INVENTION: GENE IDENTIFICATION

FILE REFERENCE: $7.03 / 8325-0007.20

CURRENT APPLICATION NUMBER: US/09/941,450

CURRENT FILING DATE: 2001-08-28

PRIOR APPLICATION NUMBER: 09/395,448

PRIOR PRILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 8
RESULT 16
US-09-918-247-25
; Sequence 25, Application US/09818247
; Patent No. US20020102657A1
; GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence:linker
US-09-941-450-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/779,451
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/235,901
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/181,543
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09941450 Patent No. US20020094529A1
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TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
FILE REFERENCE: 1900.0300003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wild, Carl T.
APPLICANT: Allaway, Gra
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: REPEAT
LOCATION: (1)..(5)
OTHER INFORMATION: (GGGGS)x, where x is 1, 2, 3,
NAME/KEY: misc_feature
OTHER INFORMATION: Preferred amino acid residues
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ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 6.2e+05;
); Mismatches 0;
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US-09-883-777-10
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CURRENT APPLICATION NUMBER: US/09/818,247
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: WD PCT/US01/09699
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/192,197
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/192,198
PRIOR APPLICATION NUMBER: US 60/192,198
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/883,777
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/172,878
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: US 60/203,347
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: PCT/US00/34755
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/742,454
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
                                                                                                          Query Match
Best Local
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SEQ ID NO 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: TWEAK RECEPTOR FILE REFERENCE: 2968-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chapin, Steven J.
APPLICANT: Richman-Eisenstat, Janice
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Secretory Component,
TITLE OF INVENTION: No. US20020102657A1-Stalk Region of plgR and Methods of Use Ther
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wiley, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mostov, Keith
                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: Description of Artificial Sequence:peptide linker
                                                                                                                                                                                                                                                                  TYPE: PRT
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GGGGS 5
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                                                                                   100.0%; Score 28; DB 10;
100.0%; Pred. No. 6.2e+05;
tive 0; Mismatches 0;
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Pred. No. 6.2e+05;
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                                                                                                                            Length 5;
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RESULT 18 US-09-867-262-3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-780-933-22
                                          CURRENT APPLICATION NUMBER: US/09/780,933
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: PA 2000 00220
PRIOR APPLICATION NUMBER: 60/184,035
PRIOR APPLICATION NUMBER: 60/184,035
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/225,558
PRIOR APPLICATION NUMBER: 60/225,558
PRIOR APPLICATION NUMBER: 60/225,558
PRIOR FILING DATE: 2000-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/09780933 Patent No. US20020127652A1
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Best Local (
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APPLICANT: FREY, Gerhard
TITLE OF INVENTION: END SELECTION IN DIRECTED EVOLUTION
FILE REFERENCE: DEVER1460-17
CURRENT APPLICATION NUMBER: US/09/867,262
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 09/267,118
PRIOR APPLICATION NUMBER: US 09/267,118
PRIOR APPLICATION NUMBER: US 09/267,178
PRIOR APPLICATION NUMBER: US 09/246,178
PRIOR APPLICATION NUMBER: US 09/246,178
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-04
                                                                                                                                                                                                                                                                                                                       APPLICANT: SCHAMBYE, HANS T.
APPLICANT: ANDERSEN, KIM V.
APPLICANT: VAN DEN HAZEL, BART
APPLICANT: CHRISTIANSEN, JESPER
APPLICANT: JEPESENT, CLAUS B.
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
FILE REFERENCE: 31-001000US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: US 08/677,112
PRIOR FILING DATE: 1996-07-09
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PRIOR FILING DATE: 1996-12-05
PRIOR APPLICATION NUMBER: US 60/008,311
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SOFTWARE: PatentIn version 3.0
                         NUMBER OF SEQ ID NOS: 30
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ORGANISM: Artificial sequence
FEATURE:
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les 5; Conserv
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5. US20020119457A1
Patentin
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US-09-731-558-6
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Best Local Similarity
Matches 5; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09731558 Patent No. US20020146691A1
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                                                                                                                                     SEQ ID NO 6
                                                                                                                                                                      APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Liu, Qiang
APPLICANT: Rebar, Edward J.
APPLICANT: Sangamo Biosciences, Inc.
APPLICANTON: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Methods of Using Randomized Libraries of Gene Function
FILE REFERENCE: 019496-003210US
CURRENT APPLICATION NUMBER: US/09/731,558
CURRENT FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
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APPLICANT: Lake, Philip
APPLICANT: Wright, Richard M.
TITLE OF INVENTION: Anti-CD3 Immu
FILE REFERENCE: CGC 4-31157A/USN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/480,236
CURRENT FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 22
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OTHER INFORMATION: Description OTHER INFORMATION: peptide
                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1
                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: peptide linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
OTHER INFORMATION: Description OTHER INFORMATION: linker
                                             FEATURE:
                                                                                                             ENGTH:
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Pred. No. 6.2
0; Mismatches
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                       of Artificial Sequence:polypeptide
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6.2e+05;
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APPLICANT: DJAVAKHISHVILI, TSOTHE

APPLICANT: FREY, Gerhard

TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN

TITLE OF INVENTION: DIRECTED EVOLUTION

FILE REFERENCE: DIVERL460-14

CURRENT APPLICATION NUMBER: US/09/885,551A

CURRENT FILING DATE: 2001-06-19

FRIOR APPLICATION NUMBER: US/09/535,754

PRIOR APPLICATION NUMBER: US/09/535,754

PRIOR APPLICATION NUMBER: US/09/535,754

PRIOR FILING DATE: 2000-03-27

PRIOR FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.0

SEQ ID NO 3
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Best Local Similarity
Matches 5; Conserve
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US-09-828-708-123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 123
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 123, Application US/09828708 Patent No. US20020146753A1
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Best Local :
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PEATURE:
OTHER INFORMATION: Antibody spacer peptide.
OTHER INFORMATION: can be repe
OTHER INFORMATION: ated more than one time
-09-885-551A-3
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TITLE OF INVENTION: autoimmune disease
FILE REFERENCE: 1361.005US1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                       ORGANISM: Artificial sequence
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Schaller, M.
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100.0%; Pred. No. 6.2e+05;
ative 0; Mismatches 0;
                                                             The entire peptide sequence
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APPLICANT: Chernajovsky, Yuti
APPLICANT: Dreja, Hanna Stina
APPLICANT: Adams, Gillian
TITLE OF INVENTION: Latent Fusion Protein
FILE REFERENCE: 0623.1000000
CURRENT APPLICATION UNMBER: US/09/756,283A
CURRENT FILING DATE: 2001-01-09
UNMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
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Sequence 4, Application US/09144886
Patent No. US20020155114A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                            APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
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Best Local Similarity
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Best Local &
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Best Local Similarity
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                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Gly4Ser linker
                                                                                                                                                              FEATURE:
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                                                                               Local Similarity
                              1 GGGGS 5
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                                                             100.0%; Score 28; DB 10; llarity 100.0%; Pred. No. 6.2e+05; Conservative 0; Mismatches 0;
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Pred. No.
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Pred. No. 6.2e+05;
D; Mismatches 0;
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. 6.2e+05;
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RESULT 26 US-09-999-745-56

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Application US/09999745

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                                                   RESULT 28
US-09-942-090-8
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; OTHER INFORMATION: Description of Artificial Sequence:linker
US-09-942-087A-8
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Sequence 8, Application US/09942090 Patent No. US20020164575A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US, Patent No. US20020160940A1
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Best Local
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CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/316,920
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gregory, Philip
TITLE OF INVENTION: MODULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
FILE REFERENCE: 8325-0002.21 / S2-US5
CURRENT APPLICATION NUMBER: US/09/942,087A
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/229,037
PRIOR FILING DATE: 1999-01-12
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APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                  Similarity
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Greqory, Philip
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Urnov, Fyodor
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                                                                                                                                                                                                 Conservative
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Pred. No. 6.2e+05;
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Pred. No. 6.2e+05;
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Query Match
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                                                          Sequence 1, Application US/09792793A Patent No. US20020168370A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 5; Conserv
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TITLE OF INVENTION: Functional Genomics Using Zinc Finger Proteins
FILE REFERENCE: 019495-002000US
CURRENT APPLICATION NUMBER: US/09/942,090
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/395,448
PRIOR FILING DATE: 1999-09-14
PRIOR FILING DATE: 1999-09-14
PRIOR PHILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
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PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/09/554,000
CURRENT FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS
TITLE OF INVENTION: DETECTION OF ANALYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. :
APPLICANT: McDonald, John R.
APPLICANT: Coggins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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OTHER INFORMATION: Linker moiety; sequence repeated indefinitely
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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Pred. No. 6.2e+05;
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Pred. No. 6.2e+05;
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; NAME/KEY: REPEAT
; LOCATION: (1)...(5)
; OTHER INFORMATION: peptide linker for use in conjugates
US-09-792-793A-2
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US-09-846-033B-212
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                                                                                                                                                                           Sequence 212, Application US/09846033B
Publication No. US20030044404A1
GENERAL INFORMATION:
APPLICANT: Rebar, Edward
APPLICANT: Jamieson, Andrew
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Best Local Similarity
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Best Local Similarity
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APPLICANT: COSGINS, Philip
TITLE OF INVENTION: MCTHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT FILING DATE: 2501-02-22
RUMBER OF SEQ 1D NOS: 93
           APPLICANT: Liu, Pei-Qi
APPLICANT: Wolffe, Alan
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Jarvis, Eric
APPLICANT: Jarvis, Eric
TITLE OF INVENTION: Regulation of Angiogenesis
TITLE OF INVENTION: Finger Proteins
FILE REFERENCE: 019496-005820US
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
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                                                                                                                                                              APPLICANT:
CURRENT APPLICATION NUMBER: US/09/846,033B
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TYPE: PRT
ORGANISM: homo sapien
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Liu, Pei-Qi
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Pred. No. 6.2e+05;
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APPLICANT: Cox III, George No. US20030087817A1bert
APPLICANT: Case, Casey Christopher
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Jarvis, Eric Edward
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Exp.
TITLE OF INVENTION: Zinc Finger Proteins
FILE REFERENCE: 019496-002200US
CURRENT APPLICATION NUMBER: US/09/897,844
CURRENT FILING DATE: 1909-01-02
PRIOR APPLICATION NUMBER: 09/229,037
PRIOR FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
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US-09-990-186-3
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Publication No. US20030068675A1
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / S11-US3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
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Matches
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Publication No. US20030087817A1
GENERAL INFORMATION:
APPLICANT: Cox III, George No. US20
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Best Local Similarity
Matches 5; Conser
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PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-12
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Pred. No. 6.2e+05;
); Mismatches 0;
                                                                                                                                                           Gene Expression in Cells Using
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FILE REFERENCE: 109845,135
CURRENT APPLICATION NUMBER: US/09/911,261A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/220,060
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
LENGTH: 5
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US-09-911-261A-23
; Sequence 23, Application US/09911261A
; Publication No. US20030134350A1
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                                                                   ; OTHER INFORMATION: Flexible linker US-09-911-261A-23
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Publication No. US20030104526A1
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,994
CURRENT APPLICATION NUMBER: US/09/989,994
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
Query Match
Best Local S
Matches 5
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Matches
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APPLICANT: Sera, Takashi
TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
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Matches 5; Conserv
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ORGANISM: Artificial Sequence
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                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: peptide linker
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Pred. No. 6.2e+05;
Score 28; DB 12;
Pred. No. 6.2e+05;
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US-09-942-024-84
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US-09-942-098-84
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APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays Fo-
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
                                                                                                                                OTHER INFORMATION: synthetic construct US-09-942-098-84
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Best Local S
Matches 5
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Best Local S
Matches 5
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Publication No. US20030143650A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 84 LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 84
                                                                                                                                                                                                                                                               TITLE OF INVENTION: Fret Protease Assays
TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Steward, Lance E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                TYPE: PRI
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                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                   FEATURE:
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Aoki, Kei Roger
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                                                                  Conservative
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                                                                               100.0%;
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                                                                Score 28; DB
Pred. No. 6.2
0; Mismatches
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RESULT 39 US-10-244-821-47 ; Sequence 47, Application US/10244821

Publication No. US20030143233A1 GENERAL INFORMATION:

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; OTHER INFORMATION: linker sequence
US-10-262-630-32
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                                Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Filikov, Anton
APPLICANT: Muchhal, Umesh
APPLICANT: Tansey, Malu Lourdas G.
APPLICANT: Zalevsky, Jonathan
TITLE OF INVENTION: PROTEIN BASED THE THE TREATMENT OF THE TREATMENT OF THE THEATMENT OF THE ALAPED DISORDERS
FILE REFERENCE: A-68990-4/RET/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/262,630
CURRENT FILING DATE: 2003-01-27
CURRENT FILING DATE: 2003-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/186,427
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 09/945,150
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 09/798,789
PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reno, John M.
APPLICANT: Dearstyne, Erica A.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THERBOF
FILB REFERENCE: 690022.547C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dahiyat, Bassil I.
APPLICANT: Desjarlais, John R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Goshorn, Stephen Charles
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Lin, Yukang
                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Gly Ser linker
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/981,289
                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                          ENGTH: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eeees 5
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                                  100.0%; Score 28; DB 12; ilarity 100.0%; Pred. No. 6.2e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                    2001-10-15
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Pred. No. 6.2e+05;
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Db 1 GGGGS 5

Search completed: December 11, 2003, 10:13:41 Job time : 19 secs

OLDER MAN TO HE HAS SHIP

9)

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Title:
Perfect score:
Sequence:
                                                                        Database :
                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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PIR 76:*
1: pir1:*
2: pir2:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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28
1 GGGGS 5
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                                                                                                                                                                                                                                                            283308 seqs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	თ	ر ت	4	w	2		No.	
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G75432	H69062	T30428	T16247	D86754	T04118	D83415	A81109	T07695	T35387	S28821	AC2391	S58673	G86252	JC4190	T02612	T25332	T49621	T48330	PQ0743	T32664	S19774	PC2047	T10550	E84686	MIEC77	H84489	A86333	S29113	ID	
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;	28	28	28	28	28	28	. 28	28	28	28	28	28	28	28	28	28
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;	155	152	150	149	148	148	145	145	144	144	144	140	139	136	136	135
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ALIGNMENTS	C86206	T04811	C86224	T23179	138881	846514	E84469	JQ1062	T34730	S35716	S04069	AC3088	C87544	T29282	T02870	S55647
	hypothetical prote	STIG1 protein homo	hypothetical prote	hypothetical prote	caudal-type homeot	puroindoline-b pre	probable glycine-r	glycine-rich prote	probable gas vesic .	glycine-rich prote	glycine-rich prote	hypothetical prote	hypothetical prote	hypothetical prote	globulin 2 precurs	hypothetical prote

Query Match 100.0%; Score 28; DB 2; Length 64; Best Local Similarity 100.0%; Pred. No. 2.1e+02;	A; Status: preliminary A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-64 <sto> A; Cross-references: GB: AE005172; NID: g8779001; PIDN: AAF79916.1; GSPDB: GN00141 C; Genetics: A; Map position: 1</sto>	Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rooney, T.; Rowley, D.; Sakano, H. Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, F. D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. quence and analysis of chromosome 1 of the plant Arabidopsis. number: A86141; MUID:21016719; PMID:11130712	RESULT 2 A86333 Apporthetical protein T20H2.25 - Arabidopsis thaliana hyporthetical protein T20H2.25 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C;Accession: A86333 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000	vative 0; Mismatc	3; DB 2; Length 37;	RESULT 1 \$29113 diptericin homolog - flesh fly (Sarcophaga peregrina) C;Species: Sarcophaga peregrina C;Species: Sarcophaga peregrina C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999 C;Accession: S29113 R;Ishikawa, M:; Kubo, T:; Natori, S. Biochem. J. 287, 573-578, 1992 A;Title: Purification and characterization of a diptericin homologue from Sarcoph A;Reference number: S29113; MUID: 93074996; PWID: 1445217
•		ykin, E.; Kim, C zi, R.; Marziali, Sun, H.; Tallon,	2001 nite, O.; Alonso, T.H.; Dewar, K.,			ay-1999 from Sarcophaga per

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A;Cross-references: EMML:X06417; NID:g41978; PIDN:CAA29725.1; PID:g41979 R;Li, Y.M.; Milne, J.C.; Madison, L.L.; Kolter, R.; Walsh, C.T. Science 274, 1188-1193, 1996 A;Title: From peptide precursors to oxazole and thiazole-containing peptide antibiotics: A;Reference number: A58368; MUID:97053605; PMID:8895467 A;Accession: A58368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M24253; NID:g341145; PIDN:AAA72741.1; PII R;Connell, N.; Han, Z.; Moreno, F.; Kolter, R. Mol. Microbiol. 1, 195-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201, 198-201
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J. Bacteriol. 171, 1126-1135, 1989
A;Title: DNA sequence, products, and transcriptional pattern A;Reference number: A32058; MUID:89123111; PMID:2644225
A;Accession: A32058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Bscherichia coli
C;Date: 30-Jun-1988 #sequence revision 01-Dec-1995 #text change 16-Jul-1999
C;Accession: A25219; A3058; I41099; A58368; S67977
R;Davagnino, J.; Herrero, M.; Furlong, D.; Moreno, F.; Kolter, R.
Proteins 1, 230-238, 1986
A;Title: The DNA replication inhibitor microcin B17 is a forty-three-amino-acid A;Reference number: A25219; MUID:88217867; PMID:3329729
A;Accession: A25219
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A; Residues: 1-66 <STO>
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Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Cess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Cess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Cess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Cess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.S.; C.S.; Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant 
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A; Residues: 1-69 < DAV >
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A;Residues: 1-14 <CON>
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A; Residues: 1-69 < GEN>
;Molecule type:
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;Map position: 2
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F;1-26/Domain: signal sequence #status predicted <SIG>F;27-68/Product: microcin B17 #status experimental <MAT>F;27-68/Product: microcin B17 #status experimental <mAT>F;39-40/Cross-link: cxazole (Gly-Ser) #status experimental F;40-41/Cross-link: thiazole (Ser-Cys) #status experimental F;47-48/Cross-link: thiazole (Gly-Cys) #status experimental F;50-51/Cross-link: thiazole (Gly-Cys) #status experimental F;54-55/Cross-link: thiazole (Gly-Cys) #status experimental F;55-65/Cross-link: cxazole (Gly-Ser) #status experimental F;51-62/Cross-link: cxazole (Gly-Ser) #status experimental F;64-65/Cross-link: cxazole (Gly-Ser) #status experimental
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A;Accession: $67977
A;Atatus: preliminary
A;Molecule type: protein
A;Residues: 27-38 <BAY>
C;Genetics:
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A;Note: mass spectroscopy of peptides and biosynthetic intermediates
A;Note: mass spectroscopy of peptides and biosynthetic intermediates
R;YOrgey, P.; Lee, J.; Koerdel, J.; Vivosas, E.; Warner, P.; Jebaratnam, D.; Kolter, R.
Proc. Natl. Acad. Sci. U.S.A. 91, 4519-4523, 1994
A;Title: Posttranslational modifications in microcin B17 define an additional class of
A;Reference number: A58375; WIID:94240167; PMID:8183941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, Leuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Censer, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Censer, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.M.; Vent
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A;Genome: plasmid pMccB17
C;Function:
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Nature 402, 761-768,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein At2g28570 (imported) - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change
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C;Keywords: antibiotic; DNA replication inhibitor; oxazole/thiazole ring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-78 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                   A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: E84686
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                                                                                               Matches
                                                                                                                                            Best
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                          Gene: At2g28570
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                                                                                          Score 28; DB
Pred. No. 2.5
); Mismatches
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Pred. No. 2.2e+02;
, Mismatches 0;
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                                                                                                                                            2.5e+02;
                                                                                                                                                                                              DB 2;
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                                                                                                                                                                                    Length 78
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RESULT 8
S19774
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submitted to the EMBL Data Library, May 1991
a Reference number: S19773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 1-18;19-24;25-31;32-38;39-45;46-51;52-56;57-60;61-65;66-71;72-77;78-81 <UCL
C;Comment: This protein is the product of the Ha locus and thus be the major factor tha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Triticum aestivum (common wheat)
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change
C;Accession: PC2047
                                                                                                                                                                                                                                                            glycine-rich protein - tomato (fragment)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-dun-1992 #sequence_revision 30-dun-1992
C;Accession: S19774
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Theor. Appl. Genet. 86, 589-597, 1993
A;Title: Characterisation of the wheat Mr 15000 grain-softness
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A;Experimental source: cultivar Columbia; BAC clone T12G13
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A; Residues: 1-80 <BEV>
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A; Accession: T10550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T10550
                                                                                                         A;Cross-references: EMBL:X59883; NID:g19321; PIDN:CAA42538.1; PID:g19322 C;Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repea
                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-82 < PAR>
                                                                                                                                                                                     A; Reference number: A; Accession: S19774
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Best Local S
Matches 5
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;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :Keywords: seed
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                                                        Query Match
Best Local
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                                   Local Similarity
nes 5; Conserv
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                                                  Score 28; DB 2;
Pred. No. 2.6e+02;
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Pred. No. 2.5e+02;
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Pred. No.
                                     Mismatches
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                                                                        Length 82;
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RESULT 10
PQ0743
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R;Davidson, S.; Wohldmann, P.; Bauer, C.; O'Neal, D.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F16B4.
                                                                       C;Date: 20-Apr-2000 #sequence_revi
C;Accession: T48330
R;Bevan, M.; Terryn, N.; Ardiles,
ewes, H.W.; Rudd, S.; Lemcke, K.;
submitted to the Protein Sequence
                                                                                                                                                                                                           RESULT 11
T48330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            grain-softness protein - wheat (fragments)
C;Species: Triticum aestivum (common wheat)
C;Date: 19-May-1994 #sequence_revision 19-May-1994
C;Accession: P00743
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A;Introns: 36/1
C;Superfamily: Arabidopsis glycine-rich protein
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                                                                                                                                                                     hypothetical protein F15A17.120 - Arabidopsis tha C; Species: Arabidopsis thallana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: seed
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A;Accession: T32664
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                                     A; Reference number: A; Accession: T48330
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: seed
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Best Local (
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preliminary
e type: DNA
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                                                         Z24491
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                                                                         W.; Buysshaert, C.; Dasseville, Mayer, K.F.X.
Database, April 2000
                                                                                                                                                                                       Arabidopsis thaliana
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Pred. No.
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Pred. No. 2.8e+02;
Mismatches 0;
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                                                                                                                  R.; De Clerck,
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A;Residues: 1-97 <BEV>
A;Cross-references: EMBL:AL163002
A;Experimental source: cultivar Co
C;Genetics:
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A;Molecule type: DNA.
A;Residues: 1-100 <SCH>
A;Residues: 1-100 <SCH>
A;Cross-references: EMBL:AL355932; GSPDB:GN00116; NCSP:B5022.30
A;Cross-references: EMBL:AL355932; GSPDB:GN00116; NCSP:B5022.30
A;Cross-references: EMBL:AL355932; GSPDB:GN00116; NCSP:B5022.30
                                                                                                                                                                                                                                                              R, Gardner, A.

R, Gardner, A.

submitted to the EMBL Data Library,

n.pafarence number: Z20017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 5
A; Introns: 7/1
A; Note: F15A17.120
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
T25332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: Z25022
A; Accession: T49621
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T49621
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                                                                                                                                                                                                                                                                                                                                  hypothetical protein T26H5.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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                                                                                                                                                                          A; Experimental source:
                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-102 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein B5022.30 [imported] - Neurospora crassa
                                                                                                                                                                                                                                         A; Status: preliminary; translated from
                                                                                                                                                                                                                                                         A; Reference number: A; Accession: T25332
                                                                                                                            , Map position: 5
                                                                                                                                                                               ;Cross-references: EMBL:Z82056; PIDN:CAB04855.1; GSPDB:GN00023; CESP:T26H5.4;Experimental source: clone T26H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene: NCSP: B5022.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000;Accession: T49621
                                                                                                                                            Gene: CESP:T26H5.4
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Best Local
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Best Local
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lly: hypothetical protein K01D12.8
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5; Conserv
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Pred. No.
                               Score 28; DB 2;
Pred. No. 3.1e+02;
Mismatches 0;
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Pred. No.
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3e+02;
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RiLee, S.Y.; Moon, H.J.; Kurata, S.; Natori, S.; Lee, B.L. Biol. Pharm. Bull. 18, 1049-1052, 1995
A;Title: Purification and cDNA cloning of an antifungal protein A;Reference number: JC4190; MUID:960737722; PMID:8535393
A;Accession: JC4190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AC004747; NID:g3413696; PID:g3413702
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; Vanhken, S.E.; Umayam, L.; Tallon, I
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhken, S.E.; Umayam, L.; Tallon, I
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein At2g26120 [imported] - Arabido N;Alternate names: hypothetical protein T19118.7 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Mar-1999 #sequence revision 24-Mar-1999 C;Accession: T02612; F84656 R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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A; Residues: 1-104 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-104 < ROU>
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A; Accession: T02612
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A;Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence
                                                                                                                                                    C;Keywords: hemolymph
F;1-20/Domain: signal sequence #status predicted
F;21-104/Product: holotricin 3 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: antifungal protein C;Species: Holotrichia diomphalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 49/3
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                                                                                                                                                                                                                               A;Cross-references: DDBJ:D13744; NID:g1088433; PIDN:BAA02889.1; PID:d1003394; PID:g17861
C;Comment: This protein is a Gly- and His-rich protein and a constitutive protein of lax
                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-104 <LEE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           holotricin 3 precursor - Holotrichia diomphalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: JC4190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Date: 04-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
                                                   Matches
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                                                                           100.0%;
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                                                Score 28; DE
Pred. No. 3.2
); Mismatches
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                                                                                                 Length 104;
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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome J. G.; Davis, R.W.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                         RNA-binding protein
C;Species: Anabaena
C;Date: 15-Feb-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          á
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M
DNA Res. 8, 205-213, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:D49424; NID:g1064776; PIDN:BAA08402.1; PID:d1008998; PID:g1064777 C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein F;1-68/Domain: ribonucleoprotein repeat homology <RRM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 23, 2161-2167, 1995
A;Title: A family of cold-regulated RNA-binding protein A;Reference number: S58673; MUID:95334368; PMID:7541909
A;Accession: S58673
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C; Superfamily:
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A; Residues: 1-108 <STO>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-109 <SAT>
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les 5; Conserv
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Pred. No. 3.3e+02;
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                       Sasamoto, S.; Watanabe, A.; Ya.; Yamada, M.; Yasuda, M.;
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Tabata, !
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A;Cross-references: EMBL:AL079348; PIDN:CAB45486.1;
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                              A; Reference number: Z21576
A; Accession: T35387
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                                                                                                                                                                                                     A; Molecule type: DNA
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                                                                ;Gene: SCOEDB:SC66T3.30c
;Superfamily: Escherichia coli ybaB protein
  Query Match
Best Local Similarity
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100.0%;

Score 28; Pred. No.

DB 2; 3.5e+02;

Length

GB/EMBL/DDBC

GSPDB:GN00070; SCOEDB:SC66T3.30c

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R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, submitted to the EMBL Data Library, June 1999
                                                           hypothetical protein SC66T3.30c - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: FlyBase:FBgn0005659
C;Superfamily: pointed protein, splice form 1; ets DNA-binding C;Keywords: DNA binding; nucleus; transcription factor F;28-109/Domain: ets DNA-binding domain homology <ETS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:M88474; NID:g157195; PIDN:AAA28451.1; C;Genetics:
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C;Species: Drosophila melanogaster
C;Date: 31-Dec1993 #sequence_revision 31-Dec-1993 #text_change 03-Nov-2000
C;Accession: $28821
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Matches
                                         Accession: T35387
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Best Local Similarity
Matches 5; Conserv
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Pred. No. 3.3
0; Mismatches
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Pred. No. 3.4e+02;
Mismatches 0
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                      J.; Barrell,
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R;Bevan, M.; Pohl, T.; Weizenegger, submitted to the Protein Sequence Da A;Reference number: Z16098
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                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R. A;Title: Complete genome sequence of Neisseria meningitidis serogroup A;Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eise; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
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A;Experimental source: cultivar Columbia; BAC clone F17N18
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A; Residues: 1-119 <B
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 22-Oct-1999
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                                       hypothetical
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ypornetical protein PA1842 [imported] - Pseudomonas aeruginosa;Species: Pseudomonas aeruginosa;Date: 15-Sep-2000 #sequence revision 15-Sep-2000 #ran-
                                                                                                                                                                                                                                                                              Superfamily: Neisseria
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;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
;Accession: A81109
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Introns: 5/2; 48/1
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Pred. No. 3.6
0; Mismatches
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                                                                                                                                                                                                       Score 28; DB 2;
Pred. No. 3.6e+02;
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A;Status: pressure Rype: DNA A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-122 <STO> A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; PID:g12723988; A;Cross-references: GB.AE005176; A;Cr
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C;Superfamily: mitochondrial
C;Keywords: mitochondrion
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A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1842
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A;Molecule type: DNA
A;Residues: 1-120 <STO>
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C;Date: 23-Mar-2001
C;Accession: D86754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, Genome Res. 11, 731-753, 2001
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Pred. No. 3.6e+02;
; Mismatches 0;
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K.R.; Kas,
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C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C:Accession: T16247
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               molybdenum transport protein ModA related protein - Methanobacterium thermoautotrophicum (;Speciles: Methanobacterium thermoautotrophicum C;Speciles: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C;Accession: H69062 R;Cacession: H69062 R;Cacession: H69062 R;Cales, C.; Lee, H.; Dubois, J.; Aldredge, T.; R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Sequence and analysis of the genome of a baculovirus A; Reference number: Z20836; MUID:99124785; PMID:9887315 A; Accession: T30428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein ORF80 - Lymantria dispar nuclear polyhedrosis virus
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: T16247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F35A5.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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A; Residues: 1-128 < KUZ>
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A; Residues: 1-125 <LEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, January 1996 A;Description: The sequence of C. elegans cosmid
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Matches
Qiu, D.; Spadafora, R.; Vicaire, R.; Wan
i, S.; Church, G.M.; Daniels, C.J.; Mao,
. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession:
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Pred. No. 3.7e+02;
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Pred. No.
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A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta A;Reference number: A69000; MUID:98037514; PMID:9371463 A;Accession: H69062
                                                              A,Cross-references: GB:U20824; NID:g695172; PIDN:AAC13840.1; PID:g695225 A,Note: the nucleotide sequence was submitted to the EMBL Data Library, C,Superfamily: ateline herpesvirus 3 hypothetical protein 52
                                                                                                                                                                                            R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783, Recession: S55647
                                                                                                                                                                                                                                                                                                               hypothetical protein 52 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 18-Nov-2002
C;Accession: $55647
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A;Accession: G75432
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Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein - Deinococcus radiodurans (strain c;Species: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #tex C;Accession: G75432
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                                                                                                                                A;Status: preliminary; nucleic acid
A;Molecule type: DNA
A;Residues: 1-135 <TEL>
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A;Experimental source: strain R1
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ilarity 100.0%;
Conservative 0
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Pred. No.
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Pred. No. 3.9e+02;
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PMID:7783207
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C;Gene: gb2
A;Gene: gb2
C;Superfamily: vicilin
C;Superfamily: seed; stora
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A;Accession: T02870
A;Status: preliminary; translated
A;Molecule type: mRNA
A;Residues: 1-136 <POS>
A;Cessidues: 1-136 <POS>
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C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 11-Jan-2000
C;Accession: T02870
C;Accession: T02870
R;Postma-Haarsma, A.D.; Verwoert, I.I.G.S.; Stronk, O.P.; Koster, J.; Lamers submitted to the EMBL Data Library, February 1998
hypothetical protein CC2380 [imported] - Caulobacter crescentus c;Species: Caulobacter crescentus c;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: C87544
C;Accession: C87544
C;Accession: C87544
C;Neierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, R;Nierman, W.C.; Feldblyum, T.V.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residue: 1-136 <DUZ>
A;Cross-references: EMBL:U58755; PIDN:AAB00696.1; GSPDB:GN00022; CESP:C34D4.11
A;Cross-rimental source: strain Bristol N2; clone C34D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Du, Z.; Le, T.T.

submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid C34D4
A;Reference number: Z20600
A;Accession: T29282
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Best Local Similarity
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T29282
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Best Local
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      Query Match
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A;Cross-references: EMBL:X14067; NID:gl8147; A;Note: the authors translated the codon ATC C;Superfamily: Arabidopsis glycine-rich prote C;Keywords: transmembrane
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87544
                                                                                                                                                                                                                                                 glycine-rich protein - red goosefoot
C;Species: Chenopodium rubrum (red goosefoot)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jul-2000
C;Accession: S04069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Atu4327 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-139 <STO>
A,Cross-references: GB:AE005673;
                                                                                                                                                                            R;Kaldenhoff, R.; Richter, G.
Nucletc Acids Res. 17, 2853, 1989
A;Title: Sequence of cDNA for a novel light-induced glycin-rich
A;Reference number: S04069; MUID:89240041; PMID:2717413
                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-144 <KAL>
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Score Pred.

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RESULT 36
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C;Species: Daucus carota (carrot)
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Ride Oliveira, D.B.; Seurinck, J.; Inze, D.; Van Montagu, M.; Botterman, J. Plant Cell 2, 427-436, 1990
A;Title: Differential expression of five Arabidopsis genes encoding glycine-rich protein A;Reference number: JQ1060; MUID:93044485; PMID:2152168
A;Accession: JQ1062
                                                                                                   glycine-rich protein 3 precursor - Arabidopsis thaliana (;Speckes: Arabidopsis thaliana (mouse-ear cress) C;Date: 31-Dec-1991 #sequence_revision 19-May-1994 #text_change 13-Jun-1997 C;Accession: JQ1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable gas vesicle synthesis protein gvpA - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 19-May-2000 C;Accession: T34730
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                                                                                                                                                                                                         RESULT 38
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A;Cross-references: EMBL:AL033505; PIDN:CAA22037.1; GSPDB:GN00070; SCOEDB:SC1E6.09
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A; Accession: T34730
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;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change;Accession: S35716
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Pred. No. 4.2e+02;
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Pred. No. 4.2e+02;
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puroindoline-b precursor - wheat
C;Species: Triticum aestivum (common wheat)
C;Date: 06-Feb-1995 #sequence_revision 06-F
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
C;Accession: E84469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-145/Product: glycine-rich protein 3 #status predicted <MAT>
F;59-100/Region: 7-residue repeats (G-G-G-G-[NR]-Y-Q)
                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-148 <GAU>
                                                                                                                                                                                                                                                                        A;Title: Triticum aestivum puroindolines, two basic cystine-rich seed proteins: cDNA seq A;Reference number: S46514; MUID:94272013; PMID:7516201
                                                                                                                                                                                                                                                                                                                        R; Gautier, M.F.; Aleman, M.E.; Guirao, A.; Marion, D.; Joudrier, Plant Mol. Biol. 25, 43-57, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S46514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           문. 왕
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C; Superfamily: Arabidopsis glycine-rich protein
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A; Residues: 1-145 < STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
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A;Experimental source: strain C24
C;Superfamily: Arabidopsis glycine-rich protein
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                                                                                                                                                                                  A;Cross-references: EMBL:X69912; NID:g509087; PIDN:CAA49537.1; PID:g509088
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                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S46514
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Matches
                                                                                                             Superfamily: glycinin;1-29/Domain: signal sequence #status predicted <SIG>;30-145/Product: puroindoline-a #status predicted <WAT>
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tive 0; Mismatches
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hes 0;
    4.4e+02;
hes 0;
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Conservative

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 Search completed: December 11, 2003, 09:58:54

 Job time : 9.4 secs

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Maximum DB
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Perfect score:
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SCX_CHICK
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GRP_DAUCA
TWS1_MOUSE
IM23_HUMAN
IM23_RAT
GRP2_NICSY
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ALIGNMENTS	US13_HCMVA	NAHB_PSEPU	EXB1_SYNY3	GRP1_PHAVU	EX12 ARATH	HMUX MUSDO	FLGH_BRUSU	FLGH BRUME	RTN3 MOUSE	RTN3_HUMAN	BRT1 RAT	GS28_DROME
	P09720 human cytom	Q52459 pseudomonas	Q55834 synechocyst	P10495 phaseolus v		Q25451 musca domes	Q8fxc2 brucella su		Q9es97 mus musculu	_	P55007 rattus norv	Q9ve50 drosophila

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AC P05834;
DT 01-NOV-1988 (
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P82617;
16-OCT-2001 (Rel. 40, Created).
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pyrokinin-5 (Pea-PK-5) (FXPRI-amide).
Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
NCBI TaxID=6978;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Comp. Neurol. 419:352-363 (2000).

-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
-!- MOTROPIC ACTIVITY: MAINLY IN ABDOMINAL PERISYMPATHETIC ORGANS .
-!- TISSUE SPECIFICITY: MAINLY IN ABDOMINAL PERISYMPATHETIC ORGANS .
-!- TO A LESSER EXTENT IN RETROCEREBRAL COMPLEX.
-!- MASS SPECTROMETRY: MW=1651.7; METHOD=MALDI.
-!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
InterPro; IPR001484; Pyrokinin.
PROSITE; P800539; PYROKININ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaedu "Differential distribution of pyrokinin-isoforms in cerebral and abdominal neurohemal organs of the American cockroach."; Insect Biochem. Mol. Biol. 29:139-144(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, FUNCTION, AND MASS SPECTROMETR'
TISSUE=Abdominal perisympathetic organs;
MEDLINB=99212469; PubMed=10196736;
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MOD_RES 17 17 AMIDAJ
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MEDLINE=98213789; PubMed=9545435; Roy R.S., Kim S., Baleja J.D., Walsh C.T.; "Role of the microcin B17 propeptide in substrate recognition: solution structure and mutational analysis of McbA1-26."; Chem. Biol. 5:217-228(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89123111; PubMed=2644225; Genilloud O., Moreno F., Kolter R.; "DNA sequence, products, and transcriptional production of the DNA replication involved in production of the DNA replication
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
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Davagnino J., Herrero M., Furlong D., Moreno F., Kolter R.;
"The DNA replication inhibitor microcin B17 is a
forty-three-amino-acid protein containing sixty percent glycine.";
                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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(In) Schneider C.H.,
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Conell N., Han Z., Moreno F., Kolter
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PTM: THE CYS RESIDUES AS WELL AS SOME GLY AND CYS ARE POST-
TRANSLATIONALLY MODIFIED. MODIFICATIONS INCLUDE THE FORMATION
FOUR THIAZOLE AND FOUR OXAZOLE RINGS THAT RESULT, RESPECTIVELY
FROM THE CONDENSATION OF FOUR SERINE SIDE CHAINS WITH THE CARE
GROUP OF THE PRECEDING AMINO ACID.
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M15469;
M24253;
X06417;
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ndez-Chico C., del
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n inhibitor
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double-strand
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                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                   Watson J.D., Beckett-Jones B., Roy R.N., Green N.C., Flynn '"Genomic sequence, structural organization and evolutionary conservation of the 13.2-kDa subunit of rat NADH:ubiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
NADH-ubiquinone oxidoreductase 13 kDa-A subunit
(EC 1.6.99.3) (Complex I-13KD-A) (CI-13KD-A) (Fa
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01-OCT-1996
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NCBI_TaxID=10090;
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                                                                 EMBL; L38438; AAB64010.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                     FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED TO BE UBIQUINONE. THIS IS A COMPONENT OF THE IRON-SULFUR (IP) FRAGMENT OF THE ENZYME.

CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + reduced acceptor.

CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.

SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
                                                                                                                                                                                           SUBCELLULAR LOCATION: Mitochondrial inner membrane; matrix side
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"raductase; NAD; Ubiquinone;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee S.Y., Moon H.J., Kurata S., Natori S., Lee B.L.;
"Purification and cDNA cloning of an antifungal protein from hemolymph of Holotrichia diomphalia larvae.";
Biol. Pharm. Bull. 18:1049-1052(1995).
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01-NOV-1997
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01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOL3
                                                                                                                       REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                   EMBL; D13744; BAA02889.1; -. PIR; JC4190; JC4190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiform Scarabaeidae; Melolonthinae; Holotrichia.
                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Larval hemolymph;
MEDLINE=96073722; PubMed=8535393;
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                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                        nsect immunity; Antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.ALBICANS.
SIMILARITY: TO TENECIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: HOLOTRICIN 3 HAS ANTIFUNGAL ACTIVITY AGAINST
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesfey B.
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075896;
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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                                                           SEQUENCE
                                                                                                                                                                      MIM;
                                                                                                                                                                                                   EMBL; AF055479;
EMBL; BC023976;
                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Overexpression of candidate tumor suppressor gene FUS1 isolated from the 3p21.3 homozygous deletion region leads to G1 arrest and growth inhibition of lung cancer cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUS1 OR LGCC
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Yokota J., Kashuba
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               formation, causing G1 arrest and ultimately inducing apoptosis homozygous 3p21.3 120-kb region-deficient cells.
TISSUE SPECIFICITY: Strong expression in heart, lung, skeletal muscle, kidney, and pancreas, followed by brain and liver, lower the strong expression in heart and liver, lower than the strong expression in heart and liver, lower than the strong expression in heart and liver, lower than the strong expression in heart and liver.
                                                                                                                GO:0008283; P:cell proliferation; GO:0007267; P:cell-cell signaling;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       levels in placenta.
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oa V., Zabarovsky
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E., Kuzmin
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Nature 417:141-147(2002).
-!- SUBUNIT: Homodimer (By similarity).
-!- SIMILARITY: Belongs to the UPF0133 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF151381; AAD34031.2; -. EMBL; AL939117; CAB45486.1; -. PIR; T35387; T35387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0133 protein SCO3619.
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InterPro; IPR004401; Cons_hypoth103.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -I- SUBCELLULAR LOCATION: CELL WALL OF AERIAL HYPHAE AND SPORULA STRUCTURES. ABUNDANTLY SECRETED.
-I- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED ON DAY 2 AND 3 AFTER INOCULATION, A TIME WHEN THE FUNGUS IS IN A RAPID PHASE OF C AFTER A STATIONARY PHASE ON DAY 4, THE EXPRESSION DECREASES.
-I- SIMILARITY: BELONGS TO THE CERATO-ULMIN HYDROPHOBIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cryphonectria parasitica.";

Gene 139:59-64(1994).

-i- FUNCTION: CONTRIBUTES TO SURFACE HYDROPHOBICITY, WHICH IS
-IMPORTANT FOR PROCESSES SUCH AS ASSOCIATION OF HYPHAE IN
REPRODUCTIVE STRUCTURES, DISPERSAL OF AERIAL SPORES AND AL
OF PATHOGENS TO HOST STRUCTURES. PRODUCED ABUNDANTLY, EXCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang L., Villalon D., Sun Y., Kazmierczak P., van Alfen N.K.; "Virus-associated down-regulation of the gene encoding cryparin, abundant cell-surface protein from the chestnut blight fungus,
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16-OCT-2001 (Rel.
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thia complex; Cryphonectria.
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01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Glycine-rich protein HC1.
Chenopodium rubrum (Red goosefoot) (Pigweed).
"Gene expression during cell suspensions."; Planta 183:17-24(1990).
                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; campanulids; Apiales; Apiaceae; Daucus.
                                                                                                        Glycine-rich protein DC9.1. Daucus carota (Carrot).
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"Sequence of cDNA for a novel light-induced glycine-rich protein.";
Nucleic Acids Res. 17:2853-2853(1989).
-!- INDUCTION: By light.
                                  Aleith F.,
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                      somatic embryogenesis in carrot
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                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable gas vesicle structural protein 1 (GVP)
GVPA1 OR GVPA OR SCO6500 OR SC1E6.09.
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                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Bacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                               PUNCTION: Gas vesicles are small, hollow, gas filled protein structures that are found in several microbial planktonic microorganisms. They allow the positioning of the organism at the favorable depth for growth. GvpA type proteins form the essential core of the structure.

SUBCELLULAR LOCATION: Gas vesicle membrane.
SIMILARITY: BELONGS TO THE GAS VESICLE PROTEIN TYPE A FAMILY.
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AL033505;
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Puroindoline-B precursor
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InterPro; IPR00063B; Gas vesicle.
Pfam; PF00741; Gas vesicle; 1.
ProDom; PD00359B; Gas vesicle; 1.
PROSITE; PS00359B; Gas VESICLE A 1; 1.
PROSITE; PS00669; GAS VESICLE A 2; FALSE_NEG.
PROSITE; PS00669; GAS_VESICLE A 2; FALSE_NEG.
Gas vesicle; Complete protecome.
SEQUENCE 144 AA; 15315 MW; D1191338B63AFG
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Capitole; TISSUE=Seed; MEDLINE=94272013; PubMed=7516201; Gautier M.-F., Aleman M.-F., Guirao A., Marion D., Joudrier P.; Gautier M.-F., Horao A., Marion D., Joudrier P.; "Triticum aestirum puroindolines, two basic cystine-rich seed proteins: cDNA sequence analysis and developmental gene expression."; Plant Mol. Biol. 25:43-57(1994).
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InterPro; IPR006106; Amylase_inhib
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Bushuk W., Tkachuk R. (e
en proteins, pp.314-325,
Paul (1991).
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Q03878;
01-JUN-1994 (Rel.
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28-FEB-2003 (Rel.
                    MOUSE
CGC8 MOUSE
Q9D187;
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                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Daucus carota (Carrot).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Apiales; Apiaceae; Daucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine-rich RNA-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00030; RRM_RNP_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology to single-stranded nucleic acid binding plant Physiol. 99:1689-1692(1992).

-i-FUNCTION: MAY PLAY A ROLE IN THE BIOSYNTHESIS HETEROGENEOUS NUCLEAR RNA AND IN THE MATURATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Queen Anne's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00360; RRM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X58146; CAA41152.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A wound-inducible glycine-rich protein from Daucus carota with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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INDUCTION: IN RESPONSE TO STRESS BY WOUNDING.
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                        151 GGGGS
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ilarity 100.0%;
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protein CGI-128 homolog.
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GLY-RICH.
, 73FBD644F51CB633 CRC64;
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Pred. No. 2.1
0; Mismatches
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubhi F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Fruuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Blake J., Balt C., Fletcher C., Fujita M., Gariboldi M.,
A Blake J., Balt C., Fletcher C., Waszarelli J., Mombaerts P.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
B Suzuki H., Toyo-oka K., Mang K.H., Weltz C., Whittaker C., Wilming L.,
Hayashigaki P., A Kang Y., Kawaji H., Kohtsuki S.,
Hayashigaki P., A Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 5
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01-MAY-1992
01-MAY-1992
01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                     ORYSA
                                                                                                                                                                                                                                                                                                                                                     GRP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. SEQUENCE 163 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions that its institutions modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
MEDLINE=91370862; PubMed=1716496;
Lei M., Wu R.;
"A novel glycine-rich cell wall p
                                                                                                                                                                                                                                                 Glycine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                         Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01883; DUF59; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                           Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                      Eukaryota;
                                                               STRAIN=cv.
                                                                                    SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE UPF0195 FAMILY.
                                                                                                                                                                                                                                                                                                                                                     ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AK003830; BAB23024.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
  glycine-rich cell wall protein gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR002744; DUF59.
                                                                                                                                                                                 Viridiplantae;
                                                               Indica-IR36;
                                                                                                                                                                                                                                      (Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 25, Last annotation update)
cell wall structural protein 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17667 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                              Streptophyta; Er
yta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 1;
Pred. No. 2.2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D3171D52CF3AD02F CRC64;
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                                                                                                                                                                                                                                                                                                                                                  165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.2e+02;
                                                                                                                                                              Embryophyta; Tracheophyta; a; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                  B
    in rice.";
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RESULT 15
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Best Local S
Matches 5
MEDLINE=21016721; PubMed=11130714;

X MEDLINE=21016721; PubMed=11130714;

A Tabata S., Kaneko T., Nakamura T., Hosouchi T., Kawashima K.,

A Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,

A Miyajima N., Sasamoto S., Kimura S., Waraki A., Nakayama S.,

A Kohara M., Mateumoto M., Matsuno A., Muraki A., Nakayama S.,

A Kohara M., Mareumoto M., Okumura S., Shinpo S., Takeuchi C., Wada T.,

A Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,

A Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,

A Habermann K., Yamada M., Yasuda M., Sato S., de la Bastide M.,

A Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,

A Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,

Belter E., Cordum H., Cordes M., Courttney L., Courtney W., Dante M.,

A Belter E., Cordum H., Cordes M., Courtney L., Caurtney W., Dante M.,

Belter E., Cordum H., Cordes M., Courtney L., Caurtney M.,

Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,

A Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,

A Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,

A Wagner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,

A Parnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HY5 ARATH
024646;
28-FEB-2003
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REPEAT
SEQUENCE
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REPEAT
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                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=cv. Columbi
                                                                                                                                                                                                                                                                                              Oyama T., Shimura Y., Okada K.;
"The Arabidopsis HY5 gene encodes a bZIP
stimulus induced development of root and
Genes Dev. 11:2983-2995(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       eurosids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HY5 OR AT5G11260 OR F2I11_150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein HY5
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: RESPONSIBLE FOR PLASTICITY OF THE -i- SUBCELLULAR LOCATION: Cell wall (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant Mol. Biol. 16:187-198(1991)
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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R2 (TYR-RICH).
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Pred. No. 2.2e+02;
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hypocotyl.";
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                                                                                       Becker
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A Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
A Volckaert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,
A Entian K.-D., Terryn N., Hartley N., Bent E., Johnson S.,
A Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,
A Ramsperger U., Wedler H., Balke K., Wedler E., Peters S.,
Van Staveren M., Dirkse W., Mooijman P., Klein Lankhorst R.,
A Weitzenegger T., Bothe G., Rose M., Hauf J., Berneiser S.,
A Meitzenegger T., Bothe G., Rose M., Berneiser S.,
A Feldpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,
A Bents O., Lemcke K., Kolesov G., Mayer K., Rudd S., Schoof H.,
A Bents O., Lemcke K., Kolesov G., Mayer K., Rudd S., Schoof H.,
A Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.;
Tsequence and analysis of Chromosome 5 of the plant Arabidopsis
                                                                                                                                            Query Match
Best Local
                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTION WITH COP1, AND MUTAGENESIS OF VAL-43--PRO-44. TISSUE=Etiolated seedling;

MEDLINE=21145432; PubMed=11226162;

Holm M., Hardtke C.S., Gaudet R., Deng X.-W.;

"Identification of a structural motif that confers specific interaction with the WD40 repeat domain of Arabidopsis COP1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20296352; PubMed=10839542;
Osterlund M.T., Hardtke C.S., Wei N., Do
"Targeted destabilization of HY5 during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of Arabidopsis.";
Nature 405:462-466(2000)
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InterPro; IPR001630; Leuzip CREB.
InterPro; IPR004827; TF bZIP.
Pfam; PF00170; bZIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                          DNA-binding; Nuclear protein; Phytochrome signaling pathway.
DNA_BIND 93 108 BASIC MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50217; BZIP; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
                                                                                                                                                                                                                                                                   MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: Expressed in root, hypocotyl, stem and floral organs.
MISCELLANEOUS: Interaction between HY5 and COP1 matrigeted degradation of HY5 by the 26S proteasome SIMILARITY: Belongs to the bZIP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         work as a transcriptional activator.
SUBUNIT: Interacts with COP1 WD40 domain.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: Expressed in root, hy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Promotes
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SM00338; BRLZ; 1.
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V:
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                                                          GGGGS 5
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; BAA21116.1; -.
; CAB96661.1; -.
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                                                                                                                                                                                                                                                             BASIC MOTIF.
LEUCINE-ZIPPER.
VP->AA: ABOLISHES
                                                                                                                                            Score 28; DB 1;
Pred. No. 2.3e+02;
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ng light-regulated development
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AC Q0325
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GRP7_ARATH STAN
Q03250;
01_JUN-1994 (Rel.:
01_JUN-1994 (Rel.:
28-FEB-2003 (Rel.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Cv. Columbia;
STRAIN=Cv. Columbia;
MEDLINE=20083497; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.I.
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Mierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
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GRP7 OR ATZG21660 OR F2G1.7.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       van Nocker S., Vierstra R.D.;
"Two cDNAs from Arabidopsis thaliana encode putative proteins containing glycine-rich domains.";
plant Mol. Biol. 21:695-699(1993).
                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z14987; CAA78711.1; -.
EMBL; L00648; AAA32853.1; -.
EMBL; AC007119; AAD23639.1; -
EMBL; S30147; S30147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. These restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                        PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 402:761-768(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Columbia; TISSUE=Leaf;
MEDLINE=93192529; PubMed=8448367;
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                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).

    -!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P09651; 1HA1
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000504; RNA_rec_mot
113
                                                                                                  Similarity
5; Conserv
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176
                                                                                                    Conservative
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                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                               rrm; 1.; RRM; 1.
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                                                                                                                                                                                                            16890
                                                                                                                          100.0%;
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                                                                                                                                                                                                         RNA-BINDING (RRM).
GLY-RICH.
, 3E1025477F9CF4C4 CRC64;
                                                                                                    Score 28; DB
Pred. No. 2.4
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN RNA TRANSCRIPTION
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                                                                                                                                  2.4e+02;
                                                                                                                                                           DB 1;
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RESULT 18
K2C3_BOVIN
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CBFA_MAIZE
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01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CCAAT-binding transcription factor subunit A (C
chain B) (NF-YB) (CAAT-box DNA binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CBFA
                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003956; CBFA NFYB.
InterPro; IPR003958; CBFA NFYB domain.
InterPro; IPR003957; CBFA_NFYB_topis.
InterPro; IPR003957; CBFA_NFYB_topis.
InterPro; IPR004822; Histone_core.
Pfam; PF00808; CBFD_NFYB_HMF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X59714; CAA42234.1; -. PIR; S22820; S22820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li X.-Y., Mantovani R. Benoist C., Mathis D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
PACCAD clade; Panicoideae; Andropogoneae;
                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription
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MEDLINE=92195809; PubMed=1549471;
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                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MaizeDB; 69282; -
                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evolutionary variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear.

DOMAIN: CAN BE DIVLIDED INTO THREE DOMAINS: THE WEAKLY CONSERVED DOMAIN: THE HIGHLY CONSERVED B DOMAIN THOUGHT TO BE INVOLVED IN SUBUNIT INTERACTION AND DNA BINDING, AND THE GLU-RICH C DOMAIN. SIMILARITY: BELONGS TO THE CBF-A SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: STIMULATES THE TRANSCRIPTION OF VARIOUS GENES BY RECOGNIZING AND BINDING TO A CCAAT MOTIF IN PROMOTERS, FOR EXAMPLE IN TYPE I COLLAGEN, ALEUMIN AND BETA-ACTIN GENES. SUBUNIT: HETEROTRIMERIC TRANSCRIPTION FACTOR COMPOSED OF THREE COMPONENTS, A, B AND C. NF-YB AND NF-YC MUST INTERACT AND DIMERIZE FOR NF-YA ASSOCIATION AND DNA BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAIZE
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                                                                                                                                                                                                Similarity 5; Conserv
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120
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179 /
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                                                                                                                                                                                                                                                                                                             regulation; DNA-binding; Acti
1 29 A DOMAIN.
30 119 B DOMAIN.
20 179 C DOMAIN.
20 179 C DOMAIN.
36 42 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                              AA;
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                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                0
                                                                                                                                                                                                                       Score 28; DB 1; Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Activator;
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Zea.
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                                                                                                                                                                                                                                           Length 179;
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RESULT 19
OLEC_BRANI
RRR RR COCCOGNETIC
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SITE
                                                                                                                                                                 OLEC BRANA
P29526;
01-APR-1993
                                                                                                                                                                                                        BRANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-1987 (Rel. 04, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Keratin, type II cytoskeletal 60 kDa, component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K2C3_BOV
P04261;
                                            Spermatophyta; Magnoliophyta;
eurosids II; Brassicales; Bras
NCBI TaxID=3708;
                                                                                     Brassica napus (Rape).
Eukaryota; Viridiplantae;
                                                                                                                             Oleosin C98
                                                                                                                                        01-APR-1993
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; K03535; AAA30602.1; -. PIR; A02947; A02947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KE
-i- MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND
MICROFIBRILLAR KERATIN, I (ACIDIC) AND II (NEUTRAL TO BA
(40-55 AND 56-70 KILODALTONS, RESPECTIVELY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE=85128114; PubMed=6084625;
Jorcano J.L., Franz J.K., Franke W.W.;
"Amino acid sequence divergity between
polypeptides of the basic (type II) sub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora: Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAR-1987 (Rel.
20-MAR-1987 (Rel.
16-OCT-2001 (Rel.
MEDLINE=93386188; PubMed=8374615;
            TISSUE=Anther
                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001664; IF. Pfam; PF00038; filament; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Differentiation 28:155-163(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOVIN
                                                                                                                                                                                                                                                             119
                                                                                                                                                                                                                                                                                    μ,
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(Rel. 25, La
(Rel. 36, La
(Fragment).
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Conservative 0;
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. 25, Last seq
. 36, Last anno
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182
                                                                                                                                                                                                                                                                                                                                                                 17560 MW;
                                                                                                                                                                                                                                                                                                                                                                                   - 63
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                                                                          Streptophyta; Embryophyta; Tracheophyta; yta; eudicotyledons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rsity between bovine (type II) subfamily
                                                              Brassicaceae;
                                                                                                                                        sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                            ROD.
TAIL.
COIL 2.
STUTTER.
                                                                                                                                                                                                                                                                                                                        Score 28; DB 1;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                             coil; Keratin
                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                 C263102147632F66 CRC64;
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                                                                                                                                                                                             183
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                                                                                                                                        update)
                                                               Brassica
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                                                                                                                                                                                                                                                                                                                                      Length 182;
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                                                                           Rosidae;
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RESULT
SCX CHI
      Query Match
Best Local S
Matches 5
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28-FEB-2003
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gametophyte-specific Plant J. 3:629-636(19-1-1-FUNCTION: MAY HAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for conmodified and this statement is not removed. Usage by and for conmodified and this statement is not removed.
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Draper J., Sco
                                                                                                                                   Schweitzer R., Chyung J.H., Murtaugh L.C., Olson E.N., Lassar A., Tabin C.J.; "Analysis of the tendon cell fate using Sc."
                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amoutation update)
Basic helix-loop-helix transcription factor s
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                   SCX_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Draper J., Scott R.; 
"Characterization of
                                                                                                                                                                             MEDLINE=21469794; PubMed=11585810;
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                        Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                             for tendons and ligaments.";
Development 128:3855-3866(2001).
send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INT J. 3:629-636 (1993). TRUCTURAL ROLE TO STABILIZE THE LIPID BODY FUNCTION: MAY HAVE A STRUCTURAL ROLE TO STABILIZE THE LIPID BODY DURING DESCICCATION OF THE SEED BY PREVENTING COALESCENCE OF THE OIL. PROBABLY INTERACTS WITH BOTH LIPID AND PHOSPHOLIPID MOIETIES OF LIPID BODIES. MAY ALSO PROVIDE RECOGNITION SIGNALS FOR SPECIFIC LIPASE AUCHORAGE IN LIPOLYSIS DURING SEEDLING GROWTH.

SUBCELLULAR LOCATION: SURFACE OF OIL BODIES. OLEOSINS EXIST AT A MONOLAYER LIPID/WATER INTERFACE.

MONOLAYER LIPID/WATER INTERFACE.
TISSUE SPECIFICITY: SPECIFIC TO THE MALE GAMETOPHYTE.
                                                                                   FUNCTION: Plays an early essential well as a later role in formation (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S24960; S24960.
cPro; IPR000136; Oleosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                      123
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TE; PS00811; OLEOSINS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               body; Multigene family.
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183
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                                            binding requires and binds the E-
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Pred. No.
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     r similarity).
the intersomitic,
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somite-derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 183;
                                             consensus
                                                                                                                                                               A.E.,
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      the superficial
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                                                                                   formation, as chondrogenic
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                                                        with another
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RESULT
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Best Local
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P48793;
01-FEB-1996
01-FEB-1996
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear p
                "High-resolution structures of xyla T.harzianum identify a new folding atomic basis of the catalysis." (In) Suominen P., Reinikainen T. (e
                                                                                                                                                                                                                      "The amino acid sequence of the harzianum E58";
(In) Visser J. Beldman G., Kust Voragen A.G.J. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00038; HLH_1; 1.
PROSITE; PS50888; HLH_2; 1.
Transcription regulation; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001092; Pfam; PF00010; HLH; 1 SMART; SM00353; HLH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xylanohydrolase)
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between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                               X-RAY CRYSTALLOGRAPHY Campbell R.L., Rose D.
                                                                                                                                                                                                                                                                                                                    Saddler J.N.;
                                                                                                                                                                                                                                                                                                                                                             STRAIN=E58;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trichoderma
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                                                                                                            Yaguchi M.,
                                                                                                                                                                                                      Xylans
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SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSCRIPTION FACTORS.
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145
187 AA;
                                                                                                                                                                                                 xylanases,
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(Rel. 33, Last sequence update)
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(Rel. 41, East annotation updat)
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ilarity 100.0%;
Conservative 0
reesei cellulases and other hydrolases,
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                                                                                                                                                                                                                                                                                                                                          Watson D.C.,
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                                                                                                                                                                                                 pp.435-438,
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                                                                                                                                 Wakarchuk W.W.,
                                                                                                                                                         ANGSTROMS)
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HELIX-LOOP-HELIX MOTIF
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Pred. No. 2.5e+02;
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                       (eds.);
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                                                               B.circulans and
d implications f
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pp.63-72
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RESULT
VG49_BF
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Best Local S
Matches 5
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15-DEC-1998
15-DEC-1998
                                                    [1]
SEQUENCE FROM N.A.
MEDLINE=98300335; PubMed=9636706;
Ford M.E., Sarkis G.J., Belanger A.E.,
Ford M.E., Sarkis G.J., Belanger A.E.,
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_BPMD2
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PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

Xylan degradation; Hydrolase; HyDrosidase; 3D-structure
XYlan degradation; Hydrolase; MUCLEOPHILE.

ACT_SITE

86

NUCLEOPHILE
ACT_SITE

177

177

PROTON DONOR.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                     Mycobacteriophage D29.
Viruses; dsDNA viruses,
                                                                                                                                                                         Gene
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                                               J. Mol.
                                                                                                                        NCBI_TaxID=28369;
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PATHWAY: Xylan degradation
SIMILARITY: BELONGS TO CELI
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5; Conserv
                                              Biol. 279:143-164(1998).
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0457; Glyco_hydro_11; 1.
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                                                                                                                                                                                                                                                                                                                                                                                 190
                                                                                                                                                                      (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
:ein (GP49).
                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No.
                                                                                                                                                                                                                                PRT;
                                                                                                                                      stage; Caudovirales; Siphoviridae.
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                                                                  Hendrix R.W., Hatfull D29: implications for
                                                                                                                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                                                                                                                                        Length 190;
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InterPro; IPR002059; Cold shock. InterPro; IPR001878; Znf_CCHC. Pfam; PF00313; CSD; 1.

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RESULT 23
GR2B_ARATH
ID GR2B_
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Best Local S
Matches 5
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Goodman H.M., Somerville C.R., Carbon S.L., Fraser C.M.,
                                    EMBL; U39072; ARAYLLULL.;
EMBL; AC006264; AADZ9810.1;
F84596; F84596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q38896;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glycine-rich protein 2b (AtGRP2b).
GRP2B OR ATZCZ1060 OR FZ6H11.18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified
                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                            Goodman H.M., Somerville C.R., Copennaver w.r., rav
Nierman W.C., White O., Eisen J.A., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Columbia;
van Nocker S., Vierstra R.D.;
"Arabidopsis AtGRP2b, a glycine-rich
nucleic acid-binding motifs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF022214; AAC18489.1; -. PIR; F72805; F72805.
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STRAIN=cv. Columbia;
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Pred. No.
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                                                                                                                                                                     EMBL outstation
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                                                                                                                                                                       a collaboration -
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PF00098; zf-CCHC;

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Matches
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Q15672; Q92487; (
01-NOV-1997 (Rel
01-NOV-1997 (Rel
                                                                                                                                                                                                                                                                                                                                       TISSUE=Lung;
Wang S.M., Pignolo R.J.,
Cristofalo V.J., Sierra J
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ZN FING
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ZN FING
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SMART; P800352; COLD SHOCK; ...
PROSITE; P850158; ZF_CCHC; 2.
PROSITE; P850158; ZF_CCHC; 2.
CSD.
CSD.
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PRINTS; PRO0050; COLDSHOCK.
ProDom; PD000621; Cold shock;
SMART; SM00357; CSP; 1.
SMART; SM00343; ZnF_C2HC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                               Krebs I., Weis I., Hudler M., Rommens J.M., Roth Tsui L.-C., Fuchtbauer E.-M., Grzeschik K.-H., Tsuranslocation breakpoint maps 5 kb 3-prime from affected with Saethre-Chotzen syndrome.";
                                                                            SEQUENCE FROM N.A. MEDLINE=97358582; PubMed=9215678;
                                                                                                                                                    Ortiz de Luna
Jabs E.W.;
                                                                                                                                                             MEDLINE=97141916; PubMed=8988166;
Howard T.D., Paznekas W.A., Green
Ortiz de Luna R.I., Delgado C.G.,
                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                  "The human H-twist gene is located at 7p21 and encodes protein that is 96% similar to its murine M-twist coundamm. Genome 7:915-917(1996).
                                                                                                                                                                                                                                                                              MEDLINE=97148940; PubMed=8995765;
Bourgeois P., Stoetzel C., Bolcato-Bellemin A.-L., Mattei M.-G.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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                                                                                                                  in Saethre-Chotzen syndrome.";
Nat. Genet. 15:36-41(1997).
                                                                                                                                                                                                                                                                     Perrin-Schmitt F.;
                                                                                                                                       "Mutations in TWIST, a basic helix-loop-helix transcription factor
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91
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5; Conserv
FROM N.A
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                       Genet.
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(Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
ed protein 1 (H-twist).
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                    6:1079-1086(1997).
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                                                                                                                                                                                                             AND VARIANTS
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the EMBL/GenBank/DDBJ databases
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                                                                                                                                                              Green
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CCHC-TYPE 1.
GLY-RICH.
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; 832411B7FD890E46 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                             SCS
                                                                                                                                                              E.D., Chiang L. Gonzalez-Ramos
                                                                                                                                                                                                             PRO-119;
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                                                                                                                                                                                                                                               M-twist counterpart.";
                                             Roth H., Scherer S.W.,
H., Tsuji K., Kunz J.;
from TWIST in a patien
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Kline A.D.
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                                             Kunz J.;
1 a patient
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(BY SIMILARITY).

(C) -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER CC BHLH PROTEIN. HOMODIMER (BY SIMILARITY).

(C) -1- SUBCELLULAR LOCATION: Nuclear.

(C) -1- DISSUE SPECIFICITY: SUBSET OF MESODERMAL CELLS.

(C) -1- DISSUE SPECIFICITY: SUBSET OF MESODERMAL CELLS.

(C) -1- DISEASE: Defects in TWIST1 are one of the causes of Saethre-Chotzen syndrome (SCS) [MIM:1010400]; also known as autosomal dominant defect characterized by minor skull and limb anomalies.

(C) -1- DISEASE: Defects in TWIST1 are the cause of Robinow-Sorauf syndrome (RSS) [MIM:180750]; also known as craniosynostosis-bifid by minor skull and limb anomalies which is very similar to Saethre-Chotzen syndrome.

(C) -1- DISEASE: Defects in TWIST1 are a cause of Baller-Gerold syndrome (BSS) [MIM:218600]. BGS is a craniosynostosis with radial defects along with other features, including small, round ears with C along with other features, including small, round ears with SC along with other features, including small, round ears with SC along with other features, including small, round ears with SC along with other features, including small, round ears with SC along with other features, including small, round ears with SC along with other features, including small, round ears with SC along with other features of Saethre-Chotzen syndrome.

(C) -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRUTTOTON EXCROPSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RA Strausberg R.D., Collins F.S., Wagner L., Schammen C.M., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L., Schammen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Histon M., Madan A., Wagne A.C., Schein J.E., Jones S.J.M., Mers R.M., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Wener A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21621049; PubMed=11754069;
Seto M.L., Lee S.J., Sze R.W., Cunningham M.L.;
"Another TWIST on Baller-Gerold syndrome.";
Am. J. Med. Genet. 104:323-330(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Munnich A., Bonaventure J.; "Mutations of the TWIST gene in the Nat. Genet. 15:42-46(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               el Ghouzzi V., le Merrer M., Perrin-Schmitt F., Lajeunie E
Benit P., Renier D., Bourgeois P., Bolcato-Bellemin A.-L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: PROBABLE TRANSCRIPTION PACTOR, WHICH SEEMS TO BE INVOLVED IN THE NEGATIVE REGULATION OF CELLULAR DETERMINATION AND IN THE DIFFERENTIATION OF SEVERAL LINEAGES INCLUDING MYOGENESIS, OSTEOGENESIS, AND NEUROGENESIS. INHIBITS MYOGENESIS BY SEQUESTRATING E PROTEINS, INHIBITING TRANS-ACTIVATION BY MEF2, AND INHIBITING TRANS-ACTIVATION. THIS INHIBITING DNA-BINDING BY MYOD THROUGH PHYSICAL INTERACTION. THIS INTERACTION PROBABLY INVOLVES THE BASIC DOMAINS OF BOTH PROTEINS (BY SIMILARITY)
                                                                                                                                            TRANSCRIPTION FACTORS.
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GO; GO:0004857
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PROSITE; PS50888; HLH 2; 1.
Differentiation; Developmental protein;
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SMART; SM00353; HLH; 1
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GO; GO:0005515; F:protein binding activity; TAS.
GO; GO:000701; P:chromosome organization and biogenesis (sen.
GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
GO; GO:0000122; P:negative regulation of transcription from P.
GO; GO:0001501; P:skeletal development; TAS.
GO; GO:0001501; P:skeletal development; TAS.
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       sequence update) annotation updat
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Q -> P (in SCS).

Q -> P (no.4495.
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P -> PKIIPTLP (in SCS).
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RA Entian K.D. Errington J. Fabret C., Ferrari E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Gilseppi G. Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Kurita K., Lepidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Hedina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Rigger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Sorokin A., Tacconi E., Takahashi H., Takemaru K.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

RA Tosato V., Uchiyama S., Vandembol M., Vannier F., Vassarotti A.,

RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,

RA Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

The Complete General Server of the Gram-neatitive hacterium Bacillus

Britan Complete General Server of the Gram-neatitive hacterium Bacillus
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J. Bacteriol. 177:3045-3051(1995).

J. Bacteriol. 177:3045-3051(1995).

-i- FUNCTION: Needed for both DNA binding and transport.

-i- FUNCTION: Needed for the uptake of transforming Diagnostic transforming Diagnostic transforming Diagnostic transforming Diagnostic transforming Diagnostic transforming Diagnostic transforming Diagnostic transforming Diagnostic transforming Diagnostic transforming Diagnostic transforming Diagnostic transforming Diagnostic transport.
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Kunst F., Ogasawara N., Moszer I., Bolotin A., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
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MEDLINE=95058187; PubMed=7968523;

Hahn J., Inmanine G., Kozlov Y., Dubnau D.A.;

"Characterization of comE, a late competence subtilis required for the binding and uptake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete subtilis.";
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MEDLINE=97124195; Pi
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Bacteria; Firmicutes;
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rComEA, a Bacillus subtilis integral membrane protein required
rComEA, a Bacillus subtilis integral membrane protein required
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                                                                                                                                                                                    binding. Its role in binding may be indirect.
SUBCELLULAR LOCATION: Type II membrane protein. Inn
SIMILARITY: TO E.COLI YBAV AND H.INFLUENZAE HI1008.
                                                    SWISS-PROT entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
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S., Takemaru K.-I.,
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Hahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

AN Halms M., Touchman J.W., Green E.D., Dickson M.C.,
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Perrin-Schmitt F.;
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Hamamori Y., Wu H.Y., Sartorelli V., Kedes L.;
"The basic domain of myogenic basic helix-loop-helix is the novel target for direct inhibition by another Twist.";
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GO; GO:0005534; C:nucleus; NAS.
GO; GO:0003700; F:transcription factor activity; NAS.
GO; GO:0003700; F:transcription; IMP.
GO; GO:0030154; P:cell differentiation; IMP.
GO; GO:003026; P:limb morphogenesis; IMP.
GO; GO:004556; P:negative regulation of cell differentiation;
GO; GO:0045843; P:negative regulation of myogenesis; IDA.
GO; GO:0001679; P:neurulation; IMP.
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pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
PROSITE; PS00038; HLH 1; 1.
PROSITE; PS50088; HLH 2; 1.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC033434; AAH33434.1; -. PIR; I53066; I53066.
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CELLULAR DETERMINATION AND INVOLVED IN THE MEGATIVE REGULATION OF CELLULAR DETERMINATION AND IN THE DIFFERENTIATION OF SEVERAL LINEAGES INCLUDING MYOGENESIS, OSTEOGENESIS, AND NEUROGENESIS. INHIBITS MYOGENESIS BY SEQUESTRATING E PROTEINS, INHIBITING TRANS-ACTIVATION BY MEF2, AND INTERACTION THIS TRANS-ACTIVATION BY MEF2, AND INTERACTION PROBABLY INVOLVES THE BASIC DOMAINS OF BOTH PROTEINS. SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bauer M.F., Gempel K., Reichert A.S., Rappold G.A., Lichtner P., Gerbitz K.-D., Neupert W., Brunner M., Hofmann S.; "Genetic and structural characterization of the human mitochondr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40,
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                                                          Transport; Protein transport; Translocation;
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR005681; Tim23.
TIGRFAMs; TIGR00983; 3a0801s02tim23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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                                      TIMM23 OR TIM23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inner membrane translocase."
                                                                                                                                                                                                                                                                                                                                                          GO:0005744; C:mitochondrial GO:0006628; P:mitochondrial
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                                                                                                                                                                                                                                                                          membrane; Outer membrane; Transmembrane,
MEM 73 93 POTENTIAL.
MEM 125 145 POTENTIAL.
MEM 181 197 POTENTIAL.
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5; Conserv
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Primates;
  Chordata;
Rodentia;
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inner membrane transloca
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Pred. No. 2.8e+02
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                                                                                                                                                                                                             inner membrane translocation;
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RESULT 29
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Best Local S
Matches 5
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01-AUG-1992 (Rel. 2
01-AUG-1992 (Rel. 2
28-FEB-2003 (Rel. 4
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mitochondrial inner membrane, rTIMI, ....
J. Biochem. 123:722-732(1998).
J. Biochem
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TRANSMEM
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                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB006451; BAA21819.1; PIR; JE0154; JE0154.
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                                                                                                                                                                                                                       MEDLINE=92003709; PubMed=1912512;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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TIGRFAMs; TIGR00983; 3a0801s02tim23;
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CONDUCTING CHANNEL OF THE MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: FORMS PART OF THE TIM23 RECEPTOR COMPLEX THAT CONSISTS
AT LEAST 3 DIFFERENT PROTEINS; TIM17, TIM23 AND TIM44.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
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MEM 73 93 POTENTIAL.
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Pred. No. 2.8e+02;
; Mismatches 0;
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Matches 5
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InterPro; IPRO02159; Znf_CCHC.
Pfam; PF000313; CSD; 1.
Pfam; PF00098; Zf-CCHC; 2.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00050; COLDSHOCK.
PRODOM; PD000621; COLD SHOCK; 1.
SMART; SM00357; CSP; 1.
SMART; SM00343; ZnF_C2HC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O80340;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ethylene responsive element binding factor 4
ERF4 OR ERF-4 OR AT3G15210 OR K714.1
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SEQUENCE
                     Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B. Partmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B. Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P., De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P., Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V., Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
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                                                                                                                                                                                                                                                                                                                                                 Pujimoto S.Y., Ohta M., Usui A., Shinshi rarabidopsis ethylene responsive element transcriptional activators or repressors expression.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                         STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
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CCHC-TYPE 1.
GLY-RICH.
CCHC-TYPE 2.
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binding factors act
of GCC box mediated
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RESULT 31
SP25_CAT
ID "SP25_C
AC Q28250
AC Q28250
DT 15-JUL
DT 15-JUL
DT 28-FSB
DE Micros
DE SP25..
OS Canis
GN SP25..
OS Canis
OC Mammal
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RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA de Haan M., Maris A., Flores M., Liquori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.I., Tallon L.J., Jenkins J.,
RA Money T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Roney T., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Preuss D., Lin X., Nierman W.C., Salbers P., Gill J.E., Feldblyum T.V.,
RA Praser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Kiyokawa C., Kohara M., Matsumo A., Matsumo A., Muraki A.,
Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
"Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT Thaliana "."
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Best Local S
Matches 5
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15-JUL-1998 (Rel. 3
28-FEB-2003 (Rel. 4
Microsomal signal p
subunit) (SPC25).
NCBI_TaxID=9615;
                                                SPC25.
Canis familiaris (Dog).
Canis familiaris (Dog).
Pinsibedia; Canidae;
Pinsibedia; Canidae;
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Q28250;
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SMART; SM00380; AP2; 1.
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InterPro; IPR001471; TF ER
Pfam; PF00847; AP2-domain;
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36, Last sequence 41, Last annotation
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41, Last annotation update)
peptidase 25 kDa subunit (E
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Embryo;

MEDLINE=2108560; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Kawai J., Shinagawa A., Shibata Y., Konno H., Adachi J., Fukuda Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
                                                                                                                                                                                                                                                                                                                O9CYNZ; Q921VB; Q9CXKI;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Microsomal signal peptidase 25 kDa subunit (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
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DOMAIN
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J. Biol. Chem. 269:25354-25358(1994).
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MEDLINE=95014327; PubMed=7929230;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA-derived primary structure of the 25-kDa subunit of canine
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FUNCTION: MICROSOMAL SIGNAL PEPTIDASE IS A ME ENDOPROTESINASE THAT REMOVES SIGNAL PEPTIDES F PROTEINS AS THEY ARE TRANSLOCATED INTO THE LUENDOPLASMIC RETICULIM.
SUBUNIT: COMPLEX OF FIVE DIFFERENT PROTEINS: SPC21, SPC18, AND SPC12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO THE SPC25 FAMILY.
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Pred. No.
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 AA
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                           Ishii Y.,
Fukuda S.,
manaka I.,
Saito R.,
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RX MEDLINE=223825; PhUMede12477932;
RA KIRUNINE=223825; PhUMede12477932;
RA Altechal S.F., Zéeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S., Garcia A.M., Gay L.J., Hulyk S., Garcia A.M., Gay L.J., Hulyk S., Garcia A.M., Gay L.J., Hulyk S., Garcia A.
   Matches
                                   Query Match
Best Local
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                                                                                                                                                                                                                                          TRANSMEM
DOMAIN
TRANSMEM
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CONFLICT
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EMBL; AKO17504; BAB30777.1; -.
EMBL; BC010547; AAH10547.1; ALT INIT.
EMBL; BC01547; AAH10547.1; ALT INIT.
MGD; MGI:1913874; 5730406I15R1k.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restr
                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1913874; 573
Hydrolase; Microsome;
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                                                                                                                                                                                                                                                                                                                                                 MAIN
Similarity
5; Conser
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226 AA;
   Conservative
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112
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24977
                                   100.0%;
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CYTOPLASMIC (POTENTIAL).
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E -> D (IN REF. 1; BAB2
                                                                                                                                                                                                                                          POTENTIAL
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                                       Score 28;
Pred. No.
                                                                                                                                      F8516C51FFED4DF9
   Mismatches
                                                                                                                                                                                                                                                                          (POTENTIAL)
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  (See http://www.isb-sib.ch/announce/
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CRC64;
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RESULT 33
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GS28_DROME
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30-MAY-2000
30-MAY-2000
15-SEP-2003
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30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat-
Ribonuclease H (EC 3.1.26.4) (RNase H).
RNHA OR SCO7284 OR SC5H1.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                          entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- COPACTOR: Binds 1 magnesium ion per subunit (B)
--- SUBUNIT: Monomer (By similarity).
---- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
---- SIMILARITY: BELONGS TO THE RNASE H FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
-i- FUNCTION: THIS ENZYME IS AN ENDONUCLEASE THAT DEGRADES THE RU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA-DNA HYBRIDS SPECIFICALLY (BY SIM-
-!- CATALYTIC ACTIVITY: Endonucleolytic
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                             Hydrolase;
                                                                                                                                                                                                                                                                                                             HAMAP; MF_00042; -; 1.
InterPro; IPR002156; RNaseH.
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COFACTOR: Binds 1 magnesium
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                                                                                                                                                Similarity
                                                                   GGGGS 188
                                                                                                                                                                                                                                                                                                                                                                                          equires a license agreement (Semail to license@isb-sib.ch).
                                                                                                                                                                                               138
231 /
                                                                                                                                                                                                                                                                             Nuclease;
                                                                                                                               Conservative
                                                                                                                                                                                                 A
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                                                                                                                                                                                                                                                                                                                                                            CAB42933.1;
                                                                                                                                                                                               138
24297
                                                                                                                                                                                  H; 1.

Endonuclease; Magnesium; Complete proteome.

MAGNESIUM (BY SIMILARITY).

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Pred. No.
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Y (BY SIMILARITY).
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Ewans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., W., Hoskins R.A., Galle R.F., RA Adams M.D., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Sutton G.G., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D., RA Marchall J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D., Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Barlis J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler S.M., Dowles M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Gelast W., Glasset K., Ra Goldek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M., Glasset K., Ra Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.I., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C., Liu X., Wattei B., McIntosh T.C., McLeed M.P., McPherson D., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Hollan B.E., Kodira C.D., Kraff C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Ra Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Markulov G., Milshina N.V., Mobarry C., Morris J., Pacleb J.M., Ra Markulov G., Milshina N.V., Mobarry C., Wenter D.R., Smith T., Ra Palench J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GS28_DROME STANDARD;
Q9VE50; Q8SWZ4;
16-OCT-2001 (Rel. 40, Created
16-OCT-2001 (Rel. 40, Last se
15-SEP-2003 (Rel. 42, Last an
Probable 28 kDa Golgi SNARE p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOS28 OR CG//VV.

Drosophila melanogaster (Fruit L/).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; **VV.

Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;

Neoptera; Endopterygota; Drosophila.
                                                                                                   Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Rubin G.M., Celniker S.E.,

"A Drosophila full-length cDNA resource.",

Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).

-!- FUNCTION: INVOLVED IN TRANSPORT FROM THE ER TO THE GOLGI.

AS WELL AS IN INTRA-GOLGI TRANSPORT (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Type IV membrane protein. Golgi (By Similarity).
                                                                                                                                                                                                                                                                                                                                                                     Science [2]
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                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Berkeley; TISSUE=Head;
MEDLINE=22426066; PubMed=12537569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006;
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                                                                                        -!- SIMILARITY:
                                                                                        BELONGS TO THE GOSR1 FAMILY.
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Last annotation updat
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M., Henderson S
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RESULT 35
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUE=Testis;
MEDLINE=95302737; PubMed=7783423;
MEDLINE=95302737; PubMed=7783423;
MEDLINE=W V Feuerstein G.Z., Yue T.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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CONFLICT
                                      CA_BIND
DOMAIN
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                            Lab.
                                                                                                                                                                                                                                                                 Douglas S.A.;
"Use of differential display to identify differentially exmRNAs induced by rat carotid artery balloon angioplasty.";
                                                                                                                                                                                                                                                                                                                                                                                                                                 BART-1 protein (Balloon angioplasty responsive
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                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
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                                                 Calcium-binding.
CA BIND 141
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                                                                          ProDom;
                                                                                                            EMBL; U33471; AAB06590.1; -.
                                                                                     interPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0006888; P:ER to Golgi transport; ISS. GO:0006891; P:intra-Golgi transport; ISS.
                                                                                                                                                                                                                                            Invest. 72:656-661(1995)
SIMILARITY: SOME, TO EF-H
                                                                                                  156987;
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                                                                          PD000012; EF-hand;
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34
232
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                                                   152
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232
                                      188
                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                         26408 MW;
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  100.0%;
                                                                                                                                                                                                                                   TO ALLOGRAFT INFLAMMATORY FACTOR-1.
                                                                                                                                                                                                                                               EF-HAND CALCIUM BINDING PROTEINS
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ANCHOR FOR TYPE IV MEMBRANE PROTEIN
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                                     EF-HAND (POTENTIAL).
ANCESTRAL CALCIUM SITE.
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
S -> C (IN REF. 2).
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
  Score 28;
                         CAC40395D8B25FF8 CRC64;
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                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
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  DB 1;
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Length 235;
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HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTN3_HU
095197;
                                    This SWI
between
                                                                                                                                                                                                                                                                                                                                             Huang X., Zhou Y., Du G., Yuan J., Qiang B., "Cloning and expression analysis of a cDNA encoding a novel neuroendocrine-specific protein-like protein 1: NSFL1.", Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel.
15-SEP-2003 (Rel.
Reticulon protein
          modified
                           the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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Genomics 58:73-81(1999).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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foreira E.F., Jaworski C.J., Rodriguez I.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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                                                                                 reticulum (Potential).
TISSUE SPECIFICITY: WI
BRAIN. THREE TIMES MOR
                                                               SIMILARITY:
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                                   SWISS-PROT entry is copyright. It is produced sen the Swiss Institute of Bioinformatics and
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non-profit institutions as long and this statement is not removed requires a license agreement (See
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                                                               Contains 1 reticulon domain.
                                                                                  TIMES MORE ABUNDANT
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40, Last sequence update)
42, Last annotation update)
3 (Neuroendocrine-specific
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0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9ES97;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and expression profile of a novel mou
RTN3 homolog.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
                      Transmembrane;
TRANSMEM 6
                                                                    Pfam; PF02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
                                                                                                           MGD; MGI:1339970; Rtn3.
InterPro; IPR003388; Reticulon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Huang X., Zhou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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AF059526; AAD20951.1; JOINED.
AF059527; AAD20951.1; JOINED.
AF059528; AAD20951.1; JOINED.
AF119297; AAD26810.1; -...
BC010634; AAH10634.1; -...
L; BC010556; AAH10564.1; -...
L; BC011394; AAH11394.1; -...
L; BC022993; AAH22993.1; -...
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                                                                                                                                                              AF195940; AAG31360.1; -.
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236 AA;
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                                         Endoplasmic reticulum
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236 R
25609 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qiang H., Yuan J., Qiang B.; ssion profile of a novel mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Integral
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDC6A4544ABCDFB7 CRC64;
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                                                               Query Match
Best Local S
Matches 5
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Best Local Similarity
Matches 5; Conserv
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SEQUENCE
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LIPID
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-:- SUBUNIT: The basal body constitutes a major portion of the flagellar organelle and consists of four rings (L,P,S, and M) mounted on a central rod (By similarity).

-:- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
-I- FUNCTION: Assembles around the rod to form the L-ring and protects the motor/basal body from shearing forces during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=16M / ATCC 23456 / Biotype 1;

MEDLINE=20020109; PubMed=11756688;

Dellvecchio V.G., Kapatral V., Redkar R.J., Patra G., Muj

Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., R

Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M.

Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letess

Haselkorn R., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                           Flagella; Outer membrane; Lipoprotein; SIGNAL 1 16 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                PRINTS; PROLUTO; FURTHER LIPOPROTEIN; 1.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Curter membrane; Lipoprotein; Signal; Complete
                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02107; FlgH; 1. PRINTS; PR01008; FLGLRINGFLGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF_00415; -; 1.
InterPro; IPR000527; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE009740; AAL54324.1; ALT_INIT PIR; AI3644; AI3644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -|- SIMILARITY: BELONGS TO THE FLGH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brucella melitensis.";
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   1 GGGGS
                                                               Similarity 5; Conserv
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237 AA;
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25428 MW;
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                                                                                                      100.0%;
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FLAGELLAR L-RING PROTEIN.

N-ACYL DIGLYCERIDE (POTEN)

, 3A8CC345CCEA6AE0 CRC64;
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Pred. No.
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EB60A0A7AC45F0DE CRC64;
                                                                                                      Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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(Basal body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.1e+02;
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                                                                                                                                         DB 1;
                                                                                                      .le+02;
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                                                                                                                                  Length 238;
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                                                                                                                                                                                                                                               (POTENTIAL)
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1., Goltsman
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RESULT 40
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ID HMUX_MUSDO
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FLGH_BRUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-22247741; PubMed=12271122; Paulsen J.A., Heidelberg J.F., Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J., Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.; "The Brucella suis genome reveals fundamental similarities between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLGH_BRUSU
Q8FXC2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_00415; -; 1.
InterPro; IPR000527; Flag_Lring.
Pfam; PF02107; FlgH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flagella; Outer membrane; Lipoprotein; Signal; Complete proteome. SIGNAL 1 16 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01008; FLGLRINGFLGH.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; BRA0158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE014518; AAN33365.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        animal and plant pathogens and symbionts.";
Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
-I- FUNCTION: Assembles around the rod to form the L-ring and probably
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brucella suis
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15-SEP-2003 (Rel. 42,
15-SEP-2003 (Rel. 42,
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                                                                                                                                                                                                                                                                     Local Similarity
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SUBURIT: The basal body constitutes a major portion of the flagellar organelle and consists of four rings (L,P,S, and M) mounted on a central rod (By similarity).

SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE FLGH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protects the motor/basal body from shearing forces during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107
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Last annotation update)
ein precursor (Basal body L-ring protein).
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PLAGELLAR L-RING PROTEIN.
N-ACYL DIGLYCERIDE (POTENTIAL).
756D0A6155D80345 CRC64;
                                                                                                                                                                                                                                                                  Score 28; DB 1; Pred. No. 3.1e+02;
      PRT;
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Search completed: December 11, 2003, 09:56:00 Job time : 6.2 secs

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;
Muscidae; Musca.
NCBI_TaxID=7370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                           Developmental protein; Nuclear protein.

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DOMAIN 32 38 POLY-ALA.

DOMAIN 108 123 POLY-GLY.

DOMAIN 142 151 POLY-GLY.

DOMAIN 224 227 POLY-ALA.

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                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis. Binds the consensus region 5'-TTAAT[GT][GA]-3' (By similarity) -i- SUBCELLULAR LOCATION: Nuclear.
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"Conserved sequence
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InterPro; IPR001356; Homeobox.
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PS00027; HOMEOBOX. 1; PARTIAL.
PGULATION; Activator; Homeobox; DNA-binding;
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4: sp_hunan:*
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10: sp_plant:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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Qy 1 GGGGS 5 Db 2 GGGGS 6 RESULT 2 Q64450 ID Q64450 PRELIMINARY; PRT; 17 AA. AC Q64450 DT 01-NOV-1996 (TrEMBLrel. 01, Created) DT 01-NOV-1996 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) DE Uridine kinase (EC 2.7.1.48) (Fragment).	Que Bes Mat	RP SEQUENCE. RP SEQUENCE. RX MEDLINE=94245619; PubMed=8188594; RX MEDLINE=94245619; PubMed=8188594; RA Govindaraj S., Eisenstein E., Jones L.H., Sanders-Loehr J., RA Chistoserdov A.Y., Davidson V.L., Edwards S.L.; RA Chistoserdov A.Y., Davidson V.L., Edwards S.L.; RT "Aromatic amine dehydrogenase, a second tryptophan tryptophylquinone RT enzyme.":		SUL R4Y

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RESULT 3
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O8W238;

O1-MAR-2002 (TrEMBLrel. 2

O1-MAR-2002 (TrEMBLrel. 2

O1-MAR-2002 (TrEMBLrel. 2

O1-MAR-2002 (TrEMBLrel. 2

O1-Factor (Fragment).

Glycine max (Soybean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE=93307625; PubMed=8319886; Griffiths E., Stevenson P., Byfield P., Ala'Aldeen D.A., Griffiths E., Stevenson P., Byfield P., Williams P.; Borriello S.P., Holland J., Parsons T., Williams P.; "Antigenic relationships of transferrin-binding proteins from Meisseria meningitidis, N. gonorrhoeae and Haemophilus influenzae: cross-reactivity of antibodies to NH2-terminal peptides."; PEMS Microbiol. Lett. 109:85-91(1993). InterPro; IPR001677; Transferrin_bind.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
Transferrin-binding protein 2 (Fragment).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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TISSUE=Liver;
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Bacteria; Proteobacteria;
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Pierschbacher M.D., Polarek J.W.,
Sipes N.J., Harper J.R.;
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                                                     RAYMAI M., Grellet F., Laudie M., Meyer Y., Co
Submitted (PEB-1994) to the EMBL/GenBank/DDBJ
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Q9F1I5;
                                                                                                                                                                                                                                                                                                                                                                                                        Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oe
Sarcophagidae; Sarcophaga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Microbiol. 37:1327-1341(2000).
EMBL; AE002565; AAG40421.1; -.
Hypothetical protein; Plasmid.
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Bacteria; Firmi
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                              "Purification and characterization of a diptericin homologue from Sarcophaga peregrina (flesh fly)."; Biochem. J. 287:573-578(1992).

-I- FUNCTION: BACTERICIDAL ACTIVITY AGAINST GRAM-NEGATIVE BACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diptericin homolog (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Boever E.H., Clewell D.B., Fraser C.M.; "Enterococcus faecalis conjugative plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20453452; PubMed=10998166;
                                                                                                                                                                                                                                                               MBDLINE=93074996; PubMed=1445217; Ishikawa M., Kubo T., Natori S.;
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7386;
                                                                                                                                                                                                                                                                                                                 FISSUE=LARVAL HEMOLYMPH;
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DEVELOPMENTAL STAGE: EXPRESSION IN THE LARVAE STARTS AFTER THE INJURY OF THE BODY WALL REACHING A MAXIMUM 10 HOURS. THE MAXIMUM LASTS FOR AT LEAST 3 HOURS. INDUCTION: IN RESPONSE TO INJURY OF THE BODY WALL OF
                                                                                                                       E.COLI AND S.SONNEI.
TISSUE SPECIFICITY: SYNTHESIZED
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5; Conserv
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                                                                                                THE HEMOLYMPH
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(Tremblrel. 13, Last seq
(Tremblrel. 15, Last ann
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Pred. No. 2.5
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Pred. No. 2.1e+02;
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SEQUENCE
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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Q13882; PRELIMINARY;
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1996 (TrEMBLrel. 19,
Q1-DEC-2001 (TrEMBLrel. 19,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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DOMAIN 18 22
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=96209920; PubMed=8655154;
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                                                                                   "A novel sequence polymorphism bradykinin B2-receptor gene."; Hum. Genet. 97:688-689(1996).
EMBL; X91663; CAA62851.1; -.
                                                                                                                                                                                                                                         NCBI_TaxID=9606
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                                                                                                                                                              MEDLINE=96209920; PubMed=8655154; Braun A., Maier E., Kammerer S.,
                                                                                                                                                                                                     SEQUENCE FROM N.A.
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STRAIN-MAPF303099;

MEDLINE=2108290; PubMed=11214968;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0031D11.",
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003231; BAB67882.1; -.
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Gukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
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DNA Res. 7:331-338(2000).
EMBL; AP003006; BAB51739.1; -
Hypothetical protein; Complete
SEQUENCE 50 AA; 5260 MW; CE
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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                                                                                                                         "Complete genome structure Mesorhizobium loti.";
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Q8H647;
01-MAR-2003
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01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-cv. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJNBa0078001 genomic sequence.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AC079888; AAM93673.1; -.
EMBL; AC079888; AAM93673.1; -.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                       clone:OSJNBa0038F22.";
Submitted (AUG-2000) to the
EMBL; AP002838; BAC24829.1;
                                                                                                                                                                            STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Bhrhartoideae; Oryzeae; Oryza.
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                                                          SEQUENCE
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SEQUENCE 53 AA; 54
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Pred. No. 4.1
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RESULT 16
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Matches
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SEQUENCE 62 AA; 54:
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STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto
"Oryza sativa nipponbare(GA3) genc
clone:P0507H06.";
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                                                                      SEQUENCE
                                                                                     Submitted (JAN-2001) to the EMBL; AP003144; BAB44143.1;
                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                               Oryza sativa (Rice).
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01-OCT-2002 (TremBirel.
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Submitted (MAY-2002)
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Homo sapiens (Human).
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01-MAR-2003
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Mammalia; Eutheria;
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Pred. No. 5.1e+02;
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Catarrhini;
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Q8VB65;
01-MAR-2002 (TrEN
01-MAR-2002 (TrEN
01-JUN-2002 (TrEN
W8V123 (WSSV179)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Taiwan;
LO C.-F., Kou G.-H.;
LO C.-F., Kou G.-H.;
Submitted (OCT-2001) to the
EMBL; AF332093; AAL33127.1;
EMBL; AF440570; AAL89047.1;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid.
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                            Q9INS5 PRELIMINARY; PRT; 64 AA.
Q9INS5; O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
T20H2.25 protein (Hypothetical 6.0 kDa protein).
T20H2.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21844071; PubMed=11853398;
Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.
Lo C.F., Kou G.H.;
In Classification of a nucleocapsid protein (VP35) gene of shrimp
spot syndrome virus and characterization of the motif important
targeting VP35 to the nuclei of transfected insect cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
"Identification and characterization of a shrimp white spot virus (WSSV) gene that encodes a novel chimeric polypeptide cellular-type thymidine kinase and thymidylate kinase.";
Virology 277:100-110(2000).
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Yang F., He J., Lin X.,
Submitted (DEC-2000) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Viruses; dsDNA viruses, no
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e EMBL/GenBank/DDBJ
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Pred. No. 5.1e+02;
; Mismatches 0;
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RESULT 19
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

NCBI TaxID=4530, 39947;
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STRAIN-CV. Columbia;

SHAIN-CV. Columbia;

Sakano H., Vaysberg M., Lee J.M., Lenz C., Liu S., Pham P.,

Sakano H., Yu G., Chin C., Chiou J., Choi E., Chung M., Gonzalez A.,

Toriumi M., Yu G., Chin C., Chiou J., Choi E., Chung M., Gonzalez A.,

Howng B., Liu A., Altafi H., Brooks S., Buehler E., Chao Q., Conn L.,

Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,

Miranda M., Nguyen M., Palm C.J., Shinn P.,

Southwick A., Davis R.W.,

The sequence of BAC T20H2 from Arabidopsis thaliana chromosome 1.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                     SEQUENCE FROM N.A.

SPECIES=O. sativa (japonica cultivar-group);

SPECIES=O. marsumoto T., Yamamoto K., Funa (
                                                                                                                                                                                                                                                                                                                  SPECIES-O. sativa; STRAIN-cv. Nipponbare;
SPECIES-O. sativa; STRAIN-cv. Nipponbare;
Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
p0468H06.9 protein (P0496H05.30 protein).
p0468H06.9 OR p0496H05.30.
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                                                                                                Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003075; BAB55698.1; -. EMBL; AP003267; BABC3300.1; -. Gramene; Q94J57; -. Gramene; Q94J57; -.
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                                                                                                                                                                              Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, clone:P0496H05.";
                                                                                                                                                                                                                                                                                            Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, clone:P0468H06.";
                                                                                                                                                                                                                                                                Submitted [2]
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Pred. No. 5.3
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                                                                Length 65;
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RESULT 21
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MEDLINE=99282512; PubMed=10353914;

Shintani S., O'hUigin C., Toyosawa S
"Origin of gene overlap. The case of
Genetics 152:743-754(1999).

EMBL; AF143499; AAD34977.1; -.

InterPro; IPR007423; Cpn60/TCP-1.

Pfam; PF00118; Cpn60_TCP1; 1.
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Q9XT04;
01-NOV-1999
01-NOV-1999
01-MAR-2002
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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NON TER 66
SEQUENCE 66 AA; 6
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Eukaryota; Metazoa; (
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                                                                                                                                                                                         SEQUENCE
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GGGGS
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Chordata; Craniata; Vertebrata;
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Diprotodontia; Macropodidae;
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                                                                                              Score 28; DB 6;
Pred. No. 5.4e+02;
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K-A) catalytic subunit gene
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Q9SK19;
01-MAY-2000
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Q8H3Q4;
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MEDLINE=20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CV. Nipponbare;
Sasaki Tv. Matsumoto T., Yamar
"Oryza sativa nipponbare(GA3)
"Clone:P0625E02.";
Clone:P0625E02.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AC006586; AAD22697.1; -. SEQUENCE 66 AA; 6723 MW; 403DFD0812065919 CRC64;
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01-MAY-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                     Submitted (DEC-2001) to the EMBL/GenBank/DDBJ EMBL; AP004570; BAC16654.1; -. SEQUENCE 66 AA; 6306 MW; C155B63748F66372
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group).
Eukarycta; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AT2G10020.
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                                                                                                                   "Oryza sativa nipponbare(GA3) genomic clone:OCI005 B10.";
Submitted (JĀN-2002) to the EMBL/GenBa
EMBL; AP003276; BAB92387.1; -.
EMBL; AP004611; BAC05638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T
                                                                SEQUENCE
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T.,
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Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2001) to
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STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamo
"Oryza sativa nipponbare(GA3) g
clone:P0691E06.";
Submitted (FEB-2001) to the EME
EMBL; AP003293; BAB86410.1; -.
EMBL; AP003293; BAB92421.1; -.
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SEQUENCE
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Sasaki T.,
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 7.4 kDa protein.
DUPR11.15:
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Eukarycta; Viridiplantae; Etreptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                       SEQUENCE FROM N.A.

MEDLINE-20181732; PubMed=10715324;

Tarchini R., Biddle P., Wineland R., Ti
"The complete sequence of 340 kb of DNA
region reveals interrupted colinearity
Plant Cell 12:381-391(2000).

EMBL; AF172282; AAF34425.1; -.
                                                                                                                                                                                                                                                         Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Sasaki T., Matsumoto T.,
"Oryza sativa (japonica
clone:P0003D09.";
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69 AA;
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                                                                            Tingey S., Rafalski A.;
DNA around the rice Adhl
ty with maize chromosome
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a; Poales; Poaceae;
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e Adh1-adh2
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QSK01

QSK01

QSK0

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AC QSSK0

DT 01-M

DT 01-D

DE At29

GN AT26

OS AT26

OS AT26

OC SUR1

OC SUR1

OC SUR1

RP SEQ

RC STR

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Submitted (DEC-2000) t
EMBL; AF332093; AAL334
SEQUENCE 76 AA; 743
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Q8VAF7;
01-MAR-2002
01-MAR-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000
01-MAY-2000
01-DEC-2001
                       MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C
Copenhaver G.P., Preuss D., Niermann W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9SK01;
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                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatcphyta; Magnoliophyta; endicotyledons; core e

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=cv. Columbi
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MEDLINE=21548311; PubMed=11689662;
Yang F., He J., Lin X., Li Q., Pan D.,
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                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
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Similarity 100.
5; Conservative
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(TrEMBLrel.
(TrEMBLrel.
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A; 7436 MW;
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to the EM
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EMBL/GenBank/DDBJ da
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Last sequence update)
Last annotation update)
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Pred. No. 6.2
); Mismatches
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Pred.
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p white spo
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                                                                                                                                                                                                                                                                                                                                                                                     Embryophyta; Tracheophyta;
dons; core eudicots; Rosid
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                                                                                                                                                                                                                                                                                                                                                                                             Rosidae;
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1.J.E.,
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RESULT 30

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ID Q9SUF

AC Q9SUF

AC Q9SUF

AC Q9SUF

DT 01-MA

DT 01-OC

GN T12G1

OC Sperm

OC Sperm

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  RESULT 31
Q8L4N9
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AC Q8L4N
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DT 01-01-MZ
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DT 0J-MZ
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Best Local
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 7.9 kDa protein.
T12G13.70 OCR ATG08230.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
Q8L4N9 PRI
Q8L4N9;
01-OCT-2002 (T)
01-OCT-2002 (T)
01-MAR-2003 (T)
OJ1103_E04.15 [
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Submitted (MAR-2000) to the
EMBL; AC006587; AAD21491.1;
SECTITENCE 78 AA; 7909 MW;
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STRAIN=CV.
                                                                                                                                                                                                                                                                                                                                                                        Hypothetical SEQUENCE 8
                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL080252; CAB45793.1; -.
EMBL; AL161510; CAB81159.1; -.
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Mewes H.W., Lemcke K.,
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t I., Mewes H.W.,

    22, Created)
    22, Last sequence update)
    23, Last annotation update)
    (P0675B10.5 protein).

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Pred. No.
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Pred. No.
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Mayer K.F.X., I
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RESULT 32
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SEQUENCE
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                                                                     PARSONS B.L., Mattoo A.K.;
PARSONS B.L., Mattoo A.K.;
"A wound-repressible glycine-rich protein transcript
"A wound-repressible glycine-rich protein transcript
vascular bundles of tomato fruit and stem.";
Plant Cell Physiol 35:27-35(1994).

EMBL; X59883; CAA42538.L;
EMBL; X59883; CAA42538.L;
PRINTS; PRO1228; EGGSHELL.
                                                                                                                                                                                                                                                                                                                                        Glycine-rich protein (Fragment).
Lycoppersicon esculentum (Tomato).
Lycoppersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Solanum.
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01-NOV-1996 (TrEMBLrel. 01, Creat
01-NOV-1996 (TrEMBLrel. 01, Last
01-MAR-2003 (TrEMBLrel. 23, Last
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Oryza Sativa (japonica cultivar-group).
Cutar Sativa (japonica cultivar-group).
Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
                                                               PRINTS;
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                                                                                                                                                                  STRAIN=pik-red; TISSUE=Pericarp;
MEDLINE=94340224; PubMed=8061936;
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MEDLINE=91355936; PubMed=1715787;
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Sasaki T., Matsumoto T.,
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                                                   SEQUENCE
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                    "Wound regulated accumulation of specific transcripts in tinteractions with fruit development, ethylene and light.", Plant Mol. Biol. 17:453-464(1991).
                                                                                                                                                                                                                                                            Parsons B.L., Mattoo A.K.;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4081;
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Similarity 5; Conserv
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100.0%; Score 28; Di
llarity 100.0%; Pred. No. 6.0
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          6.6e+02;
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Q8H799;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Root cap-specific protein (Fragment).
Zea mays (Maize)
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                            "The quiescent center controls the expression of three cap
the maize root meristem.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Ponce G., Lujan R., Campos M.E.,

Feldman L.J., Cassab G.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; Liliopsida; Poal
PACCAD clade; Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Signal Peptide Selection derived cDNAs from Arabidopsis leaves and guard cells.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF083775; AAN60333.1; -.
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01-MAR-2003
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Pred. No.
                                                                                                                     Pred. No.
                                                                                                                                         Score 28; DB 10;
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Matches 5; Conserv
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OJ1123_B01.5 protein.
OJ1123_B01.5.
Oryza Bativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Q8H5X1, 20H5X1,
Q1+MAR-2003 (TrEMBLrel. 23,
Q1-MAR-2003 (TrEMBLrel. 23,
Q1-MAR-2003 (TrEMBLrel. 23,
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NON_TER
SEQUENCE
O44629 PRELIMINARY;
O44629;
01-JUN-1998 (TrEMBLrel. 06,
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
EMBL; AF347017; AAK30134.1; -.
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
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Q98ZK1;
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submitted (JUN-2001) to the
EMBL; AP003745; BAC15816.1;
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Farnetti E., Nicoli D., Rivasi F., Portioli I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssDNA viruses;
NCBI_TaxID=10798;
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ EMBL; AF039048; AAB94238.1; -.
WormPep; F16B4.7; CE17017.
Hypothetical protein.
                                                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based c 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion;
MEDLINE=22354683; PubMed=12466851;
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Davidson S., Wohldmann P.,
"The sequence of C. elegans
Submitted (JAN-1998) to the
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MEDLINE=99069613;
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Rhabditidae; Pelode;
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Mammalia; Eutheria; Rodentia;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoekins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoekins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Baridon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Ffannkooh C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayrakaroglu L., Beasley E.M.,
RA Baridon R.C., Benson P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benson P.V., Berman B.P., Bhandari D., Botsies P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Keaft C., Kra K.E., Kemison J.A., Ketchum K.A.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D. Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D. Lai Z.,
RA Lisko P., Lei Y., Leviteky A.A., Li J., Li Z., Lidang Y., Lin X.,
RA Harls N., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Musskern D.R., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos R., Shue B., Shue H.,
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Evans C.A., Go
Banzon J., An
Carlson J.W.,
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BCDNA:RE36972 OR CG32738.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygot
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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n D., Banzon J., Beeson K.
Champe M., Davenport L.B.
                                                                                          Kronmiller B., Wan K.H.,
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   Wan K.H., Holt R.A.,
, Brandon R.C., Roger,
Beeson K.Y., Busam D.,
port L.B., Dietz S.M.
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fan D., Frise
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Emerman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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